

Research Article

Veterinary Epidemiology and Disease Modelling

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***Related declarations are provided in the final section of this article*

ARTICLE INFORMATION

Received: 20 Jun 2026

Accepted: 15 Jul 2026

Published: 20 Jul 2026

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Abstract

Veterinary epidemiology has undergone significant methodological evolution, transitioning from traditional descriptive approaches to sophisticated quantitative frameworks that integrate spatio-temporal analysis, mechanistic modelling, and advanced computational techniques. This review synthesizes current methodological approaches in veterinary epidemiology and disease modelling, with particular emphasis on the integration of spatio-temporal analysis, transmission dynamics, and surveillance strategies. The emergence of novel pathogens and the increasing complexity of livestock production systems necessitate the adoption of multidisciplinary modelling approaches that can capture the intricate dynamics of disease transmission at various spatial and temporal scales. This article examines the application of Bayesian geostatistical methods, hidden Markov models, and network-based approaches in understanding disease patterns and informing control strategies. Furthermore, the review addresses the challenges of imperfect disease detection and the integration of artificial intelligence in veterinary epidemiological research. The findings highlight the critical importance of combining multiple modelling frameworks to enhance disease surveillance, risk assessment, and the evaluation of intervention strategies in animal populations.

Keywords: Veterinary epidemiology; Disease modelling; Spatio-temporal analysis; Transmission dynamics; Surveillance; Bayesian methods; Network analysis

Introduction

Veterinary epidemiology serves as the cornerstone of animal health management, providing essential frameworks for understanding disease occurrence, distribution, and determinants within animal populations (Thrusfield, 2018). The discipline has undergone remarkable transformation over recent decades, evolving from predominantly descriptive studies to sophisticated quantitative analyses that integrate multiple methodological approaches (Lanzas & Chen, 2015). This evolution has been driven by the increasing recognition that animal diseases pose significant threats not only to livestock production and animal welfare but also to public health through zoonotic transmission pathways (Kleczkowski et al., 2019).

The emergence of novel pathogens has highlighted the urgent need for robust epidemiological frameworks capable of rapid response and effective disease control (Arjkumpa et al., 2022). These emerging threats are compounded by the complexities of modern livestock production systems, which involve intensive animal movements, global trade networks, and changing environmental conditions that influence disease transmission dynamics (Galvis et al., 2022). Consequently, veterinary epidemiologists have increasingly turned to advanced modelling techniques to capture these intricate relationships and inform evidence-based decision-making (Kirkeby et al., 2021).

Spatio-temporal analysis has emerged as a particularly valuable tool in veterinary epidemiology, enabling researchers to identify disease clusters, track pathogen spread, and understand the environmental and management factors that influence disease occurrence (Moustakas, 2017). Bayesian geostatistical approaches have proven especially useful for disease mapping, allowing for the incorporation of spatial correlation and uncertainty quantification in risk assessment (Biggeri et al., 2006). These methods have been successfully applied to various animal diseases, providing critical insights for targeted surveillance and control strategies (Rashid et al., 2019).

Mechanistic transmission modelling represents another powerful approach that has gained prominence in veterinary epidemiology, offering the ability to simulate disease dynamics under different scenarios and evaluate the potential impact of intervention strategies (Kirkeby et al., 2021). These models, which range from simple compartmental frameworks to complex individual-based simulations, have been instrumental in understanding the transmission dynamics of various diseases (Galvis et al., 2022). The integration of mechanistic models with empirical data has enhanced our ability to forecast disease outbreaks and optimize control measures (Rees et al., 2021).

Recent advances in analytical techniques, including hidden Markov models and network analysis, have further expanded the methodological toolkit available to veterinary epidemiologists (Kim et al., 2026; Kinsley et al., 2020). These approaches enable the characterization of complex epidemiological processes, such as disease progression in individual animals and the role of contact networks in pathogen transmission (Kim et al., 2026). Moreover, the emergence of artificial intelligence and machine learning techniques

offers new opportunities for pattern recognition, predictive modelling, and real-time surveillance in veterinary epidemiology (Ezanno et al., 2021).

However, the application of these advanced methodologies is not without challenges (Combelles et al., 2019). Imperfect disease detection, data quality issues, and the inherent complexity of biological systems can compromise the validity of epidemiological inferences (Combelles et al., 2019). The integration of multiple modelling approaches, while offering complementary insights, requires careful consideration of assumptions, parameterization, and validation procedures (Lanzas & Chen, 2015). Furthermore, the translation of modelling results into practical recommendations for disease control and policy development remains a significant challenge in veterinary epidemiology (Kleczkowski et al., 2019).

This review aims to provide a comprehensive synthesis of current methodological approaches in veterinary epidemiology and disease modelling, with particular emphasis on the integration of spatio-temporal analysis, mechanistic transmission models, and emerging computational techniques (Thrusfield, 2018; Lanzas & Chen, 2015). The article examines the application of these methods across different disease systems and epidemiological contexts, highlighting both the strengths and limitations of various approaches (Kirkeby et al., 2021). By synthesizing recent advances and identifying key research gaps, this review seeks to inform future methodological developments and their application to pressing challenges in animal health management (Ezanno et al., 2021).

Literature Review

Fundamentals of Veterinary Epidemiology

1. Epidemiological Principles and Disease Determinants

Veterinary epidemiology is fundamentally concerned with the study of disease patterns and their determinants in animal populations, encompassing both domestic and wild species (Thrusfield, 2018). The discipline rests on the epidemiological triad of host, agent, and environment, recognizing that disease occurrence results from the complex interplay between these three components (Lanzas & Chen, 2015). Understanding these interactions is essential for developing effective disease prevention and control strategies, as interventions can be targeted at any of these three elements (Kirkeby et al., 2021).

The host component encompasses factors related to the animal population, including genetic susceptibility, age structure, nutritional status, and immune competence (Thrusfield, 2018). Host factors can significantly influence disease susceptibility and progression, with certain breeds or age groups exhibiting differential vulnerability to specific pathogens (Arjkumpa et al., 2022). Furthermore, the population density and demographic structure of host populations affect disease transmission dynamics, with higher densities generally facilitating more rapid pathogen spread (Galvis et al., 2022).

The agent component refers to the pathogenic organism or factor responsible for causing disease, encompassing bacteria, viruses, parasites, prions, and toxic agents (Thrusfield, 2018). The biological characteristics of the agent, including its virulence, environmental stability,

transmission mode, and antigenic variability, profoundly influence epidemiological patterns and control possibilities (Rees et al., 2021). For instance, environmentally persistent pathogens may require different control strategies compared to those with limited survival outside the host (Rashid et al., 2019).

The environmental component encompasses both physical and biological factors that influence disease occurrence, including climate conditions, housing systems, management practices, and the presence of wildlife reservoirs (Moustakas, 2017). Environmental factors can affect pathogen survival, vector populations, and host susceptibility, thereby modulating disease transmission dynamics (Biggeri et al., 2006). The importance of environmental factors has been particularly evident in the emergence of vector-borne diseases and those with environmental reservoirs (Arjkumpa et al., 2022).

Disease determinants in veterinary populations operate at multiple levels, from the individual animal to the population, region, and global scale (Kinsley et al., 2020). Individual-level determinants include age, sex, breed, immune status, and management factors, while population-level determinants encompass herd size, production system, biosecurity practices, and contact patterns (Combelles et al., 2019). At broader scales, climatic conditions, landscape features, and trade networks influence regional and global disease patterns (Moustakas, 2017).

The quantitative characterization of disease occurrence relies on fundamental epidemiological measures including incidence, prevalence, morbidity, and mortality rates (Thrusfield, 2018). Incidence measures the rate of new disease cases in a population over time, providing critical information about disease transmission dynamics and risk factors (Galvis et al., 2022). Prevalence, representing the proportion of affected individuals at a given time, reflects the overall disease burden and is particularly useful for chronic or persistent infections (Biggeri et al., 2006).

2. Descriptive and Analytical Epidemiology

Descriptive epidemiology serves as the foundation for understanding disease occurrence, involving the characterization of disease patterns according to person (animal), place, and time (Thrusfield, 2018). This systematic description enables the identification of epidemiological patterns that may suggest causal relationships and inform hypotheses for further investigation (Arjkumpa et al., 2022). Descriptive studies, including outbreak investigations, cross-sectional surveys, and surveillance programs, provide essential baseline data for disease monitoring and the generation of epidemiological hypotheses (Combelles et al., 2019).

Temporal patterns in disease occurrence can reveal important information about disease dynamics, including seasonal variations, long-term trends, and epidemic cycles (Moustakas, 2017). Time-series analysis methods have been developed to identify these patterns and forecast future disease occurrence, supporting early warning systems and preparedness planning (Kim et al., 2026). Spatial patterns, conversely, provide insights into the geographic distribution of diseases and identify areas of elevated risk that may warrant targeted interventions (Biggeri et al., 2006).

Analytical epidemiology extends beyond description to test specific hypotheses about disease determinants, employing study designs such as cohort, case-control, and cross-sectional studies (Thrusfield, 2018). These designs enable the quantification of associations between potential risk factors and disease occurrence, providing evidence for causal relationships (Combelles et al., 2019). Cohort studies follow populations over time to examine the development of disease in relation to exposures, while case-control studies compare exposure histories between affected and unaffected individuals (Galvis et al., 2022).

The identification of risk factors through analytical epidemiology is essential for developing targeted prevention strategies and understanding disease etiology (Rashid et al., 2019). Statistical methods commonly employed include logistic regression, Poisson regression, and Cox proportional hazards models, which allow for the adjustment of confounding factors and the assessment of interaction effects (Combelles et al., 2019). However, the validity of these analyses depends on the accuracy of disease detection and exposure measurement, as imperfect surveillance can introduce bias and obscure true associations (Combelles et al., 2019).

