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DECIDE

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

Deliverable 4.1

Generic framework for determining the economic

burden of animal disease

WP4 – Multidimensional burden of disease metric and prioritisation of interventions

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D4.1 – Generic framework for determining
the economic burden of animal disease
Version 1.0

Content

Abbreviations

Abbreviation	Description
AHLE	Animal Health Loss Envelope
EU	European Union
GBADs	Global Burden of Animal Diseases
WP	Work Package

Partner short names

Short name	Organisation
UU	Universiteit Utrecht
UoL	The University of Liverpool
UCD	University College Dublin
ETHZ	Eidgenössische Technische Hochschule Zürich
SVA	Statens Veterinärmedicinska Anstalt
NVI	Veterinærinstituttet – Norwegian Veterinary Institute
IRTA	Institut de Recerca i Tecnologia Agroalimentàries
AHI	Animal Health Ireland Initiative
accelCH	accelopment Schweiz AG

Executive Summary

- This deliverable reports on the development of a framework for quantifying the farm-level economic burden of endemic diseases in livestock and aquaculture production systems.
- This framework considers takes a generic perspective, with the intention of being applicable across the diverse species and production types found with Europe, but also with potential for application globally.
- The deliverable also presents the first steps in the application of this framework to pilot implementation populations in pigs, broiler chickens, cattle and salmon.

Utility of this deliverable:

- The framework evaluates total disease burden in the system, thus enabling the calculation of the relative contribution of specific causes or risk factors to this total. This facilitates the selection or design of interventions to priority risks or hazards.
- The total disease burden therefore also aids in decision making when choices have to be made between different funding interventions in different systems.

Activities performed:

- This framework was developed in collaboration with the Global Burden of Animal Diseases programme.
- A consideration of the biological consequences of disease and how these effect the efficiency of livestock and aquatic production systems leads to a conceptual model which is generic in its scope.
- Operationalising this conceptual model is done by describing the inputs, outputs and dynamic processes in livestock systems both algebraically and with examples.
- The first step toward applying this pilot framework began with the description of biomass flows and population structure in pilot implementations for each of the species of interest to DECIDE: Norwegian Atlantic salmon farming, cattle in Ireland, pigs in Spain and Netherlands, and broiler chickens in the UK.

Outcomes:

- A framework for the total burden of disease in livestock and aquaculture production is in place for use within the DECIDE project.
- A description of biomass flows in pilot implementations is presented.

Next steps:

- Total burden of disease estimates can provide important context when assessing resource allocations to animal health across multiple production systems in different geographies and species groups.
- This is a precursor to developing burden estimates to specific causes or risk factors and describing the effectiveness of interventions.
- When calculated, this work will have particular application within Work Package 3 (decision tools) and will be combined with the findings of Work Package 5 (social) to present a picture of the economic and social environment and incentives faced by farm-level decision makers in animal health.

1   Introduction

Global demand for livestock and aquaculture products has been increasing for several decades, in line with increasing population, urbanisation and wealth (FAO, 2011). Recognising the important roles played by animals in the supply of protein and essential micronutrients in people's diets, the United Nations Sustainable Development goals have identified improvements in animal health as a means to enhancing the sustainability of global good supplies (UN General Assembly, 2015). Concurrent with increasing demand for animal-source food products, the parts played by livestock in climate change, environmental degradation and infectious disease epidemiology are being recognised and must be better understood, while the welfare consequences for animals in food production systems are now societal concerns (Bayvel, Diesch, & Cross, 2012).

The Global Burden of Animal Diseases (GBADs) programme has been initiated in recognition of the contribution improvements in animal health may make to productive efficiency in livestock (Rushton et al., 2018). At the conception of the DECIDE project, it was envisioned that synergies between DE-CIDE and GBADs in the need for economic analysis of disease burden would allow harmonisation of methods leading to efficiencies in resource use for both programmes. While both DECIDE and GBADs are still in their early stages, both are developing methods which are intended to be suitably generic to allow disease burden to be calculated in diverse livestock systems. This report presents the progress in developing these methods ready for application within DECIDE.

To measure the burden of disease at farm level, there are a number of basic questions that need to be addressed to ensure consistency in approach and definition. Firstly, a generic framework requires a generic description of what disease is and how it affects livestock production, from this we attempt to determine where disease burden manifests in a conceptual model of livestock production. Moving from a concept to a working measurement model where formal relationships are proposed which define metrics to quantify disease burden. In this case, the burden is defined by setting a disease-free or "ideal health" counterfactual scenario to measure against. The methods are then assessed against the need to fit the data available and stated objectives of DECIDE, those being the chosen pilot implementations: farm-level burdens of disease in European pig, broiler, calf and salmon rearing. In DECIDE we focus on prevalent infectious endemic diseases that cause gastro-intestinal or respiratory problems in young and growing production animals, i.e., pigs, broilers and calves. In addition, for salmonids we focus on the infectious endemic diseases that cause most losses through mortality or growth reduction.

Addressing these questions is the first aim of this document, which presents the development of conceptual and measurement models for livestock disease burden at farm-level and the first steps toward applying the measurement model to DECIDE pilot implementations. The limitations and expansion of these models will then also be discussed.

1.1   Animal health in livestock systems

Livestock are animal populations which are domesticated and kept for an economic purpose: as the means of converting a less desirable set of inputs into a more desirable set of outputs. In biological terms, an animal requires sufficient energy to maintain its physiology and perform the behaviours necessary for survival. Livestock extend this requirement to the fulfilment of their economic purpose. Livestock keepers are therefore incentivised to actively manage this energetic equilibrium between animal and environment in a way which optimises the value they derive from the production process. This can be achieved through the supply of nutrition and by reducing the energetic demands placed on the animal through environmental management. In so doing, additional energy is available for economically useful activities.

D4.1 – Generic framework for determining
the economic burden of animal disease
Version 1.0

In addition to the background environmental conditions and basic physiological and behavioural functions which set the maintenance energy requirement of the animal, there exist hazards which can place additional energetic burden on the animal, altering the equilibrium with its environment. These hazards generate physical risks to the health of animals and draw energetic resources away from production and basic maintenance. Where growth, reproduction and yields are reduced, animal morbidity is defined; where these conditions are suitably severe, mortality is the final result. It is this set of hazards, generating morbidity and mortality, that are defined here as disease in livestock systems. Incentives therefore exist for livestock keepers to look for ways to exclude these hazards or mitigate their impact.

Disease can be defined as the "abnormality of bodily structure or function" (Marcovitch, 2017) and as an "inability to perform physiologic functions at normal levels even though nutrition and other environmental requirements are provided at adequate levels."(Studdert, Gay, & Hinchcliff, 2020). If we accept good health as being the body's state in the absence of disease, then health is the converse of the disease definition, that is: "the normality in bodily structure and function that provides the ability to perform physiologic functions at normal levels, given nutrition and other environmental requirements are provided at adequate levels."

To illustrate these concepts, Morris (1988) describes the biological connection between the effects of disease and productivity in livestock using the example of feed inputs. Disease can be shown primarily to have consequences for the performance of the individual animal, but also when diseased animals interact within a population, at six critical points: the quantity of feed ingestion, the efficiency of its digestion, the metabolism of nutrients, the quantity and quality of desired outputs of production, the survival and reproduction rates of animals in the herd, and the long-term genetic gain delivered by selective breeding efforts. These effects can be generalised to inputs other than feed, with the conclusion that animal health influences the gross allocation of resources to the animal, the efficiency of their conversion to output, and the rate at which capital is retained or accumulates in the herd.

2   Conceptual and measurement models for disease burden

To frame this relationship in quantitative terms, focusing on a single output for illustrative purposes, the production relationship in the presence of disease can be described as follows (Hennessy & Marsh, 2021; Lichtenberg & Zilberman, 1986):

Equation 1

$$Y = F(z; \theta) \times \left[1 - L\big(b_0 * (1 - C(x; \theta))\big) \right]$$

Where Y is the total output from the system and $F(z;\theta)$ is the potential or ideal production function for a set of ordinary inputs z conditional on exogenous parameters θ (such as climate, regulations, etc.). In this case, z are the inputs (feed, labour, etc) required to generate Y in the absence of disease. L $(0 \leq L \leq 1)$ is a loss function describing the action of disease hazards b_0 on the production of Y, and $C(x; \theta)$ $(0 \leq C \leq 1)$ is a control function increasing in control inputs x (vaccines, antibiotics, etc) which mitigates the effects of b_0. If $b_0 = 0$ this is the disease-free case and there is no loss of output, $L(0) = 0$, such that ideal production $Y = F(z)$ is achieved. The burden of disease is therefore found in the combined value of lost output when Y is less than $F(z; \theta)$, plus any expenditure on control or mitigation when $x > 0$.

