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Modelling Disease Transmission in Animal Populations Using Mathematics

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Abstract- The increasing threat of emerging and re-emerging infectious diseases in livestock, wildlife, and companion animals demands quantitative frameworks that transcend descriptive epidemiology. Mathematical modeling provides the essential language and toolkit for understanding disease transmission dynamics, predicting outbreak trajectories, and optimizing intervention strategies. This paper synthesizes current advances in three foundational modeling paradigms—compartmental models (SIR-type frameworks), network models, and spatially explicit models—with particular attention to applications published in 2025–2026 across major livestock diseases. We examine how these frameworks have been applied to foot-and-mouth disease, African swine fever, avian influenza, and vector-borne diseases, highlighting methodological innovations in parameter estimation, optimal control theory, and uncertainty quantification. We further identify emerging frontiers, including multiscale models linking within-host to population-level dynamics, machine learning integration for real-time outbreak prediction, and the critical role of sensitivity analysis in identifying key transmission parameters. The synthesis demonstrates that mathematical modeling has moved from retrospective explanation to prospective decision support, providing evidence-based guidance for surveillance, vaccination, culling, and biosecurity policies.

Keywords- Mathematical modeling, Disease transmission, Animal populations, Compartmental models, Network epidemiology, Optimal control, Sensitivity analysis, One Health

I. INTRODUCTION

Infectious diseases in animal populations impose staggering economic burdens and threaten food security, biodiversity, and public health. Foot-and-mouth disease (FMD) alone causes estimated annual losses of up to $21 billion in endemic regions. African swine fever (ASF) continues to reshape global pork production. Highly pathogenic avian influenza (HPAI) has expanded its host range to include dairy cattle, revealing unexpected transmission pathways. In this complex and dynamic landscape, mathematical modeling has emerged as an indispensable tool for understanding, predicting, and controlling disease spread.

Unlike traditional epidemiological approaches that rely on retrospective analysis, mathematical models provide a forward-looking framework for simulating "what-if" scenarios, quantifying the impact of

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interventions, and identifying data gaps. The foundational principle is simple but powerful: represent the population in terms of disease states, specify transition rates between these states based on biological mechanisms, and solve the resulting system of equations to predict future outcomes.
This paper provides a structured review of current mathematical modeling approaches for animal disease transmission, focusing on applications published in 2025–2026. We cover core frameworks (Section 2), disease-specific case studies (Section 3), and emerging methodological frontiers (Section 4), concluding with an integrated pipeline for model-based decision support (Section 5).

II. CORE MATHEMATICAL FRAMEWORKS

1. Compartmental Models: The SIR Paradigm and Its Extensions:
The susceptible-infected-recovered (SIR) framework and its extensions form the bedrock of mathematical epidemiology. In its simplest deterministic form, the model comprises ordinary differential equations (ODEs) tracking the number of individuals in each compartment. The basic reproduction number \(R_0 \) —the expected number of secondary cases generated by a single infected individual in a fully susceptible population—serves as the central threshold parameter: if \(R_0 < 1 \), the disease dies out; if \(R_0 > 1 \), it can establish endemic transmission.

The SEIR extension, incorporating an exposed (latent) compartment, has proven particularly valuable for diseases with significant incubation periods. In a 2025 study of FMD in Bolivia, researchers developed a stochastic SEIR metapopulation model to simulate outbreaks across administrative regions, finding that combining ring vaccination (50–90 farms/day) with depopulation (1–2 farms/day) controlled 60.3% of outbreaks, while higher depopulation rates (3–5 farms/day) eliminated outbreaks 9 days faster. Critically, vaccination alone controlled only 0.6% of outbreaks, demonstrating the complementary roles of different interventions.

For vector-borne diseases, compartmental models must incorporate the vector population explicitly. A deterministic metapopulation model for African horse sickness (AHS) in South Africa's Western Cape identified the safest months for horse importation and vaccination, with subsequent integration of random forest-derived vector abundance maps improving model realism.