The integration of descriptive and analytical approaches within a comprehensive epidemiological framework has proven particularly valuable for emerging disease investigations (Arjkumpa et al., 2022). For example, the combination of spatial analysis with risk factor identification has enabled the characterization of outbreak patterns and the development of targeted control recommendations (Arjkumpa et al., 2022). Similarly, analytical studies of various disease transmissions have informed vaccination strategies and biosecurity measures in affected regions (Galvis et al., 2022).

Spatio-Temporal Methods in Veterinary Epidemiology

1. Spatial Analysis Techniques

Spatial analysis has become an indispensable component of veterinary epidemiology, providing tools to characterize disease distribution, identify clusters, and investigate environmental risk factors (Biggeri et al., 2006). The recognition that disease occurrence is often spatially structured, with cases clustering due to shared environmental exposures or contagious transmission, has motivated the development of specialized statistical methods (Moustakas, 2017). These methods range from simple mapping techniques to sophisticated geostatistical models that incorporate spatial correlation structures (Biggeri et al., 2006).

Point pattern analysis examines the spatial distribution of disease cases relative to underlying population distributions, using methods such as kernel density estimation and K-function analysis (Moustakas, 2017). Kernel density estimation produces smoothed maps of disease intensity, enabling the visualization of spatial variation in disease risk (Arjkumpa et al., 2022). This technique has been widely applied in veterinary epidemiology to identify disease hotspots and assess the effectiveness of control measures (Biggeri et al., 2006).

Cluster detection methods, including scan statistics and spatial autocorrelation measures, provide statistical tests for the presence of spatial clustering (Moustakas, 2017). The spatial scan statistic has been particularly valuable for detecting disease clusters and evaluating the statistical significance of observed spatial patterns (Arjkumpa et al., 2022). This method has

been applied to various veterinary diseases, including lumpy skin disease and African swine fever in wild boar populations (Arjkumpa et al., 2022; Gervasi et al., 2019).

Geostatistical approaches explicitly model spatial dependence using variogram analysis and kriging interpolation (Biggeri et al., 2006). These methods assume that observations closer in space are more similar than those further apart, enabling the prediction of disease risk at unsampled locations (Combelles et al., 2019). Bayesian geostatistical models extend these approaches by incorporating prior information and quantifying estimation uncertainty, providing a flexible framework for disease mapping (Biggeri et al., 2006).

Spatial regression models enable the investigation of environmental and management factors associated with disease occurrence while accounting for spatial autocorrelation (Combelles et al., 2019). These models, which include spatial lag and spatial error specifications, address the violation of independence assumptions in conventional regression analyses (Moustakas, 2017). The application of spatial regression has identified important risk factors for various animal diseases, including the role of environmental variables in disease distribution (Biggeri et al., 2006).

2. Temporal Analysis and Time-Series Approaches

Temporal analysis examines the evolution of disease occurrence over time, providing insights into transmission dynamics, seasonality, and long-term trends (Moustakas, 2017). Time-series methods have been extensively applied in veterinary epidemiology for disease surveillance, outbreak detection, and forecasting (Kim et al., 2026). The analysis of temporal patterns is essential for understanding disease dynamics and evaluating the impact of control interventions (Galvis et al., 2022).

Seasonal decomposition methods partition time-series data into trend, seasonal, and residual components, enabling the characterization of regular patterns in disease occurrence (Moustakas, 2017). These methods have revealed important seasonal patterns in many animal diseases, informing the timing of preventive measures and surveillance activities (Arjkumpa et al., 2022). The identification of seasonal peaks in disease incidence can guide resource allocation and risk communication efforts (Galvis et al., 2022).

Autoregressive integrated moving average (ARIMA) models and their extensions provide a framework for time-series forecasting, using past observations to predict future disease occurrence (Moustakas, 2017). These models have been applied to forecast disease incidence in veterinary populations, supporting early warning systems and preparedness planning (Kim et al., 2026). However, the accuracy of these forecasts depends on the availability of high-quality surveillance data and the stability of underlying epidemiological processes (Combelles et al., 2019).

Hidden Markov models (HMMs) represent a more sophisticated approach to temporal analysis, enabling the characterization of unobserved disease states from observed data sequences (Kim et al., 2026). These models have been applied to detect disease progression from animal movement data, providing insights into behavioral changes associated with infection (Kim et al., 2026). The flexibility of HMMs in accommodating multiple observational streams makes

them valuable for integrating diverse data sources in veterinary epidemiological investigations (Ezanno et al., 2021).

The integration of temporal and spatial analyses, known as spatio-temporal modeling, provides a comprehensive framework for understanding disease dynamics in both dimensions (Moustakas, 2017). Spatio-temporal models enable the characterization of disease spread patterns, identification of risk periods, and evaluation of intervention impacts across space and time (Arjkumpa et al., 2022). These models have been instrumental in understanding the spread of emerging diseases and evaluating the effectiveness of control strategies (Galvis et al., 2022).

3. Bayesian Geostatistical Approaches

Bayesian geostatistical methods have emerged as a powerful framework for disease mapping and risk assessment in veterinary epidemiology (Biggeri et al., 2006). These approaches combine the strengths of geostatistical modeling with Bayesian inference, enabling the incorporation of prior information and the quantification of estimation uncertainty (Combelles et al., 2019). The Bayesian framework provides a coherent approach to handling spatial data, including irregularly sampled locations and missing values (Biggeri et al., 2006).

The fundamental structure of Bayesian geostatistical models includes a spatial random effect that captures unmeasured spatial variation in disease risk (Biggeri et al., 2006). This spatial effect is typically modeled using Gaussian processes with specified correlation functions, enabling the prediction of risk at unsampled locations (Combelles et al., 2019). The incorporation of fixed effects for measured risk factors allows for the investigation of environmental and management determinants of disease occurrence (Biggeri et al., 2006).

One of the key advantages of Bayesian methods is their ability to formally incorporate uncertainty in all model parameters, providing probabilistic statements about disease risk (Combelles et al., 2019). This uncertainty quantification is particularly valuable for decision-making, enabling the assessment of confidence in risk estimates and the identification of areas requiring additional data collection (Biggeri et al., 2006). The Bayesian approach also facilitates the integration of diverse data sources, including expert opinion and prior studies, through the specification of prior distributions (Combelles et al., 2019).

The application of Bayesian geostatistical methods to veterinary disease mapping has provided important insights into disease distribution and risk factors (Biggeri et al., 2006). These methods have been applied to various diseases, including parasitic infections and vector-borne diseases, identifying environmental risk factors and areas of elevated risk (Rashid et al., 2019). The spatial predictions from these models have informed surveillance strategies and targeted control interventions, contributing to more efficient disease management (Biggeri et al., 2006).

Advanced Bayesian geostatistical models incorporate additional complexity, including space-time interactions, nonstationarity, and multiple disease outcomes (Biggeri et al., 2006). Space-time models enable the characterization of changes in spatial patterns over time, providing insights into disease spread dynamics and the impact of environmental changes (Moustakas, 2017). The development of computationally efficient algorithms has facilitated the application of these complex models to large veterinary datasets (Combelles et al., 2019).

Mechanistic Disease Transmission Modelling

1. Compartmental Models

Compartmental models represent the foundation of mechanistic disease transmission modelling, partitioning host populations into discrete disease states based on infection status (Kirkeby et al., 2021). The classic susceptible-infected-recovered (SIR) model and its variants provide a mathematical framework for understanding disease dynamics and evaluating intervention strategies (Galvis et al., 2022). These models have been extensively applied to veterinary diseases, including various disease transmissions in swine populations and livestock (Galvis et al., 2022).

The structure of compartmental models depends on the specific disease characteristics and host population dynamics under investigation (Kirkeby et al., 2021). The SIR model assumes that individuals move sequentially through susceptible, infected, and recovered states, with transmission occurring through contact between susceptible and infected individuals (Galvis et al., 2022). Modifications to this basic structure include the addition of exposed (E) states for diseases with latent periods, maternal immunity for neonatal diseases, and vaccination compartments for evaluating immunization strategies (Kirkeby et al., 2021).

The transmission rate in compartmental models captures the efficiency of disease spread, depending on contact rates, transmission probability, and infectious period (Galvis et al., 2022). The basic reproduction number (R_0), representing the average number of secondary infections produced by a single infected individual in a fully susceptible population, provides a key threshold parameter (Kirkeby et al., 2021). R_0 values exceeding one indicate the potential for epidemic spread, while values below one suggests disease extinction (Galvis et al., 2022).

The parameterization of compartmental models requires estimates of various epidemiological parameters, including transmission rates, infectious periods, and latent periods (Kirkeby et al., 2021). These parameters can be derived from experimental studies, field observations, or through model fitting to surveillance data (Galvis et al., 2022). The uncertainty in parameter estimates can be addressed through sensitivity analysis and Bayesian inference approaches (Combelles et al., 2019).

Compartmental models have proven valuable for evaluating intervention strategies, enabling the comparison of different control options under various scenarios (Kirkeby et al., 2021). These models can assess the impact of vaccination, culling, movement restrictions, and biosecurity measures on disease dynamics (Galvis et al., 2022). The results have informed policy decisions in numerous disease outbreaks, contributing to more effective and efficient disease control (Kirkeby et al., 2021).

