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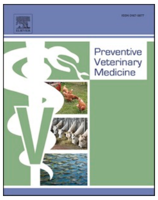

PARAMETRA: A transmission modelling database for livestock diseases

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ABSTRACT

Dynamic modelling of infectious diseases of importance to livestock production is a valuable tool for policy and decision makers. Mathematical and simulation models play an essential role in understanding complex systems, but parameterising these models can be challenging, especially in data-sparse environments. When parameters are unable to be estimated from epidemiological or experimental data, a time-consuming and labour-intensive literature review—to identify suitable literature-informed values—is often necessary. In service of this, here we present PARAMETRA, a parameter database for 20 pathogens of livestock, envisaged as an open-source collaborative tool for the research community to aid in the development of future transmission models of livestock pathogens. Pathogens included in the database so far were selected using a disease prioritisation exercise. Parameters of interest were selected by experts with a strong background in epidemiology and mathematical modelling. We populated the database with over 2000 individual values, covering a wide range of different parameters including transmission rates, diagnostic test efficacies, pathogen survival on surfaces, and the farm and regional level prevalences of selected diseases. Finally, we present an initial illustrative analysis of the database contents and the associated metadata of studies included. One of the principal conclusions we can draw from the data available is that in many cases research is reactive, rather than proactive, with research only tending to focus on specific diseases after outbreaks have already occurred, as is the case for African swine fever for example. This has important implications for future research moving to a more proactive approach for experimental and epidemiological studies based on observations of gaps in the data, and high-risk diseases. This publication represents the first step in development for the PARAMETRA database, which will be updated and expanded in the coming years.

1. Introduction

Livestock production accounts for close to half the total value of agricultural production worldwide (Schrobback et al., 2023), with demand for animal products expected to further increase in the coming years, driven in a large part by increasing population and urbanisation in low and middle-income countries (Perry et al., 2018). However, both commercialised intensive production and smallholder production alike are threatened by infectious livestock diseases (Kappes et al., 2023), with negative consequences for long term sustainability (Perry et al., 2018). Livestock diseases can have wide ranging repercussions and societal impacts. Outbreaks of epidemic diseases can lead to production

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losses and welfare issues (Knight-Jones and Rushton, 2013; Kappes et al., 2023), but also to wider economic losses due to trade restrictions (Knight-Jones and Rushton, 2013; Bradhurst et al., 2015). Infectious diseases also lead to the increased use of antibiotics which drives the selection and spread of antimicrobial resistance (Chantziaras et al., 2014; Jerab et al., 2022; Kappes et al., 2023). Finally, spillover of pathogenic agents and antimicrobial resistance from livestock can also have a deleterious effect on both wildlife and human health (Kappes et al., 2023; Ward et al., 2025). In addition to serving as bridging or amplifying hosts (McLean and Graham, 2022), certain animal species can harbour multiple strains of a virus and act as mixing vessels, as seen in the case of influenza A viral reassortment that has occurred in pigs (Ma et al., 2009).

As such, it is critically important for both animal and human health that livestock diseases are effectively controlled. However, control of livestock diseases is complex, needing to be tailored to the specificities of each different farming with control measures needing to be tailored to the specificities of each different farming and epidemiological context. Control measures can include surveillance of the disease for early detection, vaccination and/or drug treatment (where available), movements restrictions or culling of infected animals, among others (Tildesley et al., 2009). A further critical aspect of disease control is biosecurity. Within the context of livestock farming, biosecurity aims to prevent the spread of infectious agents to, within and from an animal population (Manuja et al., 2014; Alarcon et al., 2021; Huber et al., 2022). This can specifically be defined as any measure designed to reduce the probability of introduction, establishment, survival or spread of a pathogen into, within, or from a farm, area, or region. Such measures can include segregation, hygiene, or management procedures other than those using medically effective feed additives and/or prophylactic and metaphylactic treatment of animals (Huber et al., 2022). This can involve practices to prevent the introduction of pathogens to the farm through different pathways such as live animals, transport, feed, water, or movement of people, among others, which is usually named external biosecurity (Mee et al., 2012). Conversely, internal biosecurity focuses on reducing or preventing the spread of pathogens within a farm, often focusing on staff movements and hygiene, herd/flock management strategies, and cleaning and disinfection protocols (Alarcon et al., 2021). Recently, this concept has been extended to consider also those measures directed to contain the spread of pathogens out of the farm, to prevent the infection of people working or visiting the farm from zoonotic agents by implementing personal biosecurity practices and minimising the impact in the environment (e.g., use of biocides) (Renault et al., 2021; Saegerman et al., 2023).

The effectiveness of many control measures, and the spread of pathogens itself, can be difficult to measure experimentally on a large scale. Moreover in many cases the disease may not already be present within the population of interest (Bradhurst et al., 2015; Kirkeby et al., 2021). Although of great value and an invaluable source of parameter estimation for *in-silico* modelling, small scale experiments on disease transmission may not represent real-life disease epidemiology sufficiently well (Kirkeby et al., 2021). There are additionally many ethical and economic concerns that would preclude, for example, experimentally introducing epidemic pathogens into a naïve population. Within this context, *in-silico* experiment based on dynamic modelling of infectious diseases has a key role to play in evaluating the spread potential of epidemic or endemic diseases, assessing the efficacy of control measures, and supporting complex decision making for disease control. The use of modelling has expanded rapidly within the last two decades, driven by improvements in both methodology and computing power (Lanzas and Chen, 2015). Modelling has the capacity to represent complex systems and their variability, and the interconnectedness of those systems (Luke and Stamatakis, 2012). Thus, it can be of particular use in studying disease control. Models further have the capacity to identify critical elements or knowledge gaps through reconstruction of the system in question (Heffernan et al., 2005; Kirkeby et al., 2021).

When using mathematical models to assess the effectiveness of interventions, a critical aspect is the availability and quality of the input parameters (Martinez-Lopez et al., 2008). Parameters such as the transmission rate, and the infectious period are essential even for the most basic SIR (Susceptible-Infectious-Recovered) models (Heffernan et al., 2005; Blackwood and Childs, 2018). Depending on the type of disease and intervention, models necessitate the inclusion of additional parameters such as shedding rate, decay rate for environmentally transmitted pathogens,the contact rate with wildlife hosts, the probability of infection given a direct or an indirect contact or the prevalence of the disease at the herd, regional, or national level, among others (Bradhurst et al., 2015; Courtejoie et al., 2018; Benavides et al., 2020; Rees et al., 2021; Kirkeby et al., 2021; Gamza et al., 2023; Chang and de Jong, 2023). Thus, one of the initial tasks when undertaking a disease modelling project is a review of the available data and existing parameters, in addition to epidemiological considerations regarding transmission routes and control measures. The availability of data will then influence the structure of the model, how well it can represent reality, the assumptions which have to be made, and therefore how realistic the estimates are.