2. Stochastic vs. Deterministic Modeling:
Deterministic models assume large population sizes and average behavior, while stochastic models capture random variation—essential when outbreak sizes are small or extinction probabilities matter. A comparative analysis of rabies persistence in human and dog populations using both deterministic and Continuous-Time Markov Chain (CTMC) stochastic models found that while results aligned in many scenarios, stochasticity was critical at low infection rates. The multitype branching process approach was used to determine the stochastic threshold for rabies persistence, revealing how random events influence extinction probabilities.

3. Network and Metapopulation Models:
Real-world animal populations are not well-mixed; contact patterns are heterogeneous and structured. Network models represent individuals as nodes and contacts as edges, capturing the underlying connectivity that drives transmission. Metapopulation models extend this to the population level, treating farms or herds as nodes connected by animal movements.

A 2025 study on FMD transmission in mainland China constructed a metapopulation network based on the highway infrastructure map, proving the global asymptotic stability of the disease-free equilibrium and deriving the network basic reproduction number \(R_0^M \). The analysis revealed that increasing transportation of susceptible livestock can trigger outbreaks, while increasing transport of

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exposed/infected animals has the opposite effect—a non-intuitive finding with important policy implications.

Spatially embedded probabilistic models, such as the Scale-Free Percolation (SFP) model, have been applied to French cattle trade networks using Approximate Bayesian Computation for parameter estimation, demonstrating how geographical distance constraints shape disease spread risk.

III. DISEASE-SPECIFIC APPLICATIONS: 2025–2026 ADVANCES

1. African Swine Fever: Quantifying Transmission Pathways:
ASF continues to devastate global swine production. A 2025 stochastic model for free-ranging pig populations predicted that biosecurity measures implemented within 14 days of epidemic onset can avert up to 74% of pig deaths, while hypothetical vaccines conferring 70% immunity deployed prior to day 14 could avert 65% of deaths. Combined interventions saved 91% of pigs that would otherwise succumb—but if delayed beyond 60 days, only 30% of deaths were averted, underscoring the critical importance of early detection.

A mathematical analysis of ASF transmission in domestic settings identified pig recruitment rate, natural death rate, disease-induced death rate, and pig-to-pig transmission rate as the parameters most strongly influencing \(R_0 \), guiding control strategy prioritization. In the United States, the PigSpread-ASF model evaluated the National Response Plan, finding that under current protocols only 65.1% of simulated outbreaks were eliminated within 12 months. Achieving elimination required expanding control zone radii, extending movement standstills, and improving baseline detection speed.

2. Avian Influenza: Multi-Host Dynamics and Environmental Transmission:
The recent spillover of H5N1 into dairy cattle has revealed critical gaps in our understanding of multi-host transmission. A 2025 deterministic model integrating cattle (SIR framework) and wild birds (SEIR framework) with an environmental compartment derived the basic reproduction number using the next-generation matrix approach. Sensitivity analysis identified transmission among cattle, environmental contamination, and recovery rate as key drivers of epidemic outcomes.

At the waterfowl-backyard poultry interface, a stochastic compartmental model validated with historical outbreak data demonstrated that the stopover duration of migratory reservoir species—but not stopover timing—predicts HPAI infection probability in backyard poultry. This finding focuses surveillance efforts on understanding factors influencing stopover duration.

3. Foot-and-Mouth Disease: Spatial and Aerosol Dynamics:
The 2025 Bolivia FMD study exemplified the power of stochastic metapopulation modeling for national-level policy. High-risk areas were concentrated in high-density farming regions, and the most effective strategy—ring vaccination combined with depopulation—required vaccinating a median of 925,338 animals.

Aerosol transmission of FMDV, often overlooked, was quantified using a spatiotemporal dynamic model. Under sustained 0.1 m/s wind, 7-day maximum transmission distances from infected farms reached 6.2–12.07 km for cattle farms, 4.8–10.8 km for sheep farms, and 17–22.68 km for pig farms—dramatically larger than previously assumed.

Machine learning has also entered the FMD modeling landscape. An interpretable ML framework applied to FMD in the Middle East and North Africa achieved predictive accuracies exceeding 85% in identifying high-risk areas. Sheep density emerged as the dominant predictor for serotype O, while

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buffalo density and proximity to roads/cropland drove serotype A risk—enabling serotype-specific surveillance targeting.