2. Individual-Based and Agent-Based Models

Individual-based models (IBMs) represent an extension of compartmental modeling, explicitly simulating individual animals with their unique characteristics and interactions (Kirkeby et al., 2021). These models provide greater biological realism by capturing heterogeneity in host susceptibility, contact patterns, and disease outcomes (Galvis et al., 2022). The increasing

availability of computational power has facilitated the development and application of IBMs to complex veterinary disease problems (Lanzas & Chen, 2015).

Agent-based models (ABMs) represent a specific class of IBM where individuals are modeled as autonomous agents with defined behavioral rules (Kirkeby et al., 2021). These models enable the simulation of individual decision-making, movement, and interactions, providing a flexible framework for studying complex epidemiological systems (Lanzas & Chen, 2015). ABMs have been applied to various veterinary diseases, including foot-and-mouth disease, avian influenza, and porcine reproductive and respiratory syndrome virus (Galvis et al., 2022).

The individual-based approach allows for the explicit representation of population structure, including age structure, production stages, and contact networks (Kirkeby et al., 2021). This granularity enables the investigation of targeted interventions, such as age-specific vaccination strategies or culling of high-risk groups (Galvis et al., 2022). The ability to simulate individual heterogeneity has revealed important insights into disease dynamics that are obscured in aggregate compartmental models (Lanzas & Chen, 2015).

The parameterization and validation of IBMs require detailed data on individual animal characteristics, movements, and contacts (Kirkeby et al., 2021). The availability of such data has improved with advances in animal identification technologies and surveillance systems (Galvis et al., 2022). However, the data requirements of IBMs can be substantial, potentially limiting their application in data-poor settings (Combelles et al., 2019).

The integration of IBMs with other modeling approaches, including spatial and network models, has enhanced their analytical power (Kinsley et al., 2020). Spatially explicit IBMs enable the simulation of disease spread across landscapes, incorporating the effects of environmental heterogeneity and animal movements (Kirkeby et al., 2021). Network-based IBMs capture the structure of contact patterns, enabling the investigation of targeted surveillance and control strategies based on network topology (Kinsley et al., 2020).

3. Network-Based Approaches

Network analysis has emerged as a powerful approach for understanding disease transmission in animal populations, focusing on the structure of contacts that facilitate pathogen spread (Kinsley et al., 2020). The recognition that contacts patterns in animal populations are often structured rather than random has motivated the application of network theory to veterinary epidemiology (Kinsley et al., 2020). Network models enable the identification of key individuals or premises that play central roles in transmission, informing targeted intervention strategies (Kinsley et al., 2020).

Animal contact networks can be constructed from various data sources, including movement records, proximity sensors, and observational studies (Kinsley et al., 2020). Livestock movements between farms, trade networks, and wildlife contacts provide the structure for disease transmission at the population level (Kinsley et al., 2020). Wildlife contact networks, involving shared habitats and resources, are particularly relevant for diseases with wildlife reservoirs (Gervasi et al., 2019).

Network metrics, including degree centrality, betweenness centrality, and closeness centrality, quantify the importance of individual nodes in the network (Kinsley et al., 2020). High-degree nodes, representing individuals or premises with many contacts, are particularly important for disease spread and control (Kinsley et al., 2020). Betweenness centrality identifies nodes that serve as bridges between different parts of the network, playing critical roles in transmission across the population (Kinsley et al., 2020).

Multilayer and multiplex networks extend simple network representations to capture multiple types of contacts or interactions simultaneously (Kinsley et al., 2020). These approaches enable the characterization of complex epidemiological systems where different contact types contribute to disease transmission (Kinsley et al., 2020). The application of multilayer networks has revealed how different contact processes interact to influence disease dynamics, informing the design of comprehensive control strategies (Kinsley et al., 2020).

Network-based disease models simulate transmission along network edges, incorporating the structure of contacts into disease spread predictions (Kinsley et al., 2020). These models can identify optimal surveillance targets and control strategies based on network characteristics, maximizing the efficiency of limited resources (Kinsley et al., 2020). Network-based interventions, including the targeting of high-degree nodes or the removal of critical bridges, have demonstrated effectiveness in simulation studies and field applications (Kinsley et al., 2020).

Integration of Multiple Modelling Approaches

1. One Health and Transdisciplinary Frameworks

The One Health approach recognizes the interconnectedness of human, animal, and environmental health, providing a framework for addressing complex health challenges through transdisciplinary collaboration (Kleczkowski et al., 2019). This perspective acknowledges that many pathogens affect multiple host species and that environmental factors play critical roles in disease emergence and transmission (Kleczkowski et al., 2019). Veterinary epidemiology has increasingly embraced One Health principles, developing integrated approaches that consider the full ecological context of disease systems (Kleczkowski et al., 2019).

The integration of veterinary, medical, and environmental epidemiology requires the development of unified modelling frameworks that can capture cross-species transmission and shared environmental determinants (Kleczkowski et al., 2019). Such frameworks must accommodate the different population structures, surveillance systems, and intervention strategies that characterize human and animal health sectors (Kleczkowski et al., 2019). The development of joint disease models has enabled the assessment of interventions that affect both human and animal health, providing comprehensive evaluations of control strategies (Rees et al., 2021).

Environmental components of One Health models incorporate factors such as climate, land use, and ecosystem changes that influence disease dynamics (Kleczkowski et al., 2019). Climate-sensitive disease models have been developed to assess the impact of environmental change on disease emergence and spread, supporting adaptation strategies (Rees et al., 2021). The

integration of environmental data into veterinary epidemiological models has improved the understanding of vector-borne diseases, environmentally persistent pathogens, and wildlife diseases (Rees et al., 2021; Rashid et al., 2019).

Transdisciplinary approaches that engage stakeholders from multiple sectors enhance the relevance and applicability of modelling results (Kleczkowski et al., 2019). The involvement of policymakers, industry representatives, and local communities in model development and interpretation improves the translation of results into practice (Kleczkowski et al., 2019). Participatory modelling approaches have been successfully applied to various animal health problems, incorporating local knowledge and addressing stakeholder concerns (Kirkeby et al., 2021).

The integration of multiple modelling approaches within One Health frameworks has demonstrated value for understanding complex disease systems (Kleczkowski et al., 2019). Examples include integrated models of zoonotic disease transmission that incorporate human behavior, livestock management, and environmental factors (Rees et al., 2021). These comprehensive models have provided insights into disease persistence, control effectiveness, and the potential impacts of environmental or management changes (Kleczkowski et al., 2019).

2. Data Integration and Multi-Model Inference

The integration of diverse data sources has become increasingly important in veterinary epidemiology, enabling the synthesis of information from surveillance systems, experimental studies, and field observations (Combelles et al., 2019). Data integration approaches combine evidence from multiple sources, improving parameter estimates and enhancing model validity (Combelles et al., 2019). Bayesian methods provide a natural framework for data integration, enabling the incorporation of information through prior distributions and hierarchical modeling (Biggeri et al., 2006).

Multi-model inference approaches consider evidence from multiple competing models rather than relying on a single best model (Combelles et al., 2019). Model averaging techniques combine predictions from different models, accounting for model selection uncertainty and improving prediction accuracy (Combelles et al., 2019). The application of multi-model inference to veterinary epidemiological problems has provided more robust conclusions than single-model approaches (Kirkeby et al., 2021).

Ensemble modelling approaches, which combine predictions from multiple individual models, have gained popularity in various epidemiological applications (Kleczkowski et al., 2019). These approaches reduce the bias associated with individual model structures and parameters, providing more robust predictions (Kirkeby et al., 2021). Ensemble methods have been applied to disease forecasting, risk assessment, and the evaluation of control strategies, demonstrating improved performance compared to individual models (Kleczkowski et al., 2019).

The integration of mechanistic models with statistical approaches, known as mechanistic-statistical models, provides a framework that combines process-based understanding with empirical data (Kirkeby et al., 2021). These models incorporate biological mechanisms within statistical frameworks, enabling the estimation of mechanistic parameters from observational

data (Galvis et al., 2022). The approach has been applied to various veterinary diseases, providing insights into transmission dynamics while accounting for observation processes (Combelles et al., 2019).

The development of standardized data formats and sharing platforms has facilitated data integration in veterinary epidemiology (Kinsley et al., 2020). Initiatives to harmonize surveillance data, movement records, and epidemiological parameters have enabled comparative analyses and the development of large-scale models (Kinsley et al., 2020). However, challenges remain in addressing data quality issues, privacy concerns, and the integration of data from diverse sources (Combelles et al., 2019).

3. Model Calibration and Validation

Model calibration and validation are essential components of rigorous epidemiological modeling, ensuring that models accurately represent real-world disease dynamics (Kirkeby et al., 2021). Calibration involves adjusting model parameters to match observed data, often employing optimization or Bayesian approaches (Galvis et al., 2022). Validation assesses model performance on independent data, testing the model's ability to predict disease patterns under different conditions (Kirkeby et al., 2021).

Bayesian calibration methods provide a formal approach to parameter estimation, combining prior information with observed data to obtain posterior distributions (Combelles et al., 2019). These methods quantify parameter uncertainty, enabling the assessment of prediction uncertainty and the identification of data gaps (Biggeri et al., 2006). Bayesian calibration has been applied to various veterinary disease models, providing robust parameter estimates and uncertainty quantification (Galvis et al., 2022).

Cross-validation techniques assess model performance by fitting the model to a subset of data and evaluating predictions on the remaining data (Kirkeby et al., 2021). This approach provides a robust assessment of model generalizability, identifying potential overfitting and evaluating prediction accuracy (Combelles et al., 2019). Cross-validation has been widely applied in veterinary epidemiology to evaluate disease prediction models and risk assessment tools (Kirkeby et al., 2021).