The concepts so far described are illustrated in Figure 1, and this model is proposed to form the basis for the measurement of the burden of disease on livestock production at farm level. In this concept, the animal is described as a biomass unit capable of generating a particular output over a given time period. The supporting inputs provided enable the animal to perform this function at a given rate, depending on the specific production outputs required and possible population dynamics. The presence of disease hazards has the potential to alter these rates, which would be biologically defined as

morbidity and mortality producing loss of both biomass and production outputs. The outputs of this process are then any products yielded and any biomass remaining. If an ideal health state is then defined as the system functioning in the absence of disease hazards, a disease burden is then quantifiable by comparing actual system behaviour to productivity under ideal health. This burden measure is being termed the Animal Health Loss Envelope (AHLE).
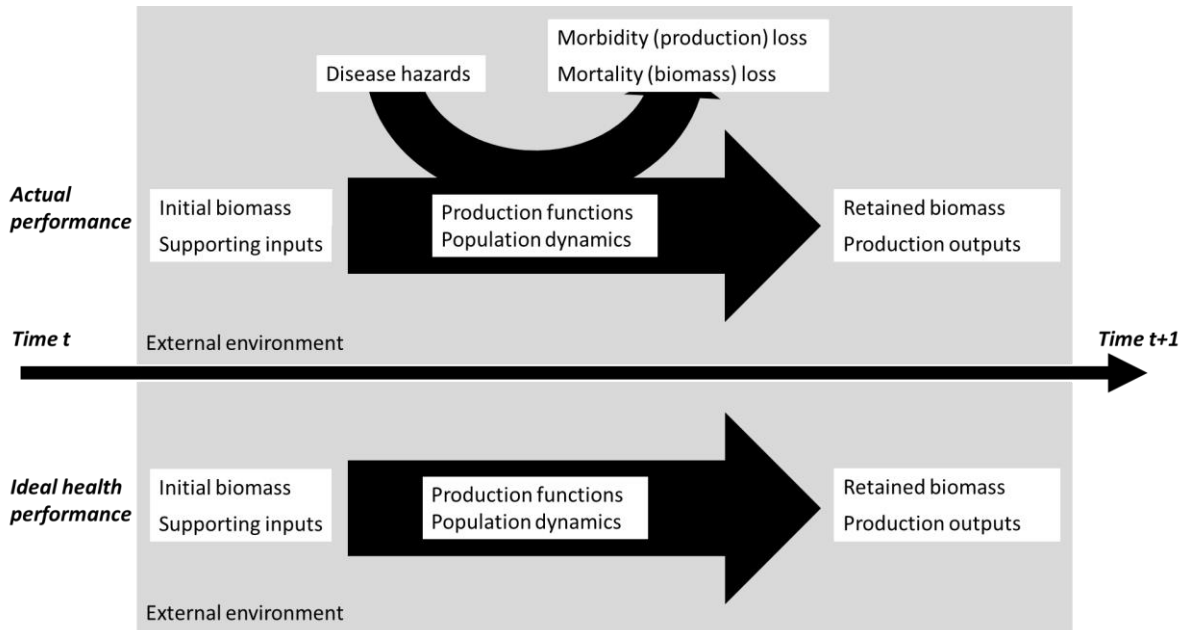

Figure 1. Conceptual model of livestock production in the presence of health hazards, and production under ideal health with which an Animal Health Loss Envelope (AHLE) can be calculated.

To move from this conceptual model to a measurement model an attempt is made to expand the model to a multiple input-output structure and describe its potential for application where population structures are more complex. After this, further consideration will be given to necessary assumptions, conventions and constraints required to operationalise the model and the datasets and resources available to refine it.

First the population of animals is divided into compartments. This division is pragmatic, based on known or hypothesised differences in input use, outputs generated, disease hazard exposure and response, as well as data availability. In other words, compartments are created where units within the total population are expected to behave differently with respect to the model structure or model outcomes. This livestock population to be evaluated is then defined by i units based on these compartments $\{1, ..., I\}$. For all compartments there is a set Y made up of j outputs $y_j = \{y_1, ..., y_J\}$. This includes both the intended outputs of the system, any intermediate outputs required to move between compartments, and any by-products produced as a result of the presence of disease. Each output is valued at price r_j. The population of live animals moving into each compartment, n_i, valued at unit price s_i and their biomass calculated by average liveweight, $n_i\overline{w}_i$, represents a special class of asset in the model. Given the timeframe of the model, biomass input to a compartment is quantified by time step t, and is therefore quantified as unit mass per unit time.

All compartments are supplied with a set Z of k ordinary inputs $z_k = \{z_1, ..., z_K\}$ which are those inputs required to meet the physiological needs of the population regardless of disease hazards, with each supplied at unit price p_k. For each output, a production function is defined as $f_j(n_i\overline{w}_i, Z_i)$. It is assumed the consequences of disease are at least partially alleviated by the application of control inputs x_i supplied at unit price q_i.

As per Equation 1 a mortality rate μ_i is defined by a loss function (M) of the hazards, b_i, present in each compartment and the efficacy of the control function D:

Equation 2

$$\mu_i = M\big(b_i(1 - D(x_i))\big)$$

Where in the disease-free case $M(0) = 0$. While the loss rate of output due to untreated morbidity is abbreviated to β_j, which is mitigated by control function C:

Equation 3

$$\beta_{ij} = L\big(b_i(1 - C(x_i))\big)$$

Again in the disease-free case, $L(0) = 0$.

The quantity of output j generated by compartment i is then the sum of outputs yielded by biomass that survives the production cycle, and the outputs yielded by biomass that suffers mortality:

Equation 4

$$Y_{ij} = f_j\big((1 - \mu_i)n_i\overline{w}_i, Z_i\big)\big(1 - \beta_{ij}\big) + f_j\big(\mu_i n_i\overline{w}_i, Z_i\big)\big(1 - \beta_{ij}\big)$$

When the hazard set is empty, b_i is equal to zero. This is the disease-free, or ideal health, state. Under these conditions, optimal mortality and morbidity rates (μ_i^* and β_{ij}^*) are defined as equal to zero, and the optimal supply of control inputs (x_i^*) is therefore also zero. In such a case, the ideal health output assumes a constant return to scale per unit and is defined as:

Equation 5

$$Y_{ij}^* = f_j(n_i\overline{w}_i, Z_i)$$

If demand for each output produced in the observed system is quantified by Y_{ij}, then the output constraint placed on the ideal health system is that for each output, demand must be met.

Equation 6

$$Y_{ij}^* \geq Y_{ij}$$

On the input side, assuming that Z_i scales with changing biomass, a cost minimisation optimisation is applied to determine the optimal n_i, termed n_i^*, which is the minimum number of units in the population n needed to satisfy this inequality for all j produced by each compartment. In that case, the total supporting input bundle for each compartment is termed Z_i^*.

Following, the disease burden is quantified by the AHLE, which is the summed difference between the ideal health and current scenarios:

Equation 7

$$AHLE = \sum_{i=1}^{I}\left(p_k(Z_{ik} - Z_{ik}^*) + q_i x_i + s_i(n_i\overline{w}_i - n_i^*\overline{w}_i) - \sum_{k=j}^{J} r_j\big(Y_{ij} - Y_{ij}^*\big)\right)$$

This represents the change in input costs of both ordinary and control inputs and the biomass change in the population, net of any additional change in output generated by meeting demand for all products under the ideal health scenario.

3 Discussion

The development of a measurement model to calculate livestock disease burden from this conceptual framework also requires making a number of measurement conventions if estimates are to be complete, consistent and comparable. These will be discussed within this section.

The dimensions of the analysis (I, J and K), being the animal populations within the system, plus the sets of inputs and outputs need to be reflected in the data used to build the model. In this respect,

**D4.1 – Generic framework for determining
the economic burden of animal disease**
Version 1.0

with greater granularity the size of these dimensions can expand, or conversely, contract when limited data is available. It is this flexibility which is an anticipated strength of this conceptual framework.