In line with this, we present here PARAMETRA, a transmission parameter database designed to aid in modelling of livestock diseases. PARAMETRA contains a wide range of information, including transmission parameters of importance for researchers and decision makers aiming to develop new, or improve existing models of disease transmission for livestock diseases. PARAMETRA thus contains parameters for a range of endemic, epidemic, and transboundary and emerging diseases, selected as important for European livestock production through a disease prioritisation exercise integrating stakeholder feedback from researchers and high-level EU decision makers. To the best of our knowledge, PARAMETRA represents the first database of its kind dedicated to collecting modelling parameters for livestock diseases into a single repository.

2. Materials and methods

2.1. Disease prioritisation

Initially, a disease prioritisation exercise was carried out for epidemic and endemic diseases in cattle, small ruminants, swine and poultry through the DISCONTOOLS database (https://www.discontools.eu/database.html). The DISCONTOOLS database was chosen as it identifies critical gaps in knowledge for the purposes of developing new disease control tools, and provides updated disease information incorporating stakeholder feedback. Among the 53 infectious diseases present in the DISCONTOOLS database, our focus was initially only on diseases affecting livestock, not zoonotic diseases, although there is naturally some overlap, particularly in the cases of avian and swine influenza. However, it must be stated unequivocally that we did not consider the potential for zoonoses as a criterion for inclusion here, as our focus was purely on animal health. Further diseases were removed as they either did not affect livestock species considered here, or were only present in a small number of countries far from Europe. This yielded an initial list of 19 endemic diseases, and 14 epidemic diseases (Supplementary Materials 1).Table 1

Next, through the Horizon Europe BIOSECURE project (https://biosecure.eu/) a qualitative stakeholder engagement exercise was then carried out with stakeholders from organisations operating at the pan-European level in farming, veterinary, public health and animal health contexts to assess their diseases of most concern for the four farming sectors.

For this an online survey was designed and disseminated. Stakeholders were first presented with information on the project and asked to indicate their consent to take part in the survey. They then answered several brief demographic details before completing a separate disease prioritisation exercise for each farming sector relevant to their

Table 1
Summary of the full list of diseases presented to EU-stakeholders for prioritisation. Diseases selected via DISCONTOOLS disease prioritisation tool (https://www.discontools.eu/database.html) are underlined.

Poultry	Swine	Cattle	Small Ruminants
Campylobacter	Porcine Reproductive and Respiratory Syndrome	Bovine Viral Diarrhoea	Peste des Petits Ruminants
Salmonella	Hepatitis E	Infectious Bovine Rhinotracheitis	Foot and Mouth Disease
Mycoplasma gallisepticum	Swine Influenza	Bovine Respiratory Syncytial Virus	Small Ruminant Lentiviruses
Colibacillosis (*E-coli*)	African Swine Fever	*Salmonella* Dublin	Contagious Agalactia
Infectious bronchitis	Classical Swine Fever	Paratuberculosis (Johne's disease)	Nematodes (worms)
Infectious bursal disease (Gumboro)	Swine Vesicular Disease	Foot and Mouth Disease	Liver fluke
Marek's disease	Porcine Circovirus Type II	Mycoplasma bovis	Bluetongue
Avian Influenza	Mycoplasma	*S. aureus* Mastitis	Sheep and Goat Pox Virus
Coccidiosis	Swine Pleuropneumonia (APP)	*S. agalactiae* Mastitis	Footrot
Poultry red mite	Swine Dysentery (Brachyspira)	Nematodes (Worms)	Contagious Pustular Dermatitis (Orf)
Newcastle disease	Swine Streptococci	Liver fluke	*E. coli*
Histomoniasis (Blackhead)	Nematodes (Worms)	Bluetongue	Q fever (*Coxiella burnetii*)
Nematodes (Worms)	Aujeszky's Disease	Lumpy skin disease	Antimicrobial resistance
Antimicrobial resistance	Post-weaning Diarrhoea	Tuberculosis (TB)	
	E. coli	*E. coli* (Diarrhoea)	
	Antimicrobial Resistance	Antimicrobial resistance	

organisation. Stakeholders were presented with a pre-defined list of sector-specific diseases and asked to select the disease of most concern to their organisation and provide a narrative explanation for that choice. They repeated this for the disease of second most concern, and third most concern. Stakeholders were then given the opportunity to add any diseases they felt were important but not listed. Narrative explanations were coded and categorised to identify commonalities in factors influencing prioritisation.

A total of 15 stakeholders, 5 males and 10 females, completed the exercise out of a total of 31 contacted (48 % response rate). Respondents came from: public health organisations ($n = 4$); policy bodies ($n = 3$); agricultural industry/farming organisations ($n = 4$); and science/research bodies ($n = 4$). Fourteen stakeholders completed the cattle disease prioritisation exercise; 10 completed the small ruminants exercise; 13 completed the swine exercise; and 11 completed the poultry exercise.

Diseases identified as a priority were therefore included in the database, in addition to further diseases considered of importance by experts within the BIOSECURE consortium.

2.2. Database design

The database has been designed to serve as an extensive repository for important parameters of use for transmission modelling of diseases of veterinary importance. Among others, these include the basic reproduction number (R_0), transmission rate (β), the probability of infection given direct or indirect contact, and the probability of reactivation of latent infection (where applicable). Furthermore, the database includes information on the durations of the latent, incubation, and infectious periods, pathogen survival on a variety of surfaces, and disinfection efficacy. Sections have also been included covering the sensitivity and specificity of diagnostic tests, the national, regional, and within herd (where applicable) prevalence of diseases, and the presence of national control programmes where appropriate.

2.3. Search strategy

To develop this database, a semi-systematic literature review (Snyder, 2019) was carried out between February 2023 – January 2024. A semi-systematic approach was taken to literature review due to the broad scope of the topic (Snyder, 2019) considered here, namely, data collection for a wide range of parameters for 20 different pathogens across four livestock categories. However, it must be noted that this semi-systematic approach does not employ a fully systematic search strategy, but rather is intended to provide an overview of the available research (Snyder, 2019), with which to populate the database as a starting foundation. The semi-systematic review focused on key parameters defined in 2. was carried out primarily in online databases of scientific literature such as PubMed and Google Scholar. The general format of the search string (PubMed) was as follows:

(disease[title/abstract] AND animal[title/abstract]) AND (parameter1[title/abstract] OR parameter2[title/abstract] OR parameter3 [title/abstract])

Search strings were then iteratively modified based on search results. Each round of iterative modification involved the addition of further terms to the search string to refine results based on title/abstract screening after each search round. This included the addition of alternative wording for parameters, for example "transmission rate" or "transmission parameter", "basic reproduction number" or "R_0". In the case of zoonotic diseases of interest (e.g. Hepatitis E influenza), or diseases with similar names to human diseases (e.g. hand, foot, and mouth disease), an additional search term (NOT human[title/abstract]) was used to ensure that studies focused on human transmission were not returned.