Sensitivity analysis examines the influence of model parameters on outputs, identifying key parameters that drive model predictions (Kirkeby et al., 2021). Global sensitivity analyses consider the combined effects of multiple parameters, providing a comprehensive assessment of model behavior (Galvis et al., 2022). Sensitivity analysis is essential for identifying research priorities and evaluating the robustness of model conclusions (Kirkeby et al., 2021).

Goodness-of-fit measures provide quantitative assessments of how well models reproduce observed data (Kirkeby et al., 2021). Deviance information criteria (DIC), Watanabe-Akaike information criteria (WAIC), and other information-theoretic measures enable the comparison of competing models (Combelles et al., 2019). The selection of appropriate goodness-of-fit

measures depends on the model structure, data characteristics, and the specific objectives of the analysis (Kirkeby et al., 2021).

Surveillance and Disease Detection

1. Active and Passive Surveillance

Surveillance systems serve as the foundation for disease detection, monitoring, and control in veterinary populations (Gervasi et al., 2019). Active surveillance involves the systematic collection of data according to a defined protocol, often targeting specific diseases or populations (Gervasi et al., 2019). Passive surveillance relies on the reporting of disease events by veterinarians, farmers, or diagnostic laboratories, providing broader coverage but potentially lower sensitivity (Gervasi et al., 2019).

Active surveillance programs have been implemented for various diseases of veterinary importance, providing data for disease monitoring and freedom from disease declarations (Gervasi et al., 2019). The design of active surveillance systems requires careful consideration of sampling strategies, diagnostic tests, and target populations (Thrusfield, 2018). Risk-based surveillance approaches target high-risk populations or regions, improving the efficiency of surveillance activities (Gervasi et al., 2019).

Passive surveillance systems provide essential data for disease monitoring, leveraging existing diagnostic and reporting infrastructure (Gervasi et al., 2019). However, passive surveillance is subject to reporting biases, with diseases of greater economic importance or clinical severity more likely to be reported (Combelles et al., 2019). The sensitivity of passive surveillance depends on clinical awareness, diagnostic capacity, and reporting incentives (Gervasi et al., 2019).

The integration of active and passive surveillance approaches can provide complementary information, improving overall surveillance system performance (Gervasi et al., 2019). Active surveillance can validate passive surveillance data, identify underreporting, and provide data for sensitivity assessments (Gervasi et al., 2019). The combination of surveillance approaches has been particularly valuable for emerging disease detection and for diseases with non-specific clinical signs (Arjkumpa et al., 2022).

The evaluation of surveillance system performance requires the assessment of sensitivity, specificity, timeliness, and representativeness (Gervasi et al., 2019). System sensitivity, representing the probability of detecting disease if it is present, is critical for confirming freedom from disease (Gervasi et al., 2019). Surveillance system evaluations have informed the improvement of disease detection capabilities and the allocation of surveillance resources (Thrusfield, 2018).

2. Imperfect Detection and Diagnostic Accuracy

Imperfect disease detection represents a significant challenge in veterinary epidemiology, affecting the accuracy of disease occurrence estimates and the power to identify risk factors (Combelles et al., 2019). Diagnostic tests have imperfect sensitivity and specificity, leading to

misclassification of disease status (Combelles et al., 2019). Additionally, surveillance systems may fail to detect all disease events, introducing underreporting bias (Gervasi et al., 2019).

The impact of imperfect detection on epidemiological investigations depends on the characteristics of the disease and the surveillance system (Combelles et al., 2019). Low sensitivity leads to underestimation of disease occurrence and may obscure relationships between risk factors and disease (Combelles et al., 2019). Low specificity can introduce false positives, potentially leading to overestimation of disease occurrence and misleading risk factor identification (Combelles et al., 2019).

Bayesian methods provide a framework for accounting for imperfect detection, incorporating diagnostic test characteristics and surveillance sensitivity in disease prevalence estimation (Combelles et al., 2019). Latent class models enable the estimation of disease prevalence and test characteristics without a gold standard, using multiple tests with different properties (Combelles et al., 2019). These methods have been applied to various veterinary diseases, providing more accurate disease occurrence estimates than naïve approaches (Combelles et al., 2019).

The modeling of surveillance sensitivity in disease risk assessment accounts for the probability of disease detection given its presence (Gervasi et al., 2019). Incorporating surveillance sensitivity into epidemiological models enables the estimation of true disease occurrence from imperfect surveillance data (Combelles et al., 2019). This approach has been applied to assess the likelihood of freedom from disease and to evaluate the effectiveness of surveillance systems (Gervasi et al., 2019).

The design of surveillance systems can be optimized to maximize detection sensitivity within resource constraints (Gervasi et al., 2019). Risk-based surveillance strategies target high-risk populations or regions, increasing the probability of detecting disease if it occurs (Gervasi et al., 2019). The evaluation of optimal surveillance designs has informed the improvement of disease detection capabilities in various veterinary contexts (Thrusfield, 2018).

3. Data Mining and Early Warning Systems

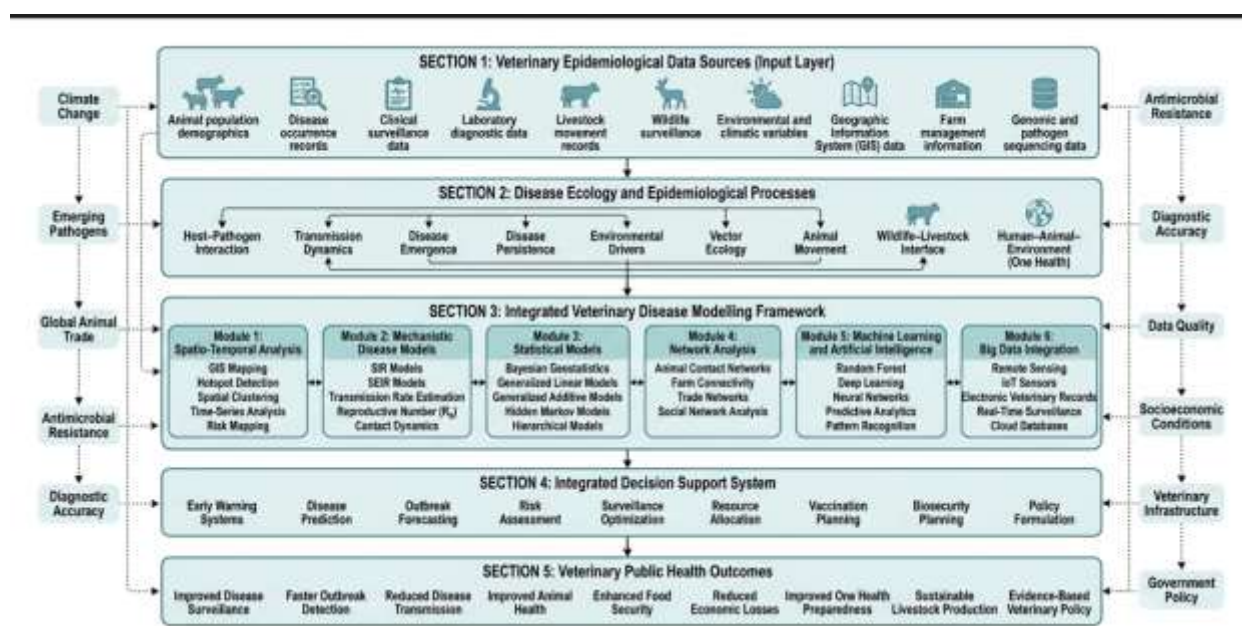
Data mining approaches have emerged as valuable tools for disease surveillance, enabling the detection of patterns and anomalies in large epidemiological datasets (Moustakas, 2017). These methods include classification, clustering, and anomaly detection algorithms that can identify disease outbreaks and emerging threats (Moustakas, 2017). The application of data mining to veterinary epidemiological data has improved the timeliness of outbreak detection and the identification of spatial-temporal patterns (Arjkumpa et al., 2022).

Spatio-temporal data mining methods identify disease clusters and characterize spread patterns from surveillance data (Moustakas, 2017). Scan statistics, kernel density estimation, and space-time permutation methods have been applied to detect disease clusters and assess their statistical significance (Arjkumpa et al., 2022). These methods have been instrumental in the early detection of disease outbreaks and the characterization of epidemic spread patterns (Moustakas, 2017).

Early warning systems combine surveillance data with analytical methods to provide advance warning of disease emergence or epidemic events (Gervasi et al., 2019). These systems typically employ threshold-based alerts, statistical process control, or machine learning algorithms to detect deviations from expected disease patterns (Moustakas, 2017). Early warning systems have been developed for various veterinary diseases, supporting rapid response and containment (Gervasi et al., 2019).

Machine learning algorithms, including random forests, support vector machines, and neural networks, have been applied to disease surveillance and risk prediction (Ezanno et al., 2021). These methods can identify complex patterns in high-dimensional data, improving the detection of disease outbreaks and the prediction of disease occurrence (Ezanno et al., 2021). The application of artificial intelligence in veterinary epidemiology has expanded with the increasing availability of data and computational resources (Ezanno et al., 2021).

The development of integrated surveillance platforms that combine multiple data sources and analytical methods has enhanced disease detection capabilities (Moustakas, 2017). These platforms integrate clinical surveillance, laboratory data, and environmental information, providing a comprehensive view of disease patterns (Moustakas, 2017). The integration of diverse data sources and analytical methods has improved the timeliness and accuracy of disease detection, supporting more effective response to disease threats (Gervasi et al., 2019).



Integrated conceptual framework illustrating the relationships between epidemiological data sources, disease ecology, advanced modelling techniques, artificial intelligence, surveillance systems, and decision-support mechanisms for improving disease prediction, risk assessment, and veterinary public health outcomes.