Where population structures are better described for example, additional compartments can be added on a single dimension, whilst maintaining high-level estimates or assumptions in other areas. This allows the generation of comparable results where data are expected to be lacking or absent for some variables or parameters, but may be quite rich on others. Enormous variation can be observed in livestock systems globally, and the datasets that describe them. To grant a degree of insight into the kind of items for which data will be required to populate the conceptual framework Table 1 expands on each of item headings listed in Figure 1 with a set of subheadings to guide the search for more data, the specification of relationships and functional forms, and measurement model design.

Table 1. Sub-dividing the conceptual framework to deconstruct livestock system performance measurement, factors common to both actual and ideal health scenarios.

Initial biomass	Population dynamics	Retained biomass
Live animal imports or purchases Biomass retained from previous time period	Age to maturity Age at retirement / culling Reproductive rates Mortality rates	Surviving biomass from start of production period Biomass added by growth and reproduction Biomass of animals sold, died, slaughtered and culled.
Supporting inputs Feed inputs Non-feed variable costs Non-livestock capital assets Labour costs Other fixed costs	**Production functions** Growth rates Product yield functions such as milk, eggs, wool.	**Production outputs** Prime slaughter products Cull animal products Milk, eggs, wool and other products Live animals sold Capital accumulation in biomass
Time Defined time point for start and end of production cycle	**External environment** Physical environment Economic environment Socio-economic and legal frameworks	

The covariance structure of the data describing the population of animals can form the basis of classification systems, an example of this will be referred to further in section 5.5. Classification systems can simplify data collection by stratifying populations, reduce noise in modelling and provide a framework for imputation of missing data. Many of the organisations working in the pilot implementations will already have functional classification systems, and these are being defined through the ontological work of WP1. Understanding what these are and how populations of animals are already being divided by the people working with them is an important consideration when mapping out likely data sources and considering methods of imputation for filling any data gaps. This is also a consideration for disease incidence and treatment cost data, where veterinary practices holding health data may specialise in particular production systems.

Many livestock populations can be disaggregated into groups of breeding, growing and producing animals which can serve to identify the purpose for which they are kept, the outputs they are intended to produce, and the relevant growth and production functions which need to be enumerated to create a functioning model for disease burden estimation. Mapping between compartment flows (see section 5.3) is also required step to ensuring population stability when estimating the ideal health scenario. With these profiles, there are also potential interactions with disease incidence and mortality

and morbidity rates. These additional covariate structures with age and weight profiles further differentiate input and output flows to and from each compartment.

Biomass as kilograms of liveweight is commonly used for describing livestock, is easily convertible into meat yield with conversion factors, and can be valued by liveweight price. Liveweight can indicate metabolic bodyweight which can be used to estimate maintenance energy requirements and therefore feed input use. Biomass also provides a denominator for productivity and resource use, and as opposed to head count can be compared between species. Describing the biomass structure of the population in greater detail, for example by genetics, sex and age categories can serve to provide covariates for the compartmentalisation of input requirements and outputs produced.

A number of international organisations have developed biomass conversion factors for livestock species per head in different geographies (FAO, 2003, 2018; IPCC, 2019), intended to reflect within-species variation as well as herd or flock structures. Additionally, some global, regional and national livestock statistics are denominated by biomass to better understand population structures and the economic value of activities and trade taking place (European Commission, 2022; United Nations, 2022). At a national level, some countries collect more detailed biomass estimations for livestock and aquaculture populations, examples of which are presented in sections 5.3, 5.5 and 5.6.

While mortality is clearly a binary scale, morbidity falls along a continuum. In the model morbidity is represented as a proportional change in output relative to the ideal. As defined, ideal health implies that the hazard set is empty, therefore morbidity, mortality and control expenditure will be zero. The ideal health case represents a theoretical rather than a practical state. It provides a zero morbidity and mortality envelope in which all observed losses could be quantified and attributed to cause or risk factor. In the absence of any means of measuring absolute morbidity levels directly, the proposed alternative is to describe production relationships in sufficient detail to allow the quantification of uncertainty around the true ideal health parameters.

Developing a sufficient array of independent models for predicting ideal health performance, and aggregating their results, is a route to countering uncertainty (Sagi & Rokach, 2018). Developing this resource is a long-term objective within the GBADs programme and DECIDE is positioned to provide some of the first contributions to this data resource across the pilot implementations. Significant volumes of literature and research are devoted to the description of livestock response to nutrition and environmental conditions, and this represents another resource available to incorporate. The impact of changes in fertility, growth and culling rates on livestock populations often necessitates herd structure modelling (Konandreas & Anderson, 1982; Matthewman & Perry, 1985; Sanders & Cartwright, 1979).

On the output side, disease effects on fertility, longevity, growth and yields are unlikely to be uniform and output product sets, product ratios, and quantities will differ between the ideal and actual scenarios. Where animals are culled or slaughtered due to disease, treated with certain drugs, or condemned post-slaughter, secondary or by-products may be generated which differ qualitatively from the primary intended output of the system and serve different markets. For example, milk from antibiotic-treated cattle can be removed from the food chain, but may be an intermediate input for rearing dairy calves, and emergency slaughter and cull animals may produce a lower quality meat, serving a different market, than prime animals. Defining the primary and secondary products of a livestock system and quantifying the changes in these sets in the disease-free condition becomes a consideration in AHLE calculation for both system dynamics in terms of sourcing alternative inputs, but also when the societal-level impact of changes in health state is considered.

Ordinary and control input costs and quantities are needed to measure change between actual and ideal health scenarios. The degree to which changes in the cost of production are retained by producers or result in price adjustment across the value chain is beyond the scope of the AHLE method in the

DECIDE project, but is an interesting consideration in qualitative terms. Similarly, the changes in market access which can result from the presence of a particular disease in a population, such as notifiable disease, are not investigated here as such listed diseases lie outside of the scope of the DECIDE project.

To model outcomes with ideal health, optimisation criteria need to be defined and those described in the previous section are proposed in the first instance. These conventions are needed to harmonise measurement. The desirability of quantifying the value of unconstrained output increase with ideal health can be debated, and unconstrained growth of populations is unlikely to be economically or socially desirable (Herrero & Thornton, 2013). From that point of view, total output generated in the ideal health scenario should not exceed the actual input capacity of the population.

Farrell (1957) expresses caution with regard using a theoretical level of maximum technical efficiency in complex production processes where this may be used to analyse the performance of individual data points. This is well noted, and the AHLE is not intended as a benchmark or target to be aimed at, but as an intermediate analytical step for attributing disease burden to cause, and as part of a suite of metrics to illustrate where disease burden is distributed.

The allocative efficiency of units of analysis will remain constant between the observed and counterfactual scenarios, that is to say, management preferences for allocation between inputs will not be adjusted for optimal efficiency in the ideal health condition, but biomass to supporting input ratios will be allowed to change only where this is the result of efficiency improvements with health.

In this case the burden of disease can be quantified as the value of this change in z, in biomass and any units of x provided to the system, and the value change for each item in the primary and secondary output sets. With a focus on measuring the benefits of improved efficiency rather than unconstrained growth, output constraints are intended to represent continuity of supply for primary products to market. Returning to equation 1, where L is greater than 0, a proportional reduction in Y is observed with respect to the quantity of z supplied. In the ideal health scenario $L = 0$, and therefore a proportional reduction in z is required to maintain a constant amount of Y. Application of all the optimisation criteria over a wider range of data will be needed to determine to whether these criteria hold up under application or need to be developed further.

Production cycles modelled as discrete or contiguous units may restrict or permit models to reflect disease burden on long-term goals such as population growth, for example. A one-year period as described accommodates variables which are commonly arranged as annual panel data for critical inputs and outputs to livestock systems, while species or commodity specific outcomes are often presented for a single life or reproductive cycle. Disease is commonly measured either through prevalence surveys (cross-sectional) or through reporting or detection rates (incidence-based). Establishing a common time frame for analysis across different species groups is necessary for producing global estimates of disease burden. Time taken to complete a single production cycle can be highly variable across livestock systems. Intensive broiler chickens can be grown and slaughtered in less than 2 months while other species, for example cattle and salmon, can require years to reach their desired size and weight. The use of an incidence-based measure of biomass maintained, i.e., kilogram-days, is intended as a means to standardising these variable lifecycles across species. How other parameters are integrated into the model structure may depend on the form of data available in a given system.