Initially, for all searches the PubMed database was screened for any studies meeting the necessary criteria using variations on the above search string. Following the identification of potential publications of interest, titles and abstracts were screened for relevance. If deemed relevant, the article was then screened in full, and relevant parameters extracted to the database, in addition to key metadata related to the article itself. Secondary searches were also conducted via Google Scholar, and CABI, and in some cases a Google search. In this case, search terms were used, rather than the pre-defined search string format used for PubMed, as this yielded preferable results. In general, preference was given to peer-reviewed scientific articles, where possible. For certain diseases, high quality systematic reviews were available, including for African swine fever (Hayes et al., 2021) and avian influenza (Kirkeby and Ward, 2022; Lambert et al., 2023). Where available, systematic reviews were included as a first preference. In the case of systematic reviews, parameters were extracted from supplementary materials and included in the database with their original reference. In some cases, grey literature has also been included. The majority of these cases were for commercial diagnostic tests, for which manufacturer specifications were often the only source reporting sensitivity and specificity. The only additional source of grey literature included in the database are WOAH disease cards, which contain information on disinfection procedures for certain diseases, where this was not available in peer-reviewed scientific literature.

3. Results and discussion

In this study we set out to build the foundations for an open-source database of modelling parameters for the purposes of facilitating the development of new models for infectious disease transmission in livestock diseases. To date, although there are a wide range of available studies, including systematic reviews of modelling approaches and transmission parameters, particularly for transboundary diseases and epidemic diseases such as ASF (Hayes et al., 2021), and avian influenza (Kirkeby and Ward, 2022; Lambert et al., 2023), there is no centralised repository collecting modelling parameters for livestock diseases. Thus, PARAMETRA seeks to fill this gap, and serve as a research tool for future modelling.

3.1. Disease prioritisation exercise

To serve as an effective tool for future modelling, however, it was necessary to determine the initial list of diseases with which to populate the database. Due to the setup of the disease prioritisation, the foundation of the database is focused on Europe. Furthermore, the stakeholders surveyed herein represented high-level EU organisations, and thus the focus of the organisations tends to be on Europe, and the EU in particular, as a whole, rather than any specific national or local contexts. This naturally represents a limitation of the exercise, however, this nonetheless served as a first step to guide the initial selection of diseases, and should not be taken as definitive. Thus, in the future, PARAMETRA should include parameters from additional diseases relevant to other regions, and specific countries within different regions of the world. Ongoing follow-up work at the time of writing from the BIOSECURE consortium is currently undertaking a stakeholder survey at the national level for veterinarians and farmers working in the swine, cattle, small ruminant, and poultry sectors. This work will examine in much greater detail the national and international trends in stakeholder attitudes relating to disease risk perception, and attitudes to biosecurity. Thus, such analysis is beyond the scope of the current study.

The prioritisation exercise showed that transboundary diseases and antimicrobial resistance were selected as the most concerning by a plurality of stakeholders for each productive animal categories considered. For cattle, the highest priority disease was reported to be foot and mouth disease, albeit only chosen by a plurality (5/14) of respondents (Fig. 1), with bacterial pathogens such as *Salmonella* Dublin, bovine tuberculosis, and bovine viral diarrhoea virus also reported as the top priority each by 2/14 respondents. For small ruminants, foot and mouth disease was also reported as the highest priority disease. A relatively high number of transboundary diseases were reported as high priority for small ruminants including bluetongue, peste des petits ruminants, and sheep and goat pox virus. For swine, the highest priority disease was reported to be African swine fever, chosen by a majority of respondents (9/13). Highly pathogenic avian influenza likewise was reported as the highest priority poultry disease by all but one of the respondents (10/11). In general, endemic diseases occupied a relatively lower position in the prioritisation exercise than epidemic diseases, with most respondents assigning them to their 2nd or 3rd priority disease, if they were selected as priorities. Further information on the disease prioritisation exercise can be found in Supplementary Materials 1

3.2. Database contents

To populate the database following disease selection (Table 2) we made use of a semi-systematic search strategy (Snyder, 2019). It must be stated that this database does not, therefore, represent a comprehensive repository of all available data, but rather, parameter values which are readily available using standard search terms and extracted primarily from published scientific articles.

PARAMETRA thus primarily contains data from peer reviewed scientific literature based on experimental and field studies, in addition to a significant number of review articles (Fig. 2). While a fully systematic review strategy may well have yielded more detailed information for

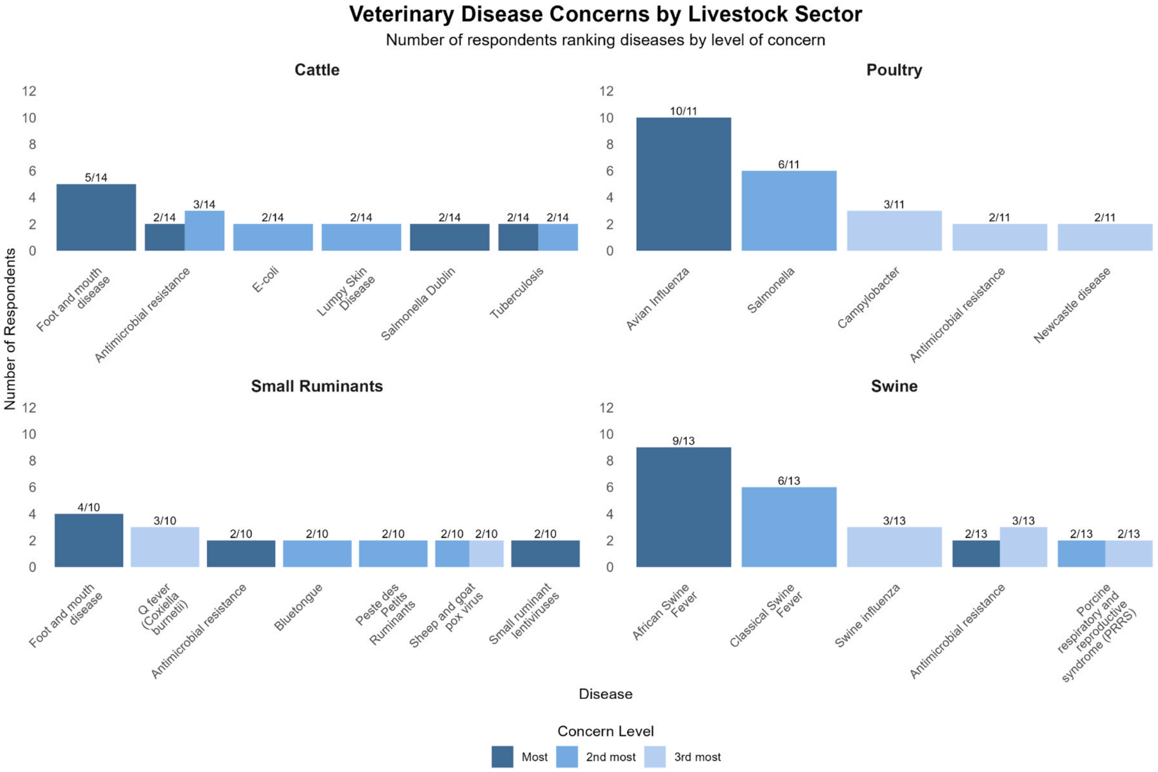


Fig. 1. Summary of the results of the EU high-level stakeholder survey exercise for disease prioritisation. Stakeholders ranked diseases based on the diseases considered most concerning, 2nd most concerning, and 3rd most concerning for their organisations, and sectors. Values above the bars above the bars represent the number of stakeholders who selected the disease/the total number of stakeholders surveyed. The same disease may occur in the most concern, 2nd most concern, and/or 3rd most concern bins, as these results represent an aggregate of all stakeholders results.