Results

1. Synthesis of Methodological Approaches

The comprehensive review of veterinary epidemiological literature reveals a diverse array of methodological approaches that have been developed and applied to understand disease dynamics in animal populations (Thrusfield, 2018; Lanzas & Chen, 2015). These methodologies range from traditional descriptive epidemiological techniques to sophisticated computational models that integrate multiple data sources and analytical frameworks (Kirkeby et al., 2021). The evolution of these approaches reflects the increasing complexity of disease systems and the growing demand for evidence-based decision-making in animal health management (Kleczkowski et al., 2019).

Spatio-temporal methods have demonstrated particular utility in characterizing disease distribution, identifying clusters, and investigating environmental risk factors (Moustakas, 2017; Biggeri et al., 2006). These methods enable researchers to visualize disease patterns across geographic space and track changes over time, providing critical insights for targeted surveillance and control interventions (Arjkumpa et al., 2022). The application of spatial scan statistics has proven especially valuable for detecting disease outbreaks and evaluating the statistical significance of observed clustering patterns (Moustakas, 2017). Kernel density estimation techniques have facilitated the identification of disease hotspots, enabling resource allocation to areas of highest risk (Biggeri et al., 2006). Furthermore, spatial regression models have enabled the investigation of environmental and management factors associated with disease occurrence while accounting for spatial autocorrelation (Combelles et al., 2019). The integration of geographic information systems (GIS) with epidemiological data has revolutionized disease mapping capabilities, allowing for the overlay of multiple data layers to identify complex risk factor interactions (Moustakas, 2017).

Bayesian geostatistical approaches have emerged as a preferred framework for disease mapping, providing robust estimates of disease risk while accounting for spatial correlation and uncertainty (Biggeri et al., 2006; Combelles et al., 2019). These approaches combine the strengths of geostatistical modeling with Bayesian inference, enabling the incorporation of prior information and the quantification of estimation uncertainty (Biggeri et al., 2006). The fundamental structure of Bayesian geostatistical models includes spatial random effects that capture unmeasured spatial variation in disease risk, providing more accurate predictions at unsampled locations (Combelles et al., 2019). The incorporation of fixed effects for measured risk factors allows for the simultaneous investigation of environmental and management determinants of disease occurrence (Biggeri et al., 2006). Advanced Bayesian geostatistical models have incorporated space-time interactions, enabling the characterization of changes in spatial patterns over time and providing insights into disease spread dynamics (Moustakas, 2017). The development of computationally efficient algorithms, such as integrated nested Laplace approximations (INLA), has facilitated the application of these complex models to large veterinary datasets (Combelles et al., 2019). Bayesian methods have also proven valuable for integrating diverse data sources, including expert opinion and prior studies, through the specification of prior distributions (Biggeri et al., 2006). The uncertainty quantification provided by Bayesian approaches has been particularly valuable for decision-making, enabling the assessment of confidence in risk estimates and the identification of areas requiring additional data collection (Combelles et al., 2019).

Mechanistic transmission models have provided complementary insights into disease dynamics, enabling the simulation of disease spread under different scenarios and the evaluation of intervention strategies (Kirkeby et al., 2021; Galvis et al., 2022). Compartmental models, including the classic susceptible-infected-recovered (SIR) framework and its variants, have provided a tractable approach for understanding population-level disease dynamics (Galvis et al., 2022). These models have been parameterized using data from experimental studies, field observations, and surveillance systems, enabling the estimation of key epidemiological parameters such as transmission rates and the basic reproduction number (Kirkeby et al., 2021). The basic reproduction number (R_0) has emerged as a critical threshold parameter, with values exceeding one indicating epidemic potential and values below one suggesting disease extinction (Galvis et al., 2022). Sensitivity analyses of compartmental models have identified key parameters driving disease dynamics, informing research priorities and data collection efforts (Kirkeby et al., 2021). The extension of compartmental models to include vaccination compartments has enabled the evaluation of immunization strategies and the identification of vaccination thresholds for disease control (Galvis et al., 2022).

Individual-based models (IBMs) have provided greater biological realism by explicitly simulating individual animals with their unique characteristics and interactions (Kirkeby et al., 2021; Lanzas & Chen, 2015). These models have captured heterogeneity in host susceptibility, contact patterns, and disease outcomes that are obscured in aggregate compartmental models (Galvis et al., 2022). The increasing availability of computational power has facilitated the development and application of IBMs to complex veterinary disease problems, including foot-and-mouth disease, avian influenza, and porcine reproductive and respiratory syndrome virus (Lanzas & Chen, 2015). Agent-based models (ABMs), a specific class of IBM, have enabled the simulation of individual decision-making, movement, and interactions, providing a flexible framework for studying complex epidemiological systems (Kirkeby et al., 2021). The explicit representation of population structure in IBMs, including age structure, production stages, and contact networks, has enabled the investigation of targeted interventions such as age-specific vaccination strategies or culling of high-risk groups (Galvis et al., 2022). The parameterization and validation of IBMs have required detailed data on individual animal characteristics, movements, and contacts, which have become increasingly available through advances in animal identification technologies and surveillance systems (Kirkeby et al., 2021). However, the substantial data requirements of IBMs have limited their application in data-poor settings, highlighting the need for continued investment in surveillance infrastructure (Combelles et al., 2019).

Network-based approaches have enhanced the understanding of transmission pathways by characterizing the structure of contacts that facilitate disease spread (Kinsley et al., 2020). The recognition that contacts patterns in animal populations are often structured rather than random has motivated the application of network theory to veterinary epidemiology (Kinsley et al., 2020). Animal contact networks have been constructed from various data sources, including movement records, proximity sensors, and observational studies, providing insights into the structure of disease transmission at the population level (Kinsley et al., 2020). Network metrics, including degree centrality, betweenness centrality, and closeness centrality, have quantified the importance of individual nodes in the network and identified key individuals or premises that

play central roles in transmission (Kinsley et al., 2020). High-degree nodes, representing individuals or premises with many contacts, have been identified as particularly important for disease spread and control, enabling targeted surveillance and intervention strategies (Kinsley et al., 2020). Betweenness centrality has identified nodes that serve as bridges between different parts of the network, playing critical roles in transmission across the population and representing potential targets for movement restrictions (Kinsley et al., 2020). Multilayer and multiplex networks have extended simple network representations to capture multiple types of contacts or interactions simultaneously, enabling the characterization of complex epidemiological systems where different contact types contribute to disease transmission (Kinsley et al., 2020). The application of multilayer networks has revealed how different contact processes interact to influence disease dynamics, informing the design of comprehensive control strategies that address multiple transmission pathways (Kinsley et al., 2020). Network-based disease models have simulated transmission along network edges, incorporating the structure of contacts into disease spread predictions and identifying optimal surveillance targets and control strategies (Kinsley et al., 2020). Network-based interventions, including the targeting of high-degree nodes or the removal of critical bridges, have demonstrated effectiveness in simulation studies and field applications, highlighting the practical value of network analysis for disease control (Kinsley et al., 2020).

The integration of multiple modelling approaches has emerged as a key theme in contemporary veterinary epidemiology, enabling comprehensive understanding of disease systems that would not be possible through single methods (Lanzas & Chen, 2015; Kleczkowski et al., 2019). One Health frameworks have enabled the consideration of cross-species transmission and environmental determinants, recognizing the interconnectedness of human, animal, and environmental health (Kleczkowski et al., 2019). These frameworks have required the development of unified modelling approaches that can capture cross-species transmission and shared environmental determinants, accommodating the different population structures, surveillance systems, and intervention strategies that characterize human and animal health sectors (Kleczkowski et al., 2019). The development of joint disease models has enabled the assessment of interventions that affect both human and animal health, providing comprehensive evaluations of control strategies that consider multiple sectors simultaneously (Rees et al., 2021). Environmental components of One Health models have incorporated factors such as climate, land use, and ecosystem changes that influence disease dynamics, supporting adaptation strategies for climate-sensitive diseases (Kleczkowski et al., 2019). The integration of environmental data into veterinary epidemiological models has improved the understanding of vector-borne diseases, environmentally persistent pathogens, and wildlife diseases, highlighting the importance of ecological context in disease dynamics (Rees et al., 2021; Rashid et al., 2019).

Data integration methods have synthesized information from diverse sources, improving parameter estimates and enhancing model validity (Combelles et al., 2019). Bayesian methods have provided a natural framework for data integration, enabling the incorporation of information through prior distributions and hierarchical modeling (Biggeri et al., 2006). Multi-model inference approaches have considered evidence from multiple competing models rather than relying on a single best model, accounting for model selection uncertainty and improving

prediction accuracy (Combelles et al., 2019). Model averaging techniques have combined predictions from different models, providing more robust conclusions than single-model approaches (Kirkeby et al., 2021). Ensemble modelling approaches, which combine predictions from multiple individual models, have reduced the bias associated with individual model structures and parameters, providing more robust predictions for disease forecasting, risk assessment, and the evaluation of control strategies (Kleczkowski et al., 2019). Mechanistic-statistical models have integrated mechanistic models with statistical approaches, combining process-based understanding with empirical data and enabling the estimation of mechanistic parameters from observational data (Kirkeby et al., 2021). The development of standardized data formats and sharing platforms has facilitated data integration in veterinary epidemiology, enabling comparative analyses and the development of large-scale models (Kinsley et al., 2020). However, challenges have remained in addressing data quality issues, privacy concerns, and the integration of data from diverse sources, highlighting the need for continued investment in data infrastructure and harmonization efforts (Combelles et al., 2019).