Input and output quantities and prices are most often recorded and presented within national data by agricultural statistics agencies or trade bodies, however the underlying datasets are rarely publicly accessible which can hinder developing a covariance structure for variables of interest. Detailed data at herd or animal level are generally not available for reasons of commercial sensitivity. Biomass can be valued by species liveweight, and prices are recorded in some international datasets, such as FAO-STAT and Eurostat, while international trade prices for animals and commodity products are recorded in UNComTrade.

4   Limitations of farm-level burden assessment

The animal health loss envelope provides a measure of the burden of animal disease through the financial cost of its effects on the productivity of livestock production systems. With the DECIDE project's focus on farm-level outcomes, the AHLE is a suitable means of quantifying disease burden. Within the wider context of food systems and society, there is scope to develop the concept further to consider the indirect consequences of production inefficiencies on consumers, society, markets and the environment which are not captured. This would form the basis for further work. The epidemiological consequences of untreated endemic disease spreading between units is also a consideration in terms of the externalities of poor health.

As an example, prophylaxis with antibiotics against common production diseases may be the most cost-effective means of reducing the direct disease burden placed on animals, leading to a low observed disease burden and higher productivity when quantified by the AHLE. Where such practices are regulated against, it is possible that a higher burden of disease is observed at the farm as the external cost of antimicrobial use, i.e., the generation of resistance, has been internalised to a greater degree within production. Given the common governance frameworks that operate across the European Union, a minimum baseline condition is provided for within DECIDE that serves to minimise this effect for between-country comparisons, as opposed to comparisons extra-EU.

The use of antimicrobials is not the only management decision that can generate externalities. The level of intensification or extensification of livestock systems can have important consequences for the environment and land use, while the interface between livestock, people and wild animals can generate zoonotic and foodborne disease consequences. Animal welfare is also considered a public good and an ethical responsibility of livestock keepers (WOAH, 2022). To generalise, the degree to which disease burden will be fully captured at farm level by the AHLE is dependent on the management practices and technologies available as well as the norms and regulatory systems in place in a given population or measurement unit. Again, the fact that we are working within a common governance framework is beneficial to the method being applied.

The positioning of a firm on these dimensions can also reflect management preferences, resource and technological availability and private and public standards and regulation. In many cases, the relationship between animal health, productivity and externalities is likely to be non-linear and covarying (Gilbert, Thomas, Coyne, & Rushton, 2020; Harvey & Hubbard, 2013; Jespersen et al., 2017). Measuring effect sizes generated by complex causal pathways, such as when estimating the impact of antimicrobial use at farm level on the spread of resistance genes and antimicrobial-resistant infections, or where valuation of non-market goods or resources such as the environment and animal welfare creates methodological challenges (Brookshire, Thayer, Schulze, & d'Arge, 1982; Mitchell & Carson, 2013).

With that in mind, the AHLE work being done at farm level in the DECIDE programme is being complemented by consideration for animal welfare and other farm level effects in Work Package 4. In that regard, Task 4.2 is to develop loss-expenditure frontiers for interventions against endemic disease while Task 4.3 is to assess the relationship between health, disease and welfare. The wider societal impact of changes in animal health is not considered here, particularly since zoonotic diseases are outside of DECIDE's scope. Application of the framework on farm level will need to be progressed to attribution to cause or risk factor to assist in the development of decision-making tools for use by farmers and vets.

D4.1 – Generic framework for determining
the economic burden of animal disease
Version 1.0

5 Framework applications - biomass and population structures

To test the framework applicability, at least one case study has been initiated for each of the species covered by DECIDE. Thus far, the following case studies are in progress:

1. Swine production, covering the Netherlands and Spain. This work is being led by UU and facilitated by GD and IRTA.

2. Cattle in Ireland, led by UCD in collaboration with AHI. This collaboration is through a PhD position located at UCD which is co-supervised by AHI and UoL, using data provided by AHI. This PhD synergises naturally with the DECIDE work of UoL and AHI and provides additional resources to WP4 at no additional cost.

3. Broiler production in the UK, led by UoL.

4. Salmon production, covering Norway. This work is being led by NVI and SRUC.

Given the need to set out population structures, and the integral part played by animal biomass in the framework, each case study has started with documenting biomass flows at country level. This has enabled the beginnings of compartmental structures to develop. This process is now described for each in the sections below. The work so far has considered national populations to describe the context. Applying the models at the individual farm, herd or flock level will follow the same principles as at a higher level of aggregation.

5.1 Standing population biomass method

The ideal scenario for biomass calculation would be to have a census dataset with the actual weight (w) of each (i) of the n individuals in the population from which the total liveweight of the population can be calculated.

$$\sum_{i=1}^{n} w_i$$

Failing that data being available, the variables n and w can be estimated, to generate an approximate population biomass by multiplication, for example:

$$\sum_{i=1}^{n} w_i \approx (n \pm \bar{\epsilon}_n)(\overline{w} \pm \bar{\epsilon}_w)$$

In this case, the method used to generate these number and liveweight estimates introduces additional sources of systematic and random error ($\bar{\epsilon}$). The objective in subsequent refinements is to minimise these errors to the greatest extent possible with the data available, while documenting uncertainty.

This is most often done by disaggregating the population structure into units J to produce a vector of values for n, and the weight distribution to create a complementary set of values for w. In this example, the additional variable c, where $0 \leq c \leq 1$, divides the total population into a set of compartments by proportion:

$$\sum_{j=1}^{J} (n \pm \bar{\epsilon}_n)\left(c_j \pm \bar{\epsilon}_{cj}\right)\left(\overline{w}_j \pm \bar{\epsilon}_{wj}\right)$$

Most frequently, population disaggregation is done based on easily assessed variables which covary with individual animal liveweight. These could be economic such as productive purpose or farm type, or biological such as genetics (species, sex, breed) or age. In addition, any information which indicates

the population structure (the proportion or number in each compartment) should be sought. When the formula is applied to each class of animals within a population, the results are summed to give total biomass. Where existing data collection aligns with administrative units or sampling frames that can aid the definition of population structure and animal liveweight estimation, this should be seen as a potential asset to be taken advantage of.

As a result of the variation in global livestock populations and data availability, there is no biomass calculation method that is optimal across all of the world's livestock. A tiered approach is therefore proposed based on how easily the population can be compartmentalised and compartmental weights estimated.

5.2 Annualised biomass estimation

A standing population biomass calculation as described in the previous section gives a snapshot of population size at a single moment in time. Many of the calculations relating to livestock system per-formance, for which biomass calculation is an important intermediate step, however, are concerned with changes in biomass over time. After all, it is the dynamics of livestock as living organisms that underlies the purpose for which they are kept. There are a number of ways of describing the dynamics of the herd. Firstly, a start and end time point need to be set (denoted as t and $t+1$), for example a single year or production cycle. Across this time the following need to be accounted for:

- Movements of biomass into each compartment
- Movements of biomass out of each compartment
- Residual change in compartment biomass between t and $t+1$
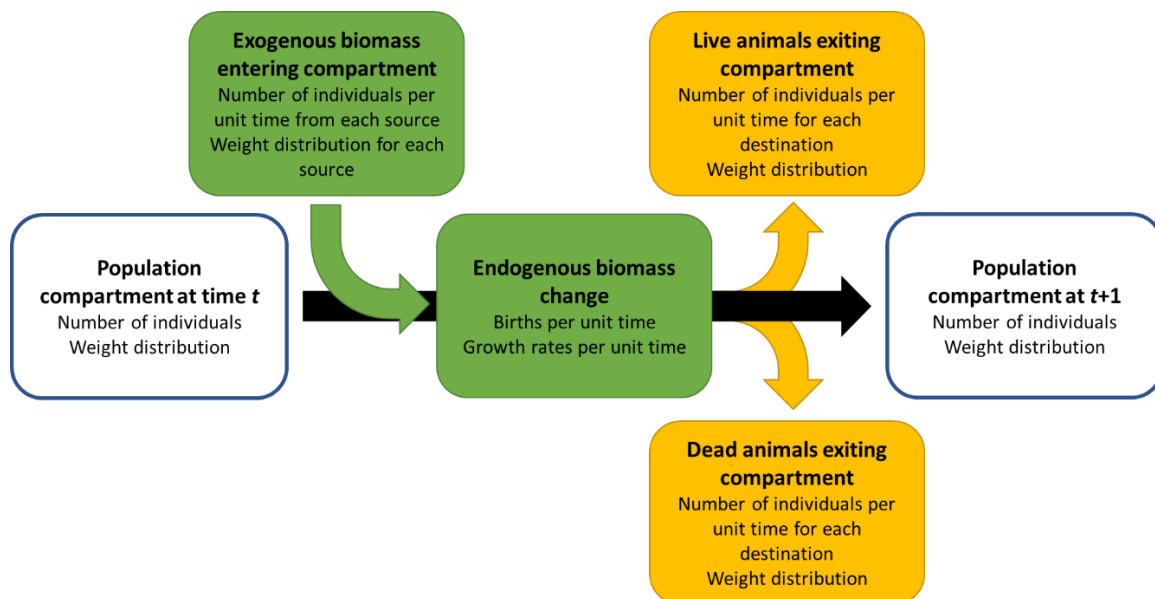
This is illustrated in Figure 2.