Table 2
Summary of diseases selected for inclusion in the PARAMETRA database at the time of publication.

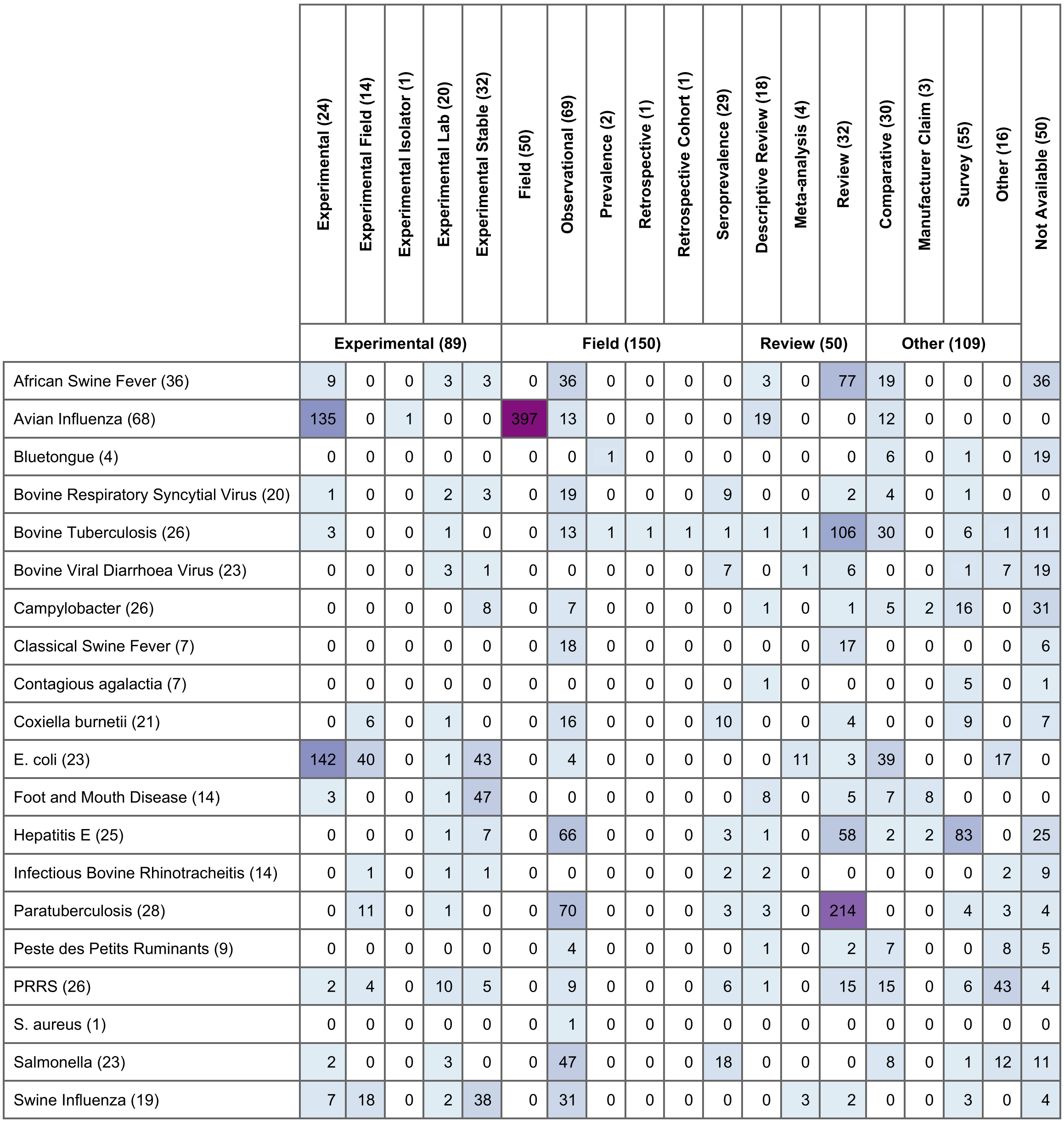
Endemic Diseases	Host
Bovine viral diarrhoea	Cattle
Infectious bovine rhinotracheitis	Cattle
***Salmonella* Dublin**	Cattle
Paratuberculosis (Johne's Disease)	Cattle
Bovine respiratory syncytial virus	Cattle
Tuberculosis (*Mycobacterium*)	Cattle
Porcine respiratory and reproductive syndrome	Pigs
Swine influenza	Pigs
Hepatitis E	Pigs
Campylobacter	Poultry
S. aureus	Cattle
Contagious agalactia (*Mycoplasma*)	Small ruminants
***Coxiella burnetti* (q-fever)**	Small ruminants
Epidemic Diseases	**Host**
Avian influenza	Poultry
Foot and mouth disease	Pigs/cattle/small ruminants
Bluetongue	Cattle/small ruminants
African swine fever	Pigs
Classical Swine Fever	Pigs
Peste des petits ruminants	Small ruminants
Antimicrobial Resistance Pathogens	**Host**
E.coli	Pigs/cattle/poultry/small ruminants

certain diseases, this was not judged to be practical for the purposes of this study, primarily due to the large number of diseases which were targeted for data collection. We have therefore focused on readily available information, rather than engaging in a systematic review of each pathogen. For example, 134 experimental studies available for avian influenza were largely derived from two systematic reviews (Kirkeby and Ward, 2022; Lambert et al., 2023). However, this does not represent an exhaustive review of all available avian influenza reviews, experimental studies, or field studies, but rather represents a foundation of avian influenza parameters with which to populate the database. Furthermore, where parameters were extracted from systematic reviews, the database also links directly to the systematic review itself. This was consciously done to recognise the contribution of these systematic reviews in populating the database, and which are invaluable resources for transboundary diseases (Hayes et al., 2021; Kirkeby and Ward, 2022; Lambert et al., 2023). This is further in line with the fact that the database presented in this publication only represents a starting point, and should be viewed accordingly, and is rather intended to serve as a resource that will grow and evolve through its use by the research community.,This does not detract from the immediate utility of this resource. PARAMETRA already contains a wealth of information, including over 2000 individual epidemiological parameters, including around 1000 transmission parameter and reproduction number values for selected diseases that are of use to disease modellers now.Furthermore, we have built the database to be downloaded directly into programming environments by URL data access. We have tested this using Python and JavaScript, as well as R (see supplementary materials 2). PARAMETRA is also available as an R package (https://biosecure-eu.github.io/parametra/).(https://biosecure-eu.github.io/parametra/). This was done to maximise utility when developing models, allowing researchers to extract specific parameters for diseases of interest without the need for extensive literature review, or even the need to manually scan the database by eye. However, this can still be done, and the currently available version can be accessed and downloaded without using programming environments. To facilitate this, the initial version of PARAMETRA is available directly on GitHub (https://github.com/BIOSECURE-EU/parametra), where each of the individual sub-databases containing transmission parameters, prevalence, diagnostic test efficacy, and so forth, can be directly accessed and extracted. However, it is also of value to note that PARAMETRA contains significant additional information related to the study type, transmission route, serotype of the pathogens, and additional information related to the study within the "notes" section. This allows users to interrogate parameters in more details once they have extracted the sections of the database corresponding to the disease(s) of interest for their study. We stress that the database values should be used with diligence and that the summary values in the database do not excuse modellers from assessing the primary sources.