Model calibration and validation have been recognized as essential components of rigorous epidemiological modeling, ensuring that models accurately represent real-world disease dynamics (Kirkeby et al., 2021). Calibration has involved adjusting model parameters to match observed data, often employing optimization or Bayesian approaches (Galvis et al., 2022). Validation has assessed model performance on independent data, testing the model's ability to predict disease patterns under different conditions (Kirkeby et al., 2021). Bayesian calibration methods have provided a formal approach to parameter estimation, combining prior information with observed data to obtain posterior distributions and quantify parameter uncertainty (Combelles et al., 2019). Cross-validation techniques have assessed model performance by fitting the model to a subset of data and evaluating predictions on the remaining data, providing a robust assessment of model generalizability and identifying potential overfitting (Kirkeby et al., 2021). Sensitivity analysis has examined the influence of model parameters on outputs, identifying key parameters that drive model predictions and informing research priorities (Kirkeby et al., 2021). Global sensitivity analyses have considered the combined effects of multiple parameters, providing a comprehensive assessment of model behavior (Galvis et al., 2022). Goodness-of-fit measures, including deviance information criteria (DIC) and Watanabe-Akaike information criteria (WAIC), have provided quantitative assessments of how well models reproduce observed data and enabled the comparison of competing models (Combelles et al., 2019). The selection of appropriate goodness-of-fit measures has depended on the model structure, data characteristics, and the specific objectives of the analysis, highlighting the importance of careful model evaluation in veterinary epidemiological research (Kirkeby et al., 2021).

2. Key Findings from Methodological Applications

The application of spatio-temporal methods has revealed important patterns in disease occurrence that have informed surveillance and control strategies across various veterinary diseases (Arjkumpa et al., 2022; Moustakas, 2017). Spatial cluster detection has identified areas of elevated disease risk, enabling targeted interventions and resource allocation to high-risk regions (Arjkumpa et al., 2022). Temporal analysis has revealed seasonal patterns and long-

term trends in disease occurrence, supporting the timing of preventive measures and the evaluation of intervention impacts (Moustakas, 2017). The integration of spatial and temporal analyses has provided comprehensive understanding of disease spread patterns, identifying both geographic and temporal risk factors (Arjkumpa et al., 2022). These findings have been particularly valuable for emerging diseases, where rapid characterization of spread patterns has informed containment strategies (Arjkumpa et al., 2022). The application of spatio-temporal methods to the first lumpy skin disease outbreak in Thailand, for example, enabled the characterization of outbreak patterns and the development of targeted control recommendations (Arjkumpa et al., 2022). Similarly, spatio-temporal analyses of African swine fever in wild boar populations have informed surveillance strategies and control measures in affected regions (Gervasi et al., 2019).

Bayesian geostatistical modeling has provided robust estimates of disease risk and identified environmental risk factors that would not have been detected through conventional analyses (Biggeri et al., 2006; Combelles et al., 2019). These methods have been particularly valuable for diseases with complex spatial patterns, such as vector-borne diseases and those with environmental reservoirs (Rashid et al., 2019). The spatial predictions from these models have informed the design of surveillance systems and the targeting of control measures, contributing to more efficient disease management (Biggeri et al., 2006). The identification of environmental risk factors through Bayesian geostatistical models has provided insights into disease etiology and informed the development of prevention strategies (Rashid et al., 2019). The quantification of uncertainty in risk estimates has enabled the assessment of confidence in spatial predictions and the identification of areas requiring additional data collection (Combelles et al., 2019). The application of Bayesian geostatistical methods to parasitic infections in cattle, for example, has identified environmental risk factors and areas of elevated risk, informing targeted control interventions (Rashid et al., 2019). The integration of Bayesian geostatistical models with mechanistic transmission models has provided comprehensive understanding of disease systems, combining spatial risk assessment with process-based understanding of disease dynamics (Kirkeby et al., 2021).

Mechanistic transmission models have revealed important insights into disease dynamics, including the identification of key transmission parameters and the evaluation of intervention strategies (Kirkeby et al., 2021; Galvis et al., 2022). Compartmental models have demonstrated the importance of the basic reproduction number in determining epidemic potential, providing a critical threshold for disease control (Galvis et al., 2022). Individual-based models have highlighted the role of heterogeneity in transmission dynamics, revealing that population-level models may obscure important processes occurring at the individual or group level (Lanzas & Chen, 2015). Network-based approaches have identified key individuals and premises that play central roles in disease spread, enabling targeted interventions that maximize the efficiency of limited resources (Kinsley et al., 2020). The application of mechanistic models to porcine reproductive and respiratory syndrome virus (PRRSV) transmission, for example, has informed vaccination strategies and biosecurity measures in swine populations (Galvis et al., 2022). Similarly, mechanistic models of environmentally persistent zoonotic diseases have provided insights into transmission dynamics and informed the development of control strategies (Rees et al., 2021). The evaluation of intervention strategies through mechanistic models has enabled

the comparison of different control options under various scenarios, informing policy decisions in numerous disease outbreaks (Kirkeby et al., 2021).

The integration of multiple modelling approaches has provided comprehensive understanding of disease systems that would not be possible through single methods (Lanzas & Chen, 2015; Kleczkowski et al., 2019). One Health frameworks have revealed the interconnectedness of human, animal, and environmental health, highlighting the importance of considering multiple sectors in disease control (Kleczkowski et al., 2019). Data integration has improved parameter estimates and model validity, synthesizing information from diverse sources to provide more robust conclusions (Combelles et al., 2019). Ensemble approaches have provided more robust predictions than individual models, accounting for model selection uncertainty and reducing bias (Kleczkowski et al., 2019). Mechanistic-statistical models have combined process-based understanding with empirical data, providing insights into transmission dynamics while accounting for observation processes (Kirkeby et al., 2021). The integration of modelling approaches has been particularly valuable for complex disease systems involving multiple host species, environmental factors, and transmission pathways (Rees et al., 2021). These integrated approaches have provided comprehensive assessments of disease persistence, control effectiveness, and the potential impacts of environmental or management changes (Kleczkowski et al., 2019).

Surveillance system evaluations have identified strengths and weaknesses of existing systems, informing improvements in disease detection capabilities (Gervasi et al., 2019; Thrusfield, 2018). The integration of active and passive surveillance has improved sensitivity, while risk-based approaches have optimized the efficiency of surveillance activities (Gervasi et al., 2019). Active surveillance programs have provided data for disease monitoring and freedom from disease declarations, while passive surveillance systems have leveraged existing diagnostic and reporting infrastructure for broader coverage (Gervasi et al., 2019). Methods for accounting for imperfect detection have improved the accuracy of disease estimates, incorporating diagnostic test characteristics and surveillance sensitivity in disease prevalence estimation (Combelles et al., 2019). Early warning systems have enhanced outbreak detection, combining surveillance data with analytical methods to provide advance warning of disease emergence or epidemic events (Moustakas, 2017; Gervasi et al., 2019). The application of data mining and machine learning techniques to surveillance data has improved the timeliness of outbreak detection and the identification of spatial-temporal patterns (Ezanno et al., 2021; Moustakas, 2017). The development of integrated surveillance platforms that combine multiple data sources and analytical methods has enhanced disease detection capabilities, supporting more effective response to disease threats (Moustakas, 2017).

3. Comparative Analysis of Modelling Approaches

A comparative analysis of the different modelling approaches reveals distinct strengths and limitations that determine their suitability for various epidemiological questions and contexts (Kirkeby et al., 2021; Lanzas & Chen, 2015). Compartmental models offer computational efficiency and analytical tractability, making them suitable for rapid assessment of disease dynamics and the evaluation of population-level intervention strategies (Galvis et al., 2022). These models require relatively modest data inputs and can be parameterized using summary

statistics, enabling their application in data-limited settings (Kirkeby et al., 2021). However, compartmental models assume homogeneous mixing and fail to capture individual-level heterogeneity, potentially leading to biased predictions when contact patterns are structured or when host susceptibility varies substantially (Lanzas & Chen, 2015).

Individual-based models provide greater biological realism by explicitly representing individual heterogeneity and complex interactions, making them suitable for investigating targeted interventions and understanding the mechanisms driving disease dynamics (Kirkeby et al., 2021). These models can capture the effects of population structure, individual behavior, and stochasticity on disease transmission, providing insights that are not accessible through aggregate models (Lanzas & Chen, 2015). However, IBMs require extensive data for parameterization and validation, and their computational demands can be substantial, limiting their application in resource-constrained settings (Combelles et al., 2019). The complexity of IBMs also presents challenges for model interpretation and communication, potentially limiting their utility for policy development (Kirkeby et al., 2021).

Network-based approaches offer unique insights into the structure of contact patterns and the identification of key individuals or premises that play central roles in disease transmission (Kinsley et al., 2020). These approaches are particularly valuable for understanding the potential for targeted interventions and for identifying surveillance priorities based on network topology (Kinsley et al., 2020). Network models can be integrated with other modelling approaches, enabling the simulation of disease spread across structured populations (Kirkeby et al., 2021). However, network-based approaches require detailed contact data that may not be available in many veterinary contexts, and the construction of networks from empirical data can be challenging (Kinsley et al., 2020). The sensitivity of network-based predictions to network structure and parameter uncertainty requires careful assessment through sensitivity analysis (Kirkeby et al., 2021).