Figure 2. Conceptual model of biomass flow in a livestock system over time.

Looking at the various in and outflows of biomass given in Figure 2, it is clear that there are various means of accounting for change over time due to interdependence between variables and rates of change. Within compartment biomass can be measured at two time points to calculate change over time, or inferred from growth rates and either a start or end-point measurement, for example. There is therefore a degree of adaptability in selection of methods for estimating movements in, out and endogenous change, depending on what is known about the population in question, what can be de-rived from data, calculated, inferred or assumed. The data points against which these three items can be measured are described further below (Table 2).

Table 2. Descriptive of variables required to populate the conceptual framework for disease burden estimation.

Item	Data	Means of calculation or estimation	Example assumption when no data or other information available
Population biomass at time t	Number of animals (head) carried over or placed Animal weights, or average weight or distribution of weight	Back calculation possible if other items are known or estimated	Constant growth rate or constant head count or weight can be assumed
Endogenous biomass change	Birth records Birth weights Weight records at intervals between t and t+1	Number of reproductive animals Growth rates, with any contingent information required Birth rates, with any contingent information required Time in compartment per animal	Assumed time point for births/hatchings Assume weight distribution of neonates/chicks/smolts Linear growth rate over time.
Exogenous biomass entry	Number of animals moving in from another compartment Live animal imports Live animal purchases Animal weight at entrance Time of entrance relative to t/t+1	Can be inferred from other entries and exits	Assumed time point for each entry source Assumed weight for each entry source
Live animals exit	Animals moving to another compartment Animals sold Animals gifted Animals sent for slaughter Weight at time of exit Time of exit relative to t/t+1	Can be inferred from other entries and exits	Assumed time point for exit to each destination All exits at a specified weight, by destination
Dead animals exit	On-farm slaughter Natural deaths Culled animals Any other animals lost (lost, stolen, assumed dead) Weight at time of exit Time of exit relative to t/t+1	Mortality rate Culling rate Total meat production from compartment Technical conversion factors for live/dead weight conversion Can be inferred from other entries and exits	Assumed time point for exit to each destination Assume weight for each destination
Population biomass at t+1	Number of animals (head) Animal weights, or average weight or distribution of weight	Can be calculated from a population growth rate	Growth rate or constant herd size/weight can be assumed

5.3   Biomass of swine populations

The biomass of swine has been calculated previously by various methods, including those developed by the World Organisation for Animal Health (WOAH[1]), European Surveillance of Veterinary Antimicrobial Consumption (ESVAC[2]), Canadian Integrated Program for Antimicrobial Resistance Surveillance

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[1] https://www.woah.org/app/uploads/2022/06/a-sixth-annual-report-amu-final.pdf
[2] https://www.ema.europa.eu/en/veterinary-regulatory/overview/antimicrobial-resistance/european-surveillance-veterinary-antimicrobial-consumption-esvac#population-correction-unit-section

(CIPARS[3]) and the U.S. Food and Drug Administration (FDA[4]). Although these methods have successfully provided a crude estimation of swine biomass on a national or global level, they are unable to disaggregate between pig life stages and production systems.

Where the ultimate goal is to analyse production efficiency, and within that, disease burden, a greater level in biomass quantification is critical to identifying where in the production chain the costliest issues occur. Considering the application of biomass as a denominator to standardise antibiotic use or greenhouse gas emissions, the same can be said. Biomass estimation is a step in the pathway to assessing the level of risk, societal burden, or the efficacy of interventions. As such, the highest-possible level of resolution is desirable. The methods referred to above tend to use on the same datasets (FAO-STAT, Eurostat).

Within DECIDE, a framework was applied that calculated quantities and dynamics of swine biomass disaggregated by life stages, using national data. To evaluate the applicability of the framework across different production systems, this was applied in two European countries: the Netherlands and Spain.

All data were retrieved from public national databases or scientific literature (Netherlands: RVO[5], CBS[6], Agrimatie[7], Handboek Kwantitatieve Informatie Veehouderij; Spain: Mapa[8], BDporc[9], Interporc[10]). Data on population structure, trade and slaughters were collected for sows and for three life stages in fattening pig production: pre-weaned piglets, weaned pigs (<50 kg) and fattening pigs (>50 kg). The yearly numbers of animals within a production stage were calculated based on the in- and outflows of animals per stage specifically. Because the life cycle of fattening pigs is shorter than one year, the in- and outflows include the flow of pigs from one stage to the next. The framework was validated by comparing calculated numbers of pigs at the end of a production year with standing population surveys, as well as through expert consultation. Ultimately, average standardised bodyweights of pigs within a certain life stage and average bodyweights at time of trade were used to convert the number of heads to live biomass.

Figure 3 presents the number of pigs for each stage and flow in fattening pig production for the Netherlands, 2019. Using the numbers from the figure, live biomass as a result from each production stage was calculated: 182 million (M) kg pre-weaned piglets, 815M kg weaned pigs and 1566M kg fattening pigs. Similarly, the framework calculates the biomass within each specific in- and outflow, including the biomass loss due to pre-slaughter mortality (48M kg).

For Spain, we are currently working on implementing the framework, although challenges arose from differences in data availability. We intend to apply the framework in several other European countries in the context of the DECIDE project, so additional issues in data availability are to be expected. To cope with this challenge, we aim to provide alternative methods of calculating specific flows of biomass within the framework. Meanwhile, this work will highlight where countries could make improvements regarding their public national data.

[3] https://publications.gc.ca/collections/collection_2020/aspc-phac/HP2-4-2018-eng-4.pdf
[4] https://www.fda.gov/files/animal%20&%20veterinary/published/FDA%E2%80%99s-Proposed-Method-for-Adjusting-Data-on-Antimicrobials-Sold-or-Distributed-for-Use-in-Food-Producing-Animals-Using-a-Biomass-Denominator--Technical-Paper.pdf
[5] https://www.rvo.nl/onderwerpen/marktinformatie/statistieken
[6] https://opendata.cbs.nl/statline/#/CBS/nl/dataset/84952NED/table?ts=1646837770301
[7] https://www.agrimatie.nl/binternet.aspx?ID=16&bedrijfstype=5
[8] https://www.mapa.gob.es/es/estadistica/temas/estadisticas-agrarias/ganaderia
[9] http://www.bdporc.irta.es
[10] https://www.sinfoporc.com/