At the time of writing, the database contains 1025 individual transmission rates, 464 individual parameters for infectious, latent, and incubation period duration, 724 individual parameters for diagnostic test efficacy, and 178 individual parameters for within herd prevalence of endemic diseases (Fig. 3). Transmission rates, infectious, latent, and incubation period duration, diagnostic test efficacy, and within herd prevalence all represent numeric values, with a single parameter per line, designed to be interfaceable directly with programming environments. We have further included, where available, information on strain or serotype, for the relevant pathogen(s) documented within the database. PARAMETRA contains additional information on regional prevalence, the presence of control plans for certain diseases, and information on the disinfection and cleaning procedures required for different diseases. However, these entries direct the user to the article itself, and are designed to aid in future literature reviews and for referencing, rather than directly downloaded into programming environments. Each category of parameters is available as a separate file.

Several interesting observations present themselves from initial analysis of database contents. The first is the tendency of research which estimates relevant parameters to cluster around certain periods of time (Fig. 4). This often corresponds to historical outbreaks. The most obvious example of this is *Coxiella burnetti*, with most relevant studies, or at least those focused on the estimation of parameters in Europe, appearing in the aftermath of the 2008 outbreak in the Netherlands (Courcoul et al., 2010, 2011; Hogerwerf et al., 2013; Pandit et al., 2016). Most subsequent studies appearing later than 2015 focused on Africa (Asamoah et al., 2022), with little information available for the European context. We have, nonetheless, when there is a relative paucity of information for certain diseases, included information from outside Europe. From our observations, there appeared to be a sharp drop in research interest in Europe after 2016, at least regarding the estimation of transmission parameters. Similarly, with African swine fever, there was relatively little research interest in estimating transmission parameters prior to 2015 (Hayes et al., 2021), with only three studies published during that period (Gulenkin et al., 2011; de Carvalho Ferreira et al., 2013; Nigsch et al., 2013). However, following the spread of ASF to Lithuania in 2014, there has been a significant growth in the quantity of publications focusing on the modelling of African swine fever (Hayes et al., 2021). Conversely, for certain other priority diseases, such as small ruminant lentiviruses (Kaba et al., 2023), and sheep and goat pox viruses, and to some extent peste des petits ruminants, there is a paucity of modelling data, despite either ongoing high levels of risk of introduction to Europe (WOAH, 2024; 2025), or high levels of prevalence in the case of small ruminant lentiviruses (Kaba et al., 2023). Although there are some studies available for PPR, including a recently produced stochastic SEIR model (EFSA, 2021), the vast majority of publications focus on African contexts (Hammami, 2016; Fournie et al., 2018).

Thus, research focusing on the estimation of transmission parameters, and building transmission models, tends to follow outbreaks, rather than prevent them. This presents a serious issue for future control of outbreaks. The estimation of transmission parameters is often a time consuming and labour-intensive process, ideally combining both epidemiological and experimental data (Blackwood and Childs, 2018; Chang and de Jong, 2023). Thus, in an ideal situation, this should be directly targeted to emerging diseases, rather than reactively pursued following an outbreak. In the case of emerging diseases, this would necessitateexperimental work aimed directly at parameterisation for