IV. VECTOR-BORNE AND ZOONOTIC DISEASES

A metapopulation model for Rift Valley fever in the Comoros archipelago evaluated three vaccine allocation strategies: proportional allocation, optimal allocation for maximizing infections averted, and equitable allocation. Optimally allocating vaccines improved effectiveness compared to proportional allocation but resulted in inequitable outcomes between islands—a trade-off that policymakers must navigate explicitly.

For West Nile virus, a modular computational framework combining compartmental models with network dynamics demonstrated that early-implemented, dual-target strategies addressing both mosquito vectors and avian reservoirs can substantially reduce transmission, providing a decision-support platform for vector control agencies.

Methodological Frontiers:

Parameter Estimation and Sensitivity Analysis

Models are only as good as their parameters. Recent advances in sensitivity analysis provide systematic approaches to identifying which parameters most influence model outputs. For avian influenza, Latin Hypercube Sampling with partial rank correlation coefficients (PRCC) identified transmission rates by humans and domestic birds as directly proportional to \(R_0 \). For brucellosis in cattle, fractional calculus with the Caputo-Fabrizio operator captured memory effects in transmission dynamics, with sensitivity analysis revealing the parameters most critical to infection rate.

Optimal Control Theory

Beyond prediction, mathematical models can identify optimal intervention strategies. A 2025 study of Q-fever transmission used Pontryagin's Maximum Principle to find optimal control solutions for vaccination, culling, environmental hygiene, and public education. Cost-effectiveness analysis using Incremental Cost-Effectiveness Ratio (ICER) identified combined livestock vaccination, gradual culling of seropositive animals, and public education as the most cost-effective strategy, achieving elimination in humans within two years.

For rodent-transmitted infections in agricultural environments, an SIR-P model with three time-dependent interventions (contact prevention, environmental sanitation, treatment) found that while full combination of controls yields maximum infection reduction, the prevention-only strategy is most economically attractive under restricted budgets.

Multiscale Modeling:

Perhaps the most exciting frontier is multiscale modeling, linking within-host viral kinetics to population-level transmission. A 2025 study of Usutu virus developed a model connecting within-host viral kinetics in birds, per-bite probability of mosquito infection, and population-level mosquito-bird transmission. Multiscale fitting to integrated laboratory and surveillance datasets improved parameter identifiability and robustness, demonstrating the power of combining microscale and macroscale data.

An Integrated Modeling Pipeline for Decision Support:

Drawing on the reviewed advances, we propose a five-step pipeline for model-based animal disease management:

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- **Data Integration:** Combine outbreak surveillance, animal movement records, environmental data, and (where available) within-host kinetics.
- **Model Selection:** Choose appropriate framework (deterministic vs. stochastic, compartmental vs. network) based on population size, heterogeneity, and question.
- **Parameter Estimation:** Use sensitivity analysis (PRCC, LHS) to identify key parameters; apply Approximate Bayesian Computation or Markov chain Monte Carlo for inference where likelihoods are intractable.
- **Simulation and Intervention Optimization:** Run scenarios under different control strategies (vaccination, culling, movement bans, biosecurity); use optimal control theory to identify cost-effective combinations.
- **Policy Translation:** Present results as actionable thresholds (e.g., "biosecurity within 14 days averts 74% of deaths") and risk maps.

V. CONCLUSION

Mathematical modeling has matured from a niche academic pursuit to a core component of animal disease preparedness and response. The frameworks reviewed—compartmental, stochastic, network, metapopulation, and multiscale—provide a versatile toolkit for understanding transmission dynamics across scales. The 2025–2026 literature demonstrates that these models are not merely descriptive but predictive and prescriptive, capable of quantifying the impact of interventions, identifying optimal resource allocation, and guiding surveillance priorities. As climate change, land-use transformation, and globalized animal trade continue to reshape disease landscapes, mathematical epidemiology will play an increasingly vital role in safeguarding animal health, food security, and the One Health interface between humans, animals, and ecosystems.

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