D4.1 – Generic framework for determining
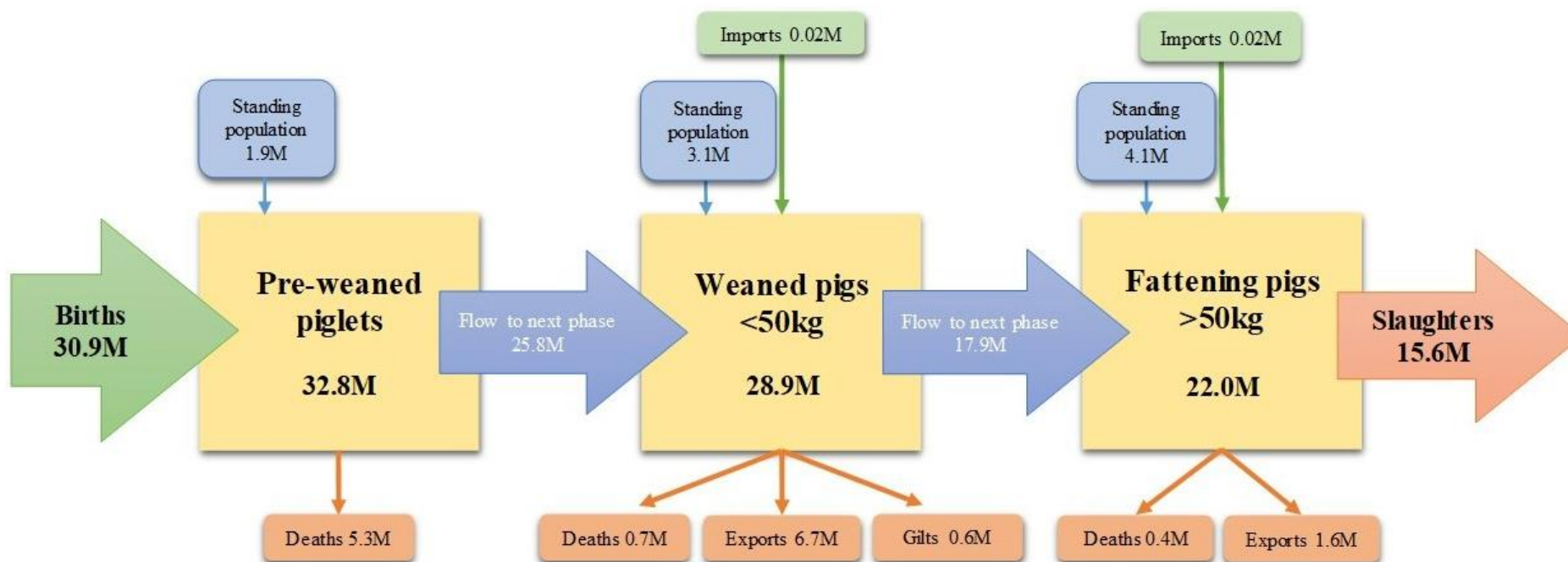the economic burden of animal disease
Version 1.0

Figure 3. Flow chart of the quantities of pigs in millions of heads (M) within each pig life stage, and for each in and outflow from each life stage compartment for the Netherlands 2019.

D4.1 – Generic framework for determining
the economic burden of animal disease
Version 1.0

5.4 Biomass of broiler populations

Publicly available datasets on British broiler sector were identified. The UK government records chicken population statistics on a monthly basis, and from these a compartmental map of the production system was devised. The framework considered the biomass in different compartments of the production chain (Figure 4).
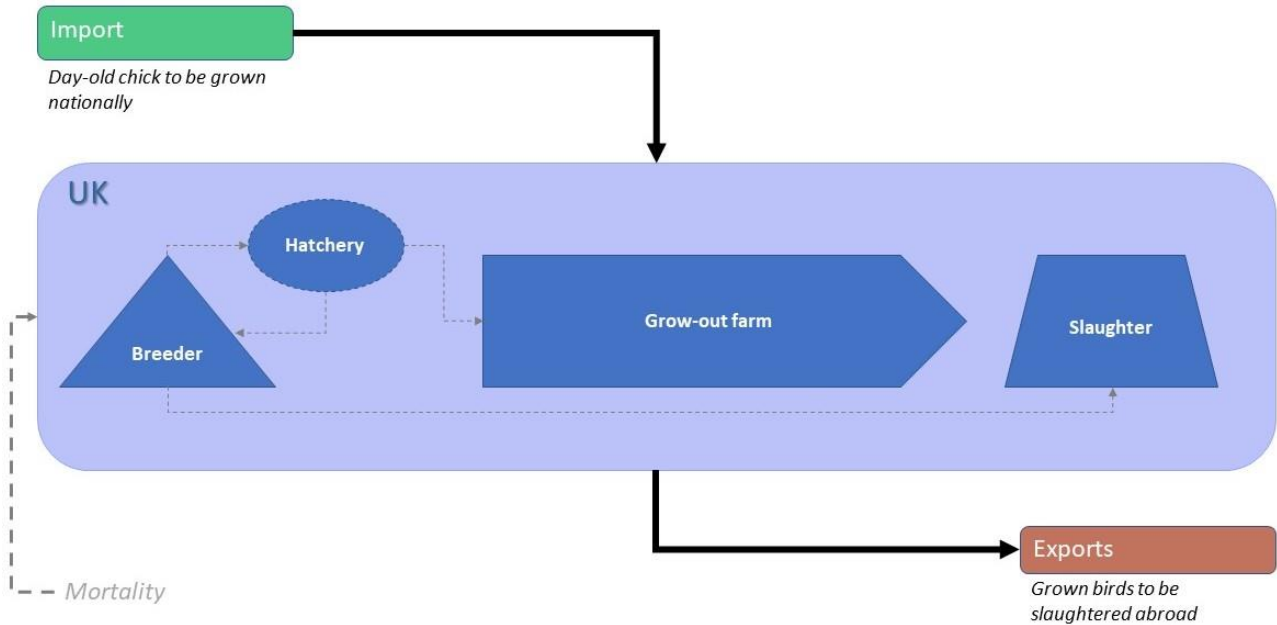
Figure 4. British commercial broiler sector and components to be considered for biomass estimation

For the chain:

$$B_t = B_s + B_{bh} + B_{exp},$$

Where B_t = total biomass (kg), B_s = for slaughter biomass (kg), B_{bh} = biomass of the breeding flock and B_{exp} = exported biomass.

The biomass in each component, accounting for the biomass lost due to mortality where needed, is described below. Mortality was assumed to be 3.5% for the grow-out stage and 1% for the breeding hens, according to Leinonen, Williams, Wiseman, Guy, and Kyriazakis (2012) and Jones, Randall, and Mills (1978) respectively. Additionally, it was assumed that birds lost to mortality would have reached half of their average liveweight before dying. Moreover, it was assumed that chicks placed for breeding purposes would have reached the weight at slaughter within one month:

$$B_s = ((N_{bs} \times \mu L w_b) + (N_{bs} \times m_b \times (\mu L w_b/2)) + ((N_{bfs} * \mu L w_{bf}) + (N_{bfs} * m_{bh} * (\mu L w_{bf}/2))$$

Where N_{bs} = number of broilers slaughtered, $\mu L w_b$ = average liveweight of a broiler, m_b = broiler mortality, N_{bfs} = number of boiling fowls slaughtered, $\mu L w_{bf}$ = average liveweight of a boiling fowl, m_{bh} = breeding hen mortality.

$$B_{bh} = (N_{bh} * (1 - m_{bh}) * \mu L w_{bf}) + (N_{bh} * m_{bh} * (\mu L w_{bf}/2)),$$

Where N_{bh} = number of breeding hens and:

$$B_{exp} = W_{elf}$$

where W_{elf} = weight of exported live fowls of the species *Gallus domesticus* > 0.185kg.

In 2020 and 2021 the yearly biomass surpassed 2.5 million tonnes. The grow-out component of the production chain represented the vast majority of the biomass for the sector (more than 99%), with the breeding stock contributing with less than 1% and traded animals even less (Table 3).

Table 3. British commercial broiler yearly biomass

Year	Total Biomass (kg)	Grow-out/Slaughtered	Breeding	Traded
2020	2,641,188,588	99.2%	0.8%	0.0%
2021	2,716,511,996	99.3%	0.7%	0.1%

The biomass present in the UK commercial broiler sector fluctuated significantly by month, with approximately 75,000 tonnes of liveweight between the lowest and highest points recorded. High points were located in April, July and October of each year, and low points in February, August and December.
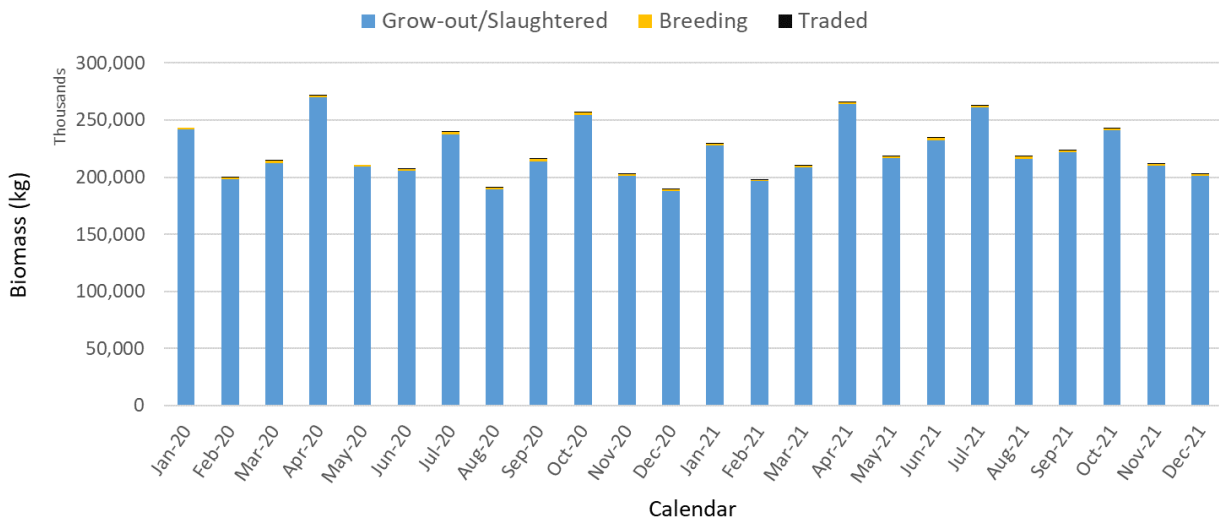

Figure 5. British commercial broiler monthly biomass

Our results indicate that the biomass of the UK commercial broiler sector was larger than 2.5 million tonnes in 2020 and 2021, with more than 99% of this figure being represented by slaughtered animals. The biomass supporting this production chain is very small compared to total biomass, and thus the systems is very sensitive to the health state of the breeding flock.