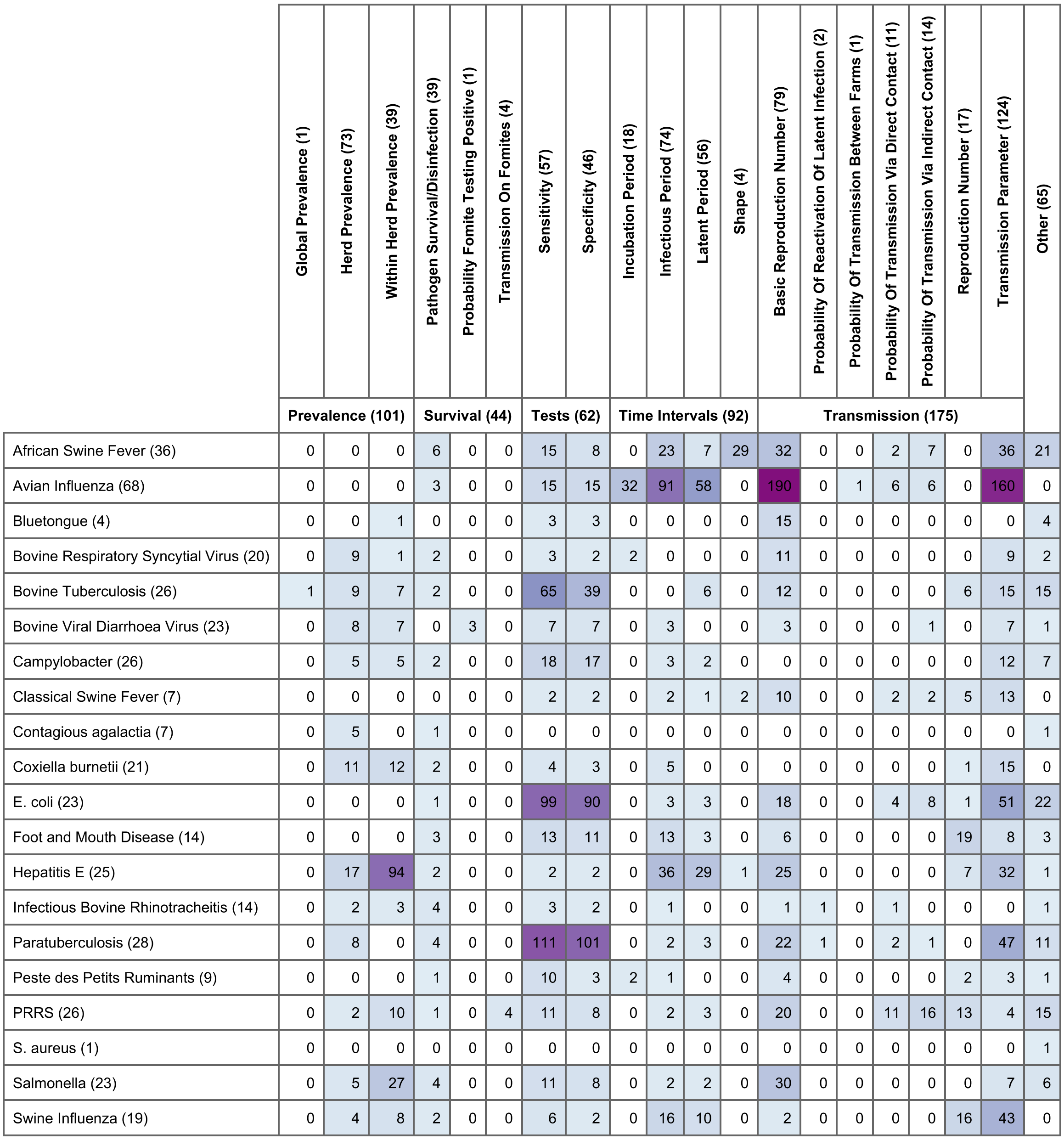


	Experimental (89)					Field (150)						Review (50)			Other (109)				
	Experimental (24)	Experimental Field (14)	Experimental Isolator (1)	Experimental Lab (20)	Experimental Stable (32)	Field (50)	Observational (69)	Prevalence (2)	Retrospective (1)	Retrospective Cohort (1)	Seroprevalence (29)	Descriptive Review (18)	Meta-analysis (4)	Review (32)	Comparative (30)	Manufacturer Claim (3)	Survey (55)	Other (16)	Not Available (50)
African Swine Fever (36)	9	0	0	3	3	0	36	0	0	0	0	3	0	77	19	0	0	0	36
Avian Influenza (68)	135	0	1	0	0	397	13	0	0	0	0	19	0	0	12	0	0	0	0
Bluetongue (4)	0	0	0	0	0	0	0	1	0	0	0	0	0	0	6	0	1	0	19
Bovine Respiratory Syncytial Virus (20)	1	0	0	2	3	0	19	0	0	0	9	0	0	2	4	0	1	0	0
Bovine Tuberculosis (26)	3	0	0	1	0	0	13	1	1	1	1	1	1	106	30	0	6	1	11
Bovine Viral Diarrhoea Virus (23)	0	0	0	3	1	0	0	0	0	0	7	0	1	6	0	0	1	7	19
Campylobacter (26)	0	0	0	0	8	0	7	0	0	0	0	1	0	1	5	2	16	0	31
Classical Swine Fever (7)	0	0	0	0	0	0	18	0	0	0	0	0	0	17	0	0	0	0	6
Contagious agalactia (7)	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	5	0	1
Coxiella burnetii (21)	0	6	0	1	0	0	16	0	0	0	10	0	0	4	0	0	9	0	7
E. coli (23)	142	40	0	1	43	0	4	0	0	0	0	0	11	3	39	0	0	17	0
Foot and Mouth Disease (14)	3	0	0	1	47	0	0	0	0	0	0	8	0	5	7	8	0	0	0
Hepatitis E (25)	0	0	0	1	7	0	66	0	0	0	3	1	0	58	2	2	83	0	25
Infectious Bovine Rhinotracheitis (14)	0	1	0	1	1	0	0	0	0	0	2	2	0	0	0	0	0	2	9
Paratuberculosis (28)	0	11	0	1	0	0	70	0	0	0	3	3	0	214	0	0	4	3	4
Peste des Petits Ruminants (9)	0	0	0	0	0	0	4	0	0	0	0	1	0	2	7	0	0	8	5
PRRS (26)	2	4	0	10	5	0	9	0	0	0	6	1	0	15	15	0	6	43	4
S. aureus (1)	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Salmonella (23)	2	0	0	3	0	0	47	0	0	0	18	0	0	0	8	0	1	12	11
Swine Influenza (19)	7	18	0	2	38	0	31	0	0	0	0	0	3	2	0	0	3	0	4

Fig. 2. Matrix Summary of database contents – types of study. The left-hand column indicates diseases, the top row the type of study. Studies are grouped by experimental, review, field, or other. Numbers indicate the counts for individual parameters present for each disease/study combination, shaded according to their relative counts, darkcounts indicating many parameters, the lighter the shade the fewer parameters, and white indicating no parameters. Number of PARAMETRA entries by pathogen and study type. The numbers in parentheses indicate the count of studies where these entries were collected. Total number of studies: 411.

future modelling, as has been done previously for African swine fever (de Carvalho Ferreira et al., 2013). Alternatively, simulationssimulations of trajectories using numerical experiments in parameter spaces can be an alternative approach to compensate for the lack of data and inform potential disease dynamics. Increased. I research coordination between EU frontier countries and near neighbour countries such as Türkiye, Morocco, and Tunisia would also be of value moving forward, particularly for transboundary diseases, especially in terms of improving surveillance in border regions in the Balkans and Eastern Europe. However, it must also be noted that modelling of past epidemics is of great value. Indeed, modelling of past epidemics is an essential part of understanding future epidemics and guiding future control efforts. Nonetheless, this should be considered synergistically with a deeper consideration of the potential for transboundary diseases, in particular, to emerge and spread from neighbouring regions to Europe.

A final important aspect of the data gathered herein, is the identification of research gaps, particularly for those of priority diseases. An initial observation that became clear during the literature review process was an overall lack of numeric parameterisation for the probability of infection given direct or indirect contacts. This information can be useful in addition to more frequently reported parameters of reproduction number (R; R_0), and transmission rate (β) because it allows for better modelling of specific transmission routes and more precise simulations of control strategies. The transmission rate (β), which was the most widely available transmission parameter based on our searches is furthermore of particular interest as it is usually the combination of the probability of infection given contact with an infectious individual and the contact rate. Probability of infection parameters are available for some diseases, such as avian influenza (Singh et al., 2018), African swine fever (Nigsch et al.,. 2013; Guinat et al., 2016), classical swine fever (Mangen et al., 2002; Weesendorp et al., 2010), porcine reproductive