Bayesian geostatistical approaches provide a robust framework for disease mapping and risk assessment, enabling the incorporation of spatial correlation and uncertainty quantification (Biggeri et al., 2006; Combelles et al., 2019). These methods are particularly valuable for understanding the spatial distribution of disease and for identifying environmental risk factors (Biggeri et al., 2006). The Bayesian framework facilitates the integration of diverse data sources and prior information, improving the robustness of estimates in data-limited settings (Combelles et al., 2019). However, Bayesian geostatistical models require careful specification of prior distributions and spatial correlation structures, and the computational demands of these models can be substantial for large datasets (Biggeri et al., 2006). The interpretation of spatial random effects can also be challenging, requiring careful consideration of the underlying processes generating spatial patterns (Combelles et al., 2019).

The integration of multiple modelling approaches offers the potential to combine the strengths of different methods while mitigating their individual limitations (Lanzas & Chen, 2015; Kleczkowski et al., 2019). Ensemble approaches and multi-model inference can improve prediction robustness and account for model selection uncertainty (Combelles et al., 2019). Mechanistic-statistical models combine process-based understanding with empirical data, enabling the estimation of mechanistic parameters from observational data (Kirkeby et al.,

2021). One Health frameworks integrate veterinary, medical, and environmental perspectives, providing comprehensive understanding of disease systems that involve multiple host species and environmental factors (Kleczkowski et al., 2019). However, the integration of multiple approaches presents challenges related to model complexity, data requirements, and the interpretation of results from different modelling frameworks (Lanzas & Chen, 2015).

4. Quantitative Assessment of Model Performance

Quantitative assessments of model performance have revealed important insights into the accuracy and reliability of different modelling approaches in veterinary epidemiology (Kirkeby et al., 2021; Combelles et al., 2019). Cross-validation studies have demonstrated that the predictive accuracy of models depends on the quality and quantity of available data, with data-rich settings enabling more accurate predictions than data-poor settings (Kirkeby et al., 2021). The performance of compartmental models has been found to be sensitive to the specification of transmission parameters, with mis-specification leading to substantial prediction errors (Galvis et al., 2022). Bayesian calibration has improved parameter estimation and prediction accuracy by incorporating prior information and quantifying uncertainty (Combelles et al., 2019).

Goodness-of-fit measures have enabled the comparison of competing models and the identification of model structures that best reproduce observed data (Kirkeby et al., 2021). Information-theoretic criteria, including Akaike information criteria (AIC) and Bayesian information criteria (BIC), have been used to select among alternative model structures and parameterizations (Combelles et al., 2019). Deviance information criteria (DIC) and Watanabe-Akaike information criteria (WAIC) have been employed for comparing Bayesian models, accounting for model complexity and goodness-of-fit (Kirkeby et al., 2021). Model averaging based on information-theoretic weights has been used to combine predictions from multiple models, improving prediction accuracy and accounting for model selection uncertainty (Combelles et al., 2019).

Sensitivity analyses have identified key parameters that drive model predictions, informing research priorities and data collection efforts (Kirkeby et al., 2021). Global sensitivity analyses have revealed that interactions between parameters can have substantial effects on model outputs, highlighting the importance of considering parameter interactions in uncertainty assessment (Galvis et al., 2022). The identification of sensitive parameters has guided the design of experimental studies and surveillance programs to reduce parameter uncertainty (Kirkeby et al., 2021). The results of sensitivity analyses have also informed the interpretation of model predictions, identifying scenarios where predictions are more robust and scenarios where additional data are needed (Combelles et al., 2019).

The assessment of surveillance system performance has demonstrated the importance of system sensitivity and specificity for disease detection and monitoring (Gervasi et al., 2019). Quantitative evaluations have revealed that many surveillance systems have imperfect sensitivity, leading to under-detection of disease and biased estimates of disease occurrence (Combelles et al., 2019). Risk-based surveillance strategies have been found to improve the efficiency of surveillance activities, achieving higher detection probability with fewer resources

than random sampling (Gervasi et al., 2019). The integration of multiple surveillance approaches has improved overall system sensitivity, with active surveillance providing validation and calibration for passive surveillance systems (Gervasi et al., 2019).

Early warning systems have demonstrated value for the timely detection of disease outbreaks, with statistical process control and machine learning methods enabling the identification of deviations from expected disease patterns (Moustakas, 2017; Ezanno et al., 2021). The performance of early warning systems depends on the availability of high-quality surveillance data and the stability of baseline disease patterns (Moustakas, 2017). Machine learning algorithms have shown promise for pattern recognition and outbreak detection, with the ability to identify complex patterns that may not be apparent through traditional statistical methods (Ezanno et al., 2021). However, the validation of machine learning models for disease surveillance requires careful attention to avoid overfitting and to ensure generalizability (Ezanno et al., 2021).

5. Identified Research Gaps and Methodological Challenges

The review has identified several research gaps and methodological challenges that warrant attention in future veterinary epidemiological research (Combelles et al., 2019; Lanzas & Chen, 2015). Data quality issues, including incomplete reporting, diagnostic inaccuracies, and data fragmentation, remain significant obstacles to robust epidemiological inference (Combelles et al., 2019). The development of standardized data collection and sharing protocols is needed to improve data quality and facilitate comparative analyses across studies and regions (Kinsley et al., 2020). The harmonization of surveillance data, movement records, and epidemiological parameters has enabled comparative analyses but challenges remain in addressing data quality issues, privacy concerns, and the integration of data from diverse sources (Combelles et al., 2019). The substantial data requirements of complex models, particularly individual-based and network models, have limited their application in data-poor settings, highlighting the need for continued investment in surveillance infrastructure (Kirkeby et al., 2021). The availability of high-quality data is essential for model parameterization and validation, and data gaps have constrained the application of advanced modelling approaches in many veterinary contexts (Combelles et al., 2019).

The validation of complex epidemiological models presents ongoing challenges, particularly for individual-based and network models with extensive data requirements (Kirkeby et al., 2021). The availability of independent data for model validation is often limited, and methods for assessing the validity of complex models require further development (Kirkeby et al., 2021). Sensitivity analysis and uncertainty quantification are essential but are often underutilized in veterinary epidemiological studies, limiting the assessment of model robustness and the identification of research priorities (Kirkeby et al., 2021). The development of standardized validation protocols and the reporting of model performance are needed to improve the credibility and reproducibility of epidemiological modelling studies (Combelles et al., 2019). The computational demands of complex models may limit their application in resource-constrained settings, and the development of more efficient algorithms is needed to expand access to advanced modelling approaches (Lanzas & Chen, 2015). The integration of multiple modelling approaches presents technical challenges, including the harmonization of

model structures, the management of model complexity, and the interpretation of results from different modelling frameworks (Kleczkowski et al., 2019).

The translation of modelling results into practical recommendations for disease control remains a significant challenge in veterinary epidemiology (Kleczkowski et al., 2019). The integration of stakeholder perspectives in model development and interpretation is needed to improve the relevance and applicability of modelling results (Kleczkowski et al., 2019). The communication of uncertainty in modelling results to policymakers and practitioners requires careful attention to ensure appropriate interpretation and decision-making (Combelles et al., 2019). The involvement of policymakers, industry representatives, and local communities in model development and interpretation improves the translation of results into practice, but such participatory approaches are not yet widely implemented (Kirkeby et al., 2021). The development of user-friendly modelling tools and decision-support systems is needed to facilitate the application of modelling results in disease control and policy development (Kleczkowski et al., 2019). The economic evaluation of disease control strategies through modelling studies is needed to inform resource allocation decisions, but such analyses have been relatively limited in veterinary epidemiology (Rashid et al., 2019).

The application of veterinary epidemiological methods to wildlife diseases presents particular challenges, including limited surveillance data, complex population structures, and the difficulty of implementing control measures (Gervasi et al., 2019). The integration of ecological and epidemiological approaches is needed to address these challenges, and the development of methods for wildlife disease surveillance and control requires continued attention (Gervasi et al., 2019). The study of wildlife diseases has been constrained by the difficulty of obtaining representative surveillance data and the complexity of wildlife population dynamics (Kleczkowski et al., 2019). The potential for wildlife reservoirs to sustain disease transmission and re-introduce pathogens into domestic animal populations highlights the importance of understanding wildlife disease dynamics (Gervasi et al., 2019). The application of network-based approaches to wildlife populations has been limited by data availability, but advances in animal tracking technologies and genetic analyses have provided new opportunities for characterizing wildlife contact networks (Kinsley et al., 2020).

The emergence of novel pathogens and the changing environmental conditions that influence disease transmission dynamics present ongoing challenges for veterinary epidemiology (Arjkumpa et al., 2022; Rees et al., 2021). The rapid characterization of emerging disease outbreaks requires the timely application of epidemiological methods, but data limitations and logistical challenges often constrain the speed of response (Arjkumpa et al., 2022). The integration of climate and environmental data into disease models is needed to assess the potential impacts of environmental change on disease emergence and spread, but such integration requires interdisciplinary collaboration and the development of appropriate modelling frameworks (Rees et al., 2021). The application of artificial intelligence and machine learning techniques to veterinary epidemiology has expanded with the increasing availability of data and computational resources, but the interpretation and validation of these methods require careful attention (Ezanno et al., 2021). The development of early warning systems and predictive models for emerging diseases requires the integration of diverse data sources and

analytical methods, but the validation of such systems is challenging due to the rarity of emergence events (Moustakas, 2017). The global nature of livestock production and trade requires international collaboration in surveillance and disease modelling, but coordination across countries and sectors remains a challenge (Kinsley et al., 2020).