Detailed knowledge about placements, growth curves and mortality rates at different moments of the productive life of the birds would be useful for developing a population dynamic model with all components of the production chain leading to a more accurate figure for the sector's biomass. Input resources required to support each compartment and prices for input and outputs as the next step toward determining health loss impact on production efficiency.

5.5   Biomass of cattle populations

The approach for the Irish case study project is to generate an estimate of the herd biomass the national cattle population from 2011 to 2021, following a method outlined by Rothman-Ostrow, Gilbert, and Rushton (2020). This requires herd structure, breed composition, age, sex, and live weight of the population in its estimation. The initial focus for the DECIDE project is on calf data. Alongside the herd biomass estimation, an estimation of the total stock value of each herd will be developed.

There are three data sources collected by the Department of Agriculture, Food and the Marine Ireland which have been used to describe the cattle population for this study:

1. Animal Health Computer System (AHCS)

2. Live Cattle Pricing (LCP) database

3. Animal Identification and Movement (AIM) database

The AHCS system is utilised for the surveillance and monitoring of animal health and welfare in Ireland, i.e., TB Eradication and Brucellosis Monitoring Programmes, and to make compensation payments to herd owners. This provided data on bTB reactor slaughter data. The LCP database stores information collected at the marts such as price, EBI, sex, breed, and quality score. The AIM system holds records of births, movements and disposals in accordance with EU requirements, tracing all bovines from birth to death (Department of Agriculture Food and the Marine, 2022) See Figure 6 for an overview of the information in data sources 1 and 2.
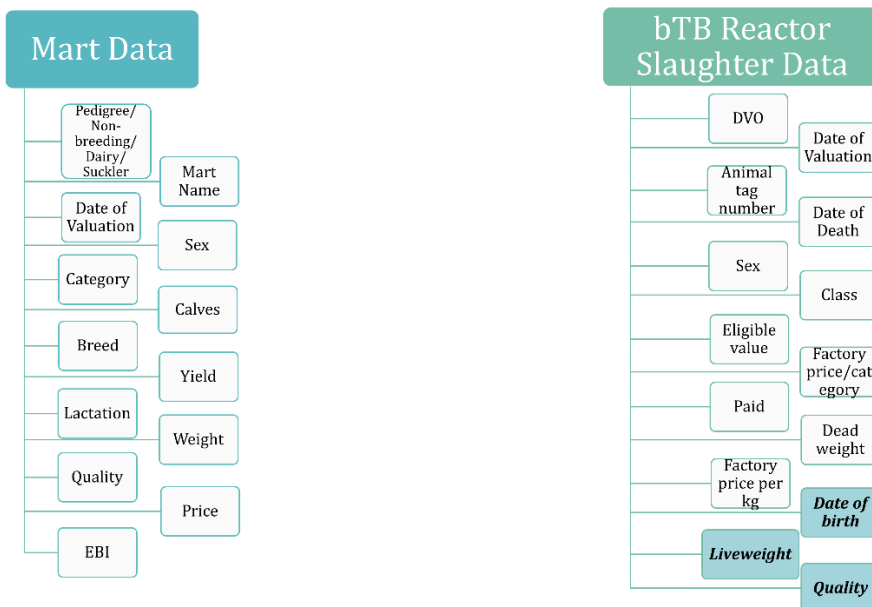

Figure 6. Data inputs in the mart and bTB reactor slaughter datasets.

The average price of an individual animal by their age, sex, breed, and live weight at a given time was calculated using the bTB reactor slaughter data. The results are then validated against the price values in the mart data. Both the bTB reactor slaughter data and mart data follow into the development of a lookup table. The lookup table is used in conjunction with data source 3 of the study. The movement data are used to create the herd population structure over the ten-year period, classifying herd types using the model developed for Irish cattle herds by Brock et al. (2021). The individual animals in the movement data were matched to their corresponding stock value in the lookup table. The individual biomass estimates and stock values are aggregated to the herd level, repeating this process monthly over a ten-year period to characterise the changes in biomass and stock value within and between years. To date, this is the first biomass study in Ireland using data spanning ten years with a total stock value per herd. The estimates will be a starting point for calculating the AHLE of the cattle sector in Ireland within the boundaries of the common methodological framework.

Data sources 1 and 2 add an economic value to the biomass estimates across the ten-year period.
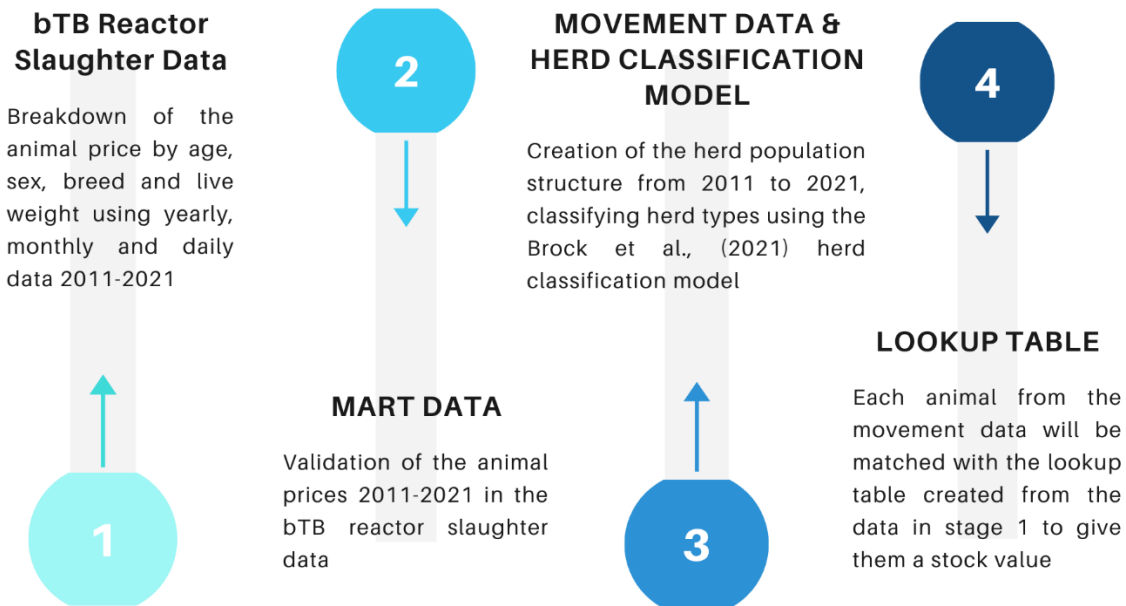
Figure 7. Four stages and data sources of the cattle biomass study in Ireland