	Global Prevalence (1)	Herd Prevalence (73)	Within Herd Prevalence (39)	Pathogen Survival/Disinfection (39)	Probability Fomite Testing Positive (1)	Transmission On Fomites (4)	Sensitivity (57)	Specificity (46)	Incubation Period (18)	Infectious Period (74)	Latent Period (56)	Shape (4)	Basic Reproduction Number (79)	Probability Of Reactivation Of Latent Infection (2)	Probability Of Transmission Between Farms (1)	Probability Of Transmission Via Direct Contact (11)	Probability Of Transmission Via Indirect Contact (14)	Reproduction Number (17)	Transmission Parameter (124)	Other (65)
	Prevalence (101)			Survival (44)			Tests (62)		Time Intervals (92)				Transmission (175)							
African Swine Fever (36)	0	0	0	6	0	0	15	8	0	23	7	29	32	0	0	2	7	0	36	21
Avian Influenza (68)	0	0	0	3	0	0	15	15	32	91	58	0	190	0	1	6	6	0	160	0
Bluetongue (4)	0	0	1	0	0	0	3	3	0	0	0	0	15	0	0	0	0	0	0	4
Bovine Respiratory Syncytial Virus (20)	0	9	1	2	0	0	3	2	2	0	0	0	11	0	0	0	0	0	9	2
Bovine Tuberculosis (26)	1	9	7	2	0	0	65	39	0	0	6	0	12	0	0	0	0	6	15	15
Bovine Viral Diarrhoea Virus (23)	0	8	7	0	3	0	7	7	0	3	0	0	3	0	0	0	1	0	7	1
Campylobacter (26)	0	5	5	2	0	0	18	17	0	3	2	0	0	0	0	0	0	0	12	7
Classical Swine Fever (7)	0	0	0	0	0	0	2	2	0	2	1	2	10	0	0	2	2	5	13	0
Contagious agalactia (7)	0	5	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Coxiella burnetii (21)	0	11	12	2	0	0	4	3	0	5	0	0	0	0	0	0	0	1	15	0
E. coli (23)	0	0	0	1	0	0	99	90	0	3	3	0	18	0	0	4	8	1	51	22
Foot and Mouth Disease (14)	0	0	0	3	0	0	13	11	0	13	3	0	6	0	0	0	0	19	8	3
Hepatitis E (25)	0	17	94	2	0	0	2	2	0	36	29	1	25	0	0	0	0	7	32	1
Infectious Bovine Rhinotracheitis (14)	0	2	3	4	0	0	3	2	0	1	0	0	1	1	0	1	0	0	0	1
Paratuberculosis (28)	0	8	0	4	0	0	111	101	0	2	3	0	22	1	0	2	1	0	47	11
Peste des Petits Ruminants (9)	0	0	0	1	0	0	10	3	2	1	0	0	4	0	0	0	0	2	3	1
PRRS (26)	0	2	10	1	0	4	11	8	0	2	3	0	20	0	0	11	16	13	4	15
S. aureus (1)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella (23)	0	5	27	4	0	0	11	8	0	2	2	0	30	0	0	0	0	0	7	6
Swine Influenza (19)	0	4	8	2	0	0	6	2	0	16	10	0	2	0	0	0	0	16	43	0

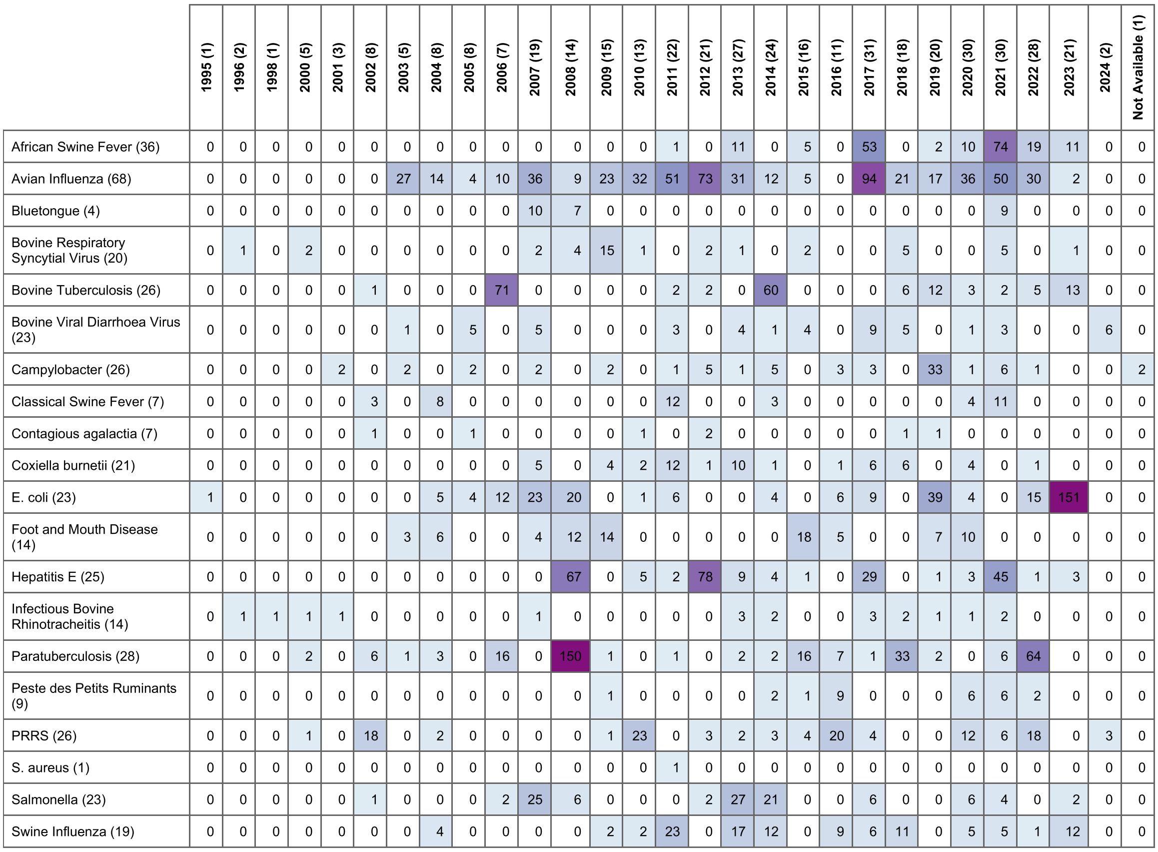
Fig. 3. Matrix Summary of database contents – specific parameters. The left-hand column indicates pathogens and the number of associated studies and the top row the parameter and the number of associated studies. Numbers indicate the counts for individual parameters present for each disease/parameter combination, shaded according to their relative counts, darkcounts indicating more parameters, the lighter the shade the fewer parameters, and white indicating no parameters. Number of PARAMETRA entries by pathogen and parameter. The numbers in parentheses indicate the count of studies where these entries were collected. Total number of studies: 411. Note that one study could report several parameter values, including for the same parameter (e.g. several parameter values for the transmission rate).

and respiratory syndrome (Thakur et al., 2015), infectious bovine rhinotracheitis (Mars et al., 2000), and *E. coli* (Cornick and VuKhac, 2008; de Freitas Costa et al., 2022). We frequently observed, however, when searching for probability of transmission, that many publications made direct mention of probability, but did not provide a numeric parameter, rather a descriptive statement such as “Airborne transmission of FMD is referred to as a low probability – high consequence event” (Brown et al., 2022).