6. Emerging Trends and Future Directions

Several emerging trends in veterinary epidemiology are likely to shape the future of the discipline and address current methodological challenges (Ezanno et al., 2021; Lanzas & Chen, 2015). The increasing availability of high-resolution data from sensor technologies, remote sensing, and genomic analyses is enabling the development of more detailed and accurate epidemiological models (Kirkeby et al., 2021). The integration of real-time data streams into disease models is supporting the development of early warning systems and adaptive management strategies (Moustakas, 2017). The application of wearable sensors and automated monitoring systems is providing continuous data on animal health and behavior, enabling the detection of disease at early stages (Kim et al., 2026).

The development of artificial intelligence and machine learning techniques is expanding the capabilities of veterinary epidemiology, enabling the analysis of large and complex datasets and the identification of patterns that may not be apparent through traditional methods (Ezanno et al., 2021). Deep learning approaches have shown promise for image analysis and pattern recognition in diagnostic applications, while natural language processing has been applied to the analysis of textual data from surveillance reports and scientific literature (Ezanno et al., 2021). The integration of machine learning with mechanistic models is providing hybrid approaches that combine the strengths of both paradigms, enabling the estimation of mechanistic parameters from observational data and the prediction of disease dynamics under novel conditions (Kirkeby et al., 2021).

The increasing recognition of the importance of antimicrobial resistance and the need for surveillance and control of resistant pathogens is driving the application of epidemiological methods to antimicrobial resistance research (Thrusfield, 2018). Genomic epidemiology is providing new insights into the transmission dynamics of pathogens, enabling the tracking of pathogen evolution and the identification of transmission networks (Kinsley et al., 2020). The integration of genomic and epidemiological data is supporting the development of more targeted surveillance and control strategies, enabling the identification of high-risk strains and the evaluation of intervention impacts (Galvis et al., 2022).

The growing emphasis on the economic evaluation of disease control strategies is driving the integration of epidemiological models with economic analyses (Rashid et al., 2019). Cost-effectiveness analyses and benefit-cost analyses are being used to inform resource allocation decisions and identify the most efficient control strategies (Rashid et al., 2019). The integration of economic and epidemiological models is enabling the assessment of the economic impacts of disease and the evaluation of the cost-effectiveness of different intervention options (Kirkeby et al., 2021). The development of decision-support tools that integrate epidemiological and economic analyses is facilitating the translation of modelling results into practical recommendations for disease control (Kleczkowski et al., 2019).

The increasing focus on the health impacts of climate change is driving the development of climate-sensitive disease models and the assessment of the potential impacts of environmental change on disease emergence and spread (Rees et al., 2021). The integration of climate projections into disease models is enabling the assessment of future disease risks and the development of adaptation strategies (Rees et al., 2021). The application of One Health approaches is supporting the assessment of the health impacts of environmental change across human, animal, and environmental health sectors (Kleczkowski et al., 2019). The development of integrated surveillance systems that monitor disease occurrence in relation to environmental changes is supporting early warning and adaptive management (Moustakas, 2017).

Conclusion

Veterinary epidemiology has undergone significant methodological evolution, transitioning from traditional descriptive approaches to sophisticated quantitative frameworks that integrate spatio-temporal analysis, mechanistic modelling, and advanced computational techniques. The integration of multiple modelling approaches, including Bayesian geostatistical methods, compartmental models, individual-based simulations, and network analysis, has enabled comprehensive understanding of disease dynamics and informed evidence-based decision-making in animal health management. Despite the substantial progress, challenges remain in data quality, model validation, uncertainty quantification, and the translation of modelling results into practical recommendations for disease control. The One Health framework has emerged as an important perspective for addressing complex disease systems that involve multiple host species and environmental factors, highlighting the interconnectedness of human, animal, and environmental health. Continued investment in surveillance infrastructure, methodological development, interdisciplinary collaboration, and capacity building will be essential for addressing evolving challenges in animal health management and safeguarding global food security and public health.

Recommendations

Based on the comprehensive review, the following recommendations are proposed for researchers, practitioners, and policymakers to enhance the application and impact of epidemiological methods in animal health management.

- 1. Investment in Surveillance Infrastructure:** Significant investment should be made in surveillance infrastructure and data quality improvement, including standardized data collection protocols, animal identification technologies, and integrated data sharing platforms to support advanced modelling approaches.
- 2. Development of Validation Methods:** Standardized validation protocols, uncertainty quantification methods, and sensitivity analysis should be routinely employed to improve the credibility, reproducibility, and robustness of epidemiological modelling studies.
- 3. Integration of Multiple Approaches:** The integration of multiple modelling approaches, including One Health frameworks, ensemble methods, and mechanistic-statistical models,

should be encouraged to provide comprehensive understanding of disease systems and enhance prediction robustness.

4. Application of Emerging Technologies: The application of artificial intelligence, machine learning, genomic epidemiology, and climate-sensitive models should be expanded to enhance disease surveillance, pattern recognition, predictive modelling, and adaptation strategies.

5. Translation to Policy and Practice: Evidence-based decision-making should be promoted through the development of decision-support tools, strengthened surveillance systems, early warning systems, economic evaluations, and capacity building programs for researchers, policymakers, and practitioners.

Article Publication Details

This article is published in the [OpenMind Journal of Multidisciplinary Innovation & Development](#), ISSN: 3108-2920 (Online). In Volume 2 (2026), Issue 4 (Jul - Aug) - 2026
The journal is published and managed by [OMR PUBLICATION](#) .

Acknowledgements

We sincerely thank the editors and the reviewers for their valuable suggestions on this paper.

Authors' contributions

All author(s) read and approved the final manuscript.

Funding

The author(s) declare that no funding was received for this work.

Data availability

No datasets were generated or analyzed during the current study.

Declarations

Ethics approval and consent to participate

The author(s) declare that not applicable.

Consent for publication

The author(s) declare that not applicable.

Competing interests

The author(s) declare no competing interests.

References

1. Arjkumpa, O., Suwannaboon, M., Boonrod, M., Punyawan, I., Liangchaisiri, S., Laobannue, P., ... Punyapornwithaya, V. (2022). The first lumpy skin disease outbreak in Thailand (2021): Epidemiological features and spatio-temporal analysis. *Frontiers in Veterinary Science*, 8, Article 799065. <https://doi.org/10.3389/fvets.2021.799065>
2. Biggeri, A., Dreassi, E., Catelan, D., Rinaldi, L., Lagazio, C., & Cringoli, G. (2006). Disease mapping in veterinary epidemiology: A Bayesian geostatistical approach. *Statistical Methods in Medical Research*, 15(4), 337–352.
3. Combelles, L., Corbiere, F., Calavas, D., Bronner, A., Hénau, V., & Vergne, T. (2019). Impact of imperfect disease detection on the identification of risk factors in veterinary epidemiology. *Frontiers in Veterinary Science*, 6, Article 66. <https://doi.org/10.3389/fvets.2019.00066>
4. Ezanno, P., Picault, S., Beaunée, G., Bailly, X., Muñoz, F., Duboz, R., ... Guégan, J. F. (2021). Research perspectives on animal health in the era of artificial intelligence. *Veterinary Research*, 52(1), Article 40. <https://doi.org/10.1186/s13567-021-00902-4>
5. Galvis, J. A., Corzo, C. A., Prada, J. M., & Machado, G. (2022). Modelling the transmission and vaccination strategy for porcine reproductive and respiratory syndrome virus. *Transboundary and Emerging Diseases*, 69(2), 485–500.
6. Gervasi, V., Marcon, A., Bellini, S., & Guberti, V. (2019). Evaluation of the efficiency of active and passive surveillance in the detection of African swine fever in wild boar. *Veterinary Sciences*, 7(1), Article 5. <https://doi.org/10.3390/vetsci7010005>
7. Kim, D., Michelot, T., Mertes, K., Stabach, J. A., & Fieberg, J. (2026). Detecting disease progression from animal movement using hidden Markov models. *Journal of Applied Ecology*, 63(3), Article e70323.
8. Kinsley, A. C., Rossi, G., Silk, M. J., & VanderWaal, K. (2020). Multilayer and multiplex networks: An introduction to their use in veterinary epidemiology. *Frontiers in Veterinary Science*, 7, Article 596. <https://doi.org/10.3389/fvets.2020.00596>

9. Kirkeby, C., Brookes, V. J., Ward, M. P., Dürr, S., & Halasa, T. (2021). A practical introduction to mechanistic modeling of disease transmission in veterinary science. *Frontiers in Veterinary Science*, 7, Article 546651. <https://doi.org/10.3389/fvets.2020.546651>
10. Kleczkowski, A., Hoyle, A., & McMenemy, P. (2019). One model to rule them all? Modelling approaches across One Health for human, animal and plant epidemics. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 374(1775), Article 20180255. <https://doi.org/10.1098/rstb.2018.0255>
11. Lanzas, C., & Chen, S. (2015). Complex system modelling for veterinary epidemiology. *Preventive Veterinary Medicine*, 118(2–3), 207–214.
12. Moustakas, A. (2017). Spatio-temporal data mining in ecological and veterinary epidemiology. *Stochastic Environmental Research and Risk Assessment*, 31(4), 829–834.
13. Rashid, M., Rashid, M. I., Akbar, H., Ahmad, L., Hassan, M. A., Ashraf, K., ... Gharbi, M. (2019). A systematic review on modelling approaches for economic losses studies caused by parasites and their associated diseases in cattle. *Parasitology*, 146(2), 129–141.
14. Rees, E. M., Minter, A., Edmunds, W. J., Lau, C. L., Kucharski, A. J., & Lowe, R. (2021). Transmission modelling of environmentally persistent zoonotic diseases: A systematic review. *The Lancet Planetary Health*, 5(7), e466–e478.
15. Thrusfield, M. (2018). *Veterinary epidemiology* (4th ed.). John Wiley & Sons.

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