5.6 Biomass of salmonid production

Production of salmonids occur in two to three phases, as shown in Figure 8. Fertilised eggs are put into the system, and the output is slaughtered round weight. For the case example Norway, data on the amount that flows from one phase to another is publicly available at the directorate of fisheries (Atlantic salmon and rainbow trout (fiskeridir.no)).
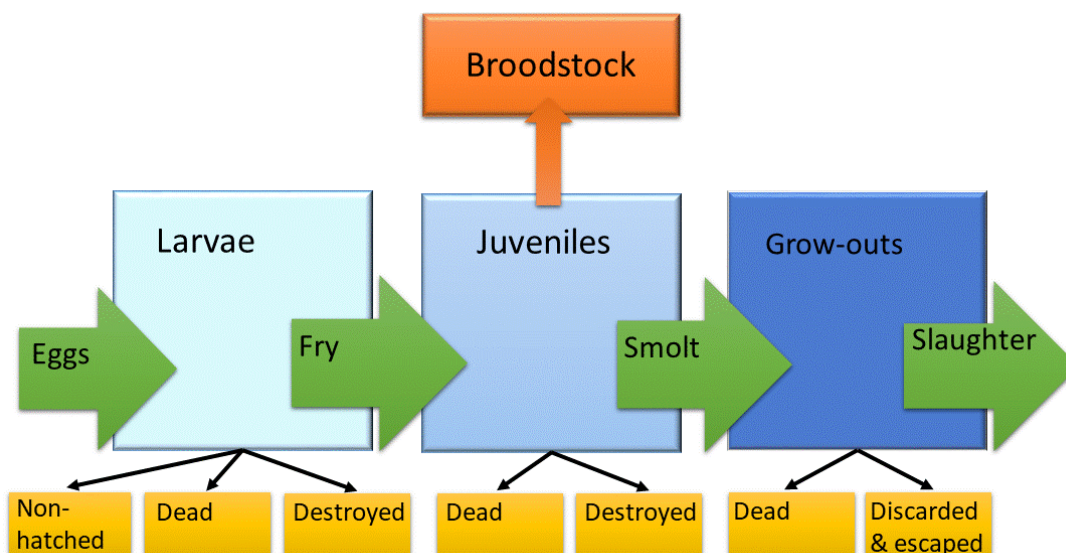

Figure 8. Flowchart of the salmonid production, indicating the flow of biomass through the production system.

Roe put into production is measured in numbers, not biomass or weight. For 2021, a total of 577.7 million roe were put into production. Not all fertilised eggs hatch, but the number of hatched larvae is reported: In 2021, this number was 557.4 million. Thus, the number of non-hatched eggs can be deduced from these two

numbers. For juveniles, the standing stock is reported every month, and by the end of the year. By the end of 2021, the standing stock of juveniles in hatcheries was 422.5 million. In addition, the monthly losses are reported in numbers; by the end of 2021, this amounted to 144.9 million. A small proportion of the juveniles are traded; in 2021 this amounted to 28.8 million, or 6.7% of the standing stock. For the juveniles, the average weight is reported monthly together with the number, but the average weight is not publicly available. These data are however, available for competent authorities and the National Reference lab, and in some cases on request. One publication describes the weight distribution in the hatcheries based on these numbers (Mortality patterns during the freshwater production phase of salmonids in Norway - Gåsnes - 2021 - Journal of Fish Diseases - Wiley Online Library). In this study, data from 2011 to 2019 was used, and across this time period, one fifth of all juveniles above 3 grams where in each of the following weight groups: 3–12.2 g; 12.3–34.2 g; 34.3–58.1 g; 58.2–89.1 g; and > 89.1 g. Thus, approximations on the biomass in hatcheries can be calculated from these numbers.

The number of juvenile fish sold for production in sea is also reported; in 2021 it totalled 429.8 million. According to definitions, these are fish weighing a maximum of 250 g. The average weight of such smolts for stocking is between 75 and 250 grams.

When it comes to grow-outs in the sea, both the number of fish and their average weight are reported every month. At the directorate of fisheries, the standing stock can be found, as exemplified in Table 4:

Table 4. Standing stock of Atlantic salmon in Norwegian marine farms, per the end of October 2022. (Note: Only Atlantic salmon is included, not other salmonid species, although this can be found in the statistics also.

	Stocked previous years		Stocked last year		Stocked present year	
Total for Norway	Number of fish	Av. weight	Number of fish	Av. weight	Number of fish	Av. weight
	326,000	0.995kg	143,787,000	3.585kg	320,873,000	1.099

Thus, estimating the standing biomass can be done by multiplying the number and the average weight.

The number of fish lost per month is also reported, divided into the categories: dead, escaped, destroyed, others, and counting error. The Norwegian Veterinary Institute provides an interactive application where the numbers of dead fish per species, area and year can be found: Laksefiskdødlighet (vetinst.no)

The average weight of the dead fish is reported, but this information is not contained in the official statistics. However, as with the hatchery data they are available for specific purposes. There are publications describing the mortality rate for different weight groups, and thus it can be estimated where the largest losses are. The amount of slaughtered fish per year is reported in metric ton round weight, and is publicly available from the directorate of Fisheries. Thus, for 2021, this totalled 1,657,473 tonnes. In the Fish Health Report, published by the Norwegian Veterinary Institute each year, the average mortality across all fish cohorts slaughtered in 2021 was 17.4%, thus indicating the amount of fish lost before the economic gain could be realised.

When regarding the biomass of the standing stock, it is of interest that there is a great deal of seasonality, due to the fact that smolt are released into the sea at specific times of the year, and growth is very much regulated by seawater temperatures (Figure 9). In addition, market prices fluctuate, and to some extent controls when fish are slaughtered.
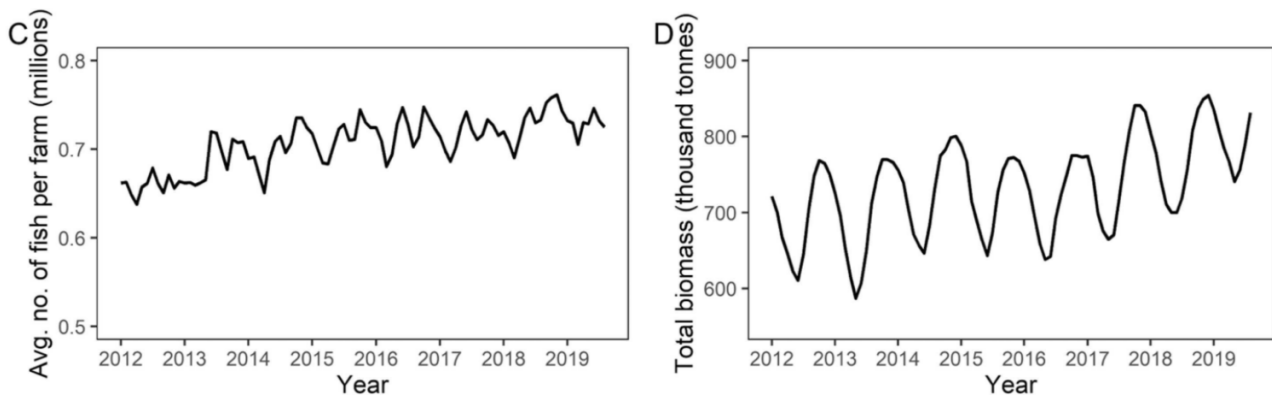
Figure 9. Salmonid production data for fish farms in Norway from January 2012-August 2019: (c) average number of salmonids per farm (in millions) per month and (d) the total biomass (in thousand tonnes) on all active farms per month. From Simulated effects of increasing salmonid production on sea lice populations in Norway - ScienceDirect

6 Next steps

This report summarises the progress made in developing a framework that can be applied to assess farm-level disease burden in livestock systems, and where that framework fits within the wider animal health context and the societal burden of diseases of livestock and aquatic production species. This framework has been developed in synergy with the Global Burden of Animal Diseases programme. So far, the application of the framework has begun with case studies in Norwegian salmon farming, United Kingdom broiler production, Irish cattle farming, and pig production in both the Netherlands and Spain. Initially these studies are working at national level, which serves to describe structure of populations to understand where farm-level data is needed before farm-level models are constructed and is possible without access to confidential data.

Within the DECIDE project, there is a need to ensure this work continues to be integrated with that being done by other work packages. Work Package 1 will be key contributors of data on study populations for example, through a federated data model which will allow individual farm data to be analysed without compromising confidentiality. In addition, health and productive performance data will need to be standardised between units, and parameters for models extracted from this data. The AHLE estimation and any subsequent attribution to cause or risk factor will provide prioritisation framework in economic metrics which can be used by Work Package 3 in developing decision support tools. The results from the AHLE may further influence the technical requirements (e.g., use of other data sources that imply connecting to additional databases), the development (e.g., adding new functions to the tools), and the evaluation of the decision support tools. The presentation of this information (e.g., framing, visualisation, richness of information) can be better informed by the output of Work Package 5, in tailoring the focus of economic analysis to-ward messaging that resonates with the users of the tools, e.g., farmers and veterinarians, and supports their decision making.

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