Given the important research gaps identified as part of the process of populating the database, moving forward, PARAMETRA is committed to ensuring the update and evolution of the database to fill these gaps as studies become available. As such, we have included a PARAMETRA submission form (https://ec.europa.eu/eusurvey/runner/parametra-submission) (https://ec.europa.eu/eusurvey/runner/parametra-submission) which will allow prospective contributors to contact the PARAMETRA coordination team with potential submissions (parameter values for existing diseases). Prospective submissions will be considered by the coordination team on an individual basis. In the medium term, we will then consider expansion to include new diseases, based on the engagement received from the wider research community.

4. Concluding remarks

In this study we sought to create a database containing a range of key parameters for diseases affecting livestock in Europe. We focused initially on 20 priority diseases and populated the database with available information using a semi-systematic search strategy. PARAMETRA presents a new open-access resource to speed up the development of disease transmission models in Europe and beyond. This supports the development of tailored disease transmission models in various



	1995 (1)	1996 (2)	1998 (1)	2000 (5)	2001 (3)	2002 (8)	2003 (5)	2004 (8)	2005 (8)	2006 (7)	2007 (19)	2008 (14)	2009 (15)	2010 (13)	2011 (22)	2012 (21)	2013 (27)	2014 (24)	2015 (16)	2016 (11)	2017 (31)	2018 (18)	2019 (20)	2020 (30)	2021 (30)	2022 (28)	2023 (21)	2024 (2)	Not Available (1)
African Swine Fever (36)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	11	0	5	0	53	0	2	10	74	19	11	0	0
Avian Influenza (68)	0	0	0	0	0	0	27	14	4	10	36	9	23	32	51	73	31	12	5	0	94	21	17	36	50	30	2	0	0
Bluetongue (4)	0	0	0	0	0	0	0	0	0	0	10	7	0	0	0	0	0	0	0	0	0	0	0	0	9	0	0	0	0
Bovine Respiratory Syncytial Virus (20)	0	1	0	2	0	0	0	0	0	0	2	4	15	1	0	2	1	0	2	0	0	5	0	0	5	0	1	0	0
Bovine Tuberculosis (26)	0	0	0	0	0	1	0	0	0	71	0	0	0	0	2	2	0	60	0	0	0	6	12	3	2	5	13	0	0
Bovine Viral Diarrhoea Virus (23)	0	0	0	0	0	0	1	0	5	0	5	0	0	0	3	0	4	1	4	0	9	5	0	1	3	0	0	6	0
Campylobacter (26)	0	0	0	0	2	0	2	0	2	0	2	0	2	0	1	5	1	5	0	3	3	0	33	1	6	1	0	0	2
Classical Swine Fever (7)	0	0	0	0	0	3	0	8	0	0	0	0	0	0	12	0	0	3	0	0	0	0	0	4	11	0	0	0	0
Contagious agalactia (7)	0	0	0	0	0	1	0	0	1	0	0	0	0	1	0	2	0	0	0	0	0	1	1	0	0	0	0	0	0
Coxiella burnetii (21)	0	0	0	0	0	0	0	0	0	0	5	0	4	2	12	1	10	1	0	1	6	6	0	4	0	1	0	0	0
E. coli (23)	1	0	0	0	0	0	0	5	4	12	23	20	0	1	6	0	0	4	0	6	9	0	39	4	0	15	151	0	0
Foot and Mouth Disease (14)	0	0	0	0	0	0	3	6	0	0	4	12	14	0	0	0	0	0	18	5	0	0	7	10	0	0	0	0	0
Hepatitis E (25)	0	0	0	0	0	0	0	0	0	0	0	67	0	5	2	78	9	4	1	0	29	0	1	3	45	1	3	0	0
Infectious Bovine Rhinotracheitis (14)	0	1	1	1	1	0	0	0	0	0	1	0	0	0	0	0	3	2	0	0	3	2	1	1	2	0	0	0	0
Paratuberculosis (28)	0	0	0	2	0	6	1	3	0	16	0	150	1	0	1	0	2	2	16	7	1	33	2	0	6	64	0	0	0
Peste des Petits Ruminants (9)	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2	1	9	0	0	0	6	6	2	0	0	0
PRRS (26)	0	0	0	1	0	18	0	2	0	0	0	0	1	23	0	3	2	3	4	20	4	0	0	12	6	18	0	3	0
S. aureus (1)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Salmonella (23)	0	0	0	0	0	1	0	0	0	2	25	6	0	0	0	2	27	21	0	0	6	0	0	6	4	0	2	0	0
Swine Influenza (19)	0	0	0	0	0	0	0	4	0	0	0	0	2	2	23	0	17	12	0	9	6	11	0	5	5	1	12	0	0

Fig. 4. Matrix Summary of database contents. The left-hand column indicates pathogens and the number of associated studies and the top row the year of reporting. Numbers indicate the counts for individual parameters present for each disease/parameter combination, shaded according to their relative counts, darkcounts indicating more parameters, the lighter colours indicating fewer parameters, and white indicating no parameter. Number of PARAMETRA entries by pathogen and year. The numbers in parentheses indicate the count of studies where these entries were collected. Total number of studies: 411.

situations and may contribute to a faster development and implementation of relevant containment protocols to control epidemic diseases in the face of outbreaks or epidemics. The true value of the database will become clear as it is used and expands to contain more parameters and diseases. In the short to medium term, we aim to gauge feedback from the wider research community, and based on the uptake of this tool, will establish procedures for researchers to begin the contribute to the database. This will require the establishment of validation procedures for inclusions from outside the original team, which will also be considered as the tool evolves. Finally, dependent on the uptake and interest in PARAMETRA, permanent web hosting may be considered, allowing the database to develop beyond its current format accessible through GitHub.

CRediT authorship contribution statement

Egil Fischer: Writing – review & editing, Visualization, Validation, Software, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Áine Regan:** Writing – review & editing, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Allepuz Alberto:** Writing – review & editing, Validation, Supervision, Software, Project administration, Methodology, Data curation, Conceptualization. **Jerrold Tubay:** Writing – review & editing, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Johannes Charlier:** Writing – review & editing, Supervision, Software, Project administration, Methodology, Investigation. **Natalia Ciria Artiga:** Writing – review & editing, Visualization, Validation, Software, Resources, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Arvo Viltrop:** Software, Methodology, Data curation. **Jeroen Dewulf:** Writing – review & editing, Validation, Supervision, Resources, Project administration, Methodology, Funding acquisition, Data curation, Conceptualization. **Alistair Antonopoulos:** Writing – review & editing, Writing – original draft, Visualization, Validation, Software, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Francisca Velkers:** Writing – review & editing, Methodology, Investigation, Data curation. **Evelien Biebaut:** Writing – review & editing, Supervision, Project administration, Methodology, Investigation, Data curation, Conceptualization. **Sébastien Lambert:** Writing – review & editing, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Timothée Vergne:** Writing – review & editing, Methodology, Investigation, Data curation, Conceptualization. **Giovanna Ciaravino:** Writing – review & editing, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Brandon Hayes:** Writing – review & editing, Methodology, Investigation, Formal analysis, Data curation, Conceptualization.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.prevetmed.2025.106668.

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