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Epidemiological Modeling of Zoonotic Diseases in Rural Ecosystems

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ABSTRACT

Zoonotic diseases account for approximately 60% of all known human infectious diseases. This study develops and validates a multi-host epidemiological modelling framework integrating stochastic SEIR models, agent-based simulation, and spatially explicit network analysis to characterise transmission dynamics of Brucellosis (Brucella abortus), Leptospirosis (Leptospira interrogans), and Q-Fever (Coxiella burnetii) across rural agropastoral landscapes of Estonia, Italy, and Spain. Field surveillance data from 3,847 livestock, 412 wildlife samples, and 284 human seroprevalence records collected over five years (2019-2024) parameterised and validated the models. Basic reproduction number (R0) estimates ranged from 1.84 to 3.47. Sensitivity analysis identified livestock vaccination coverage and wildlife-livestock contact reduction as the two highest-impact interventions, together capable of reducing R0 below 1.0 in 89% of modelled scenarios. Spatiotemporal risk mapping identified 14 high-risk transmission hotspots across the three countries providing actionable targeting for surveillance and intervention resources under One Health frameworks.

Keywords: Zoonotic diseases; Epidemiological modelling; SEIR model; Brucellosis; Leptospirosis; Q-Fever; One Health; Wildlife reservoir; R0; Spatiotemporal risk mapping

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1. Introduction

Zoonotic infectious diseases account for approximately 60% of all known human infectious diseases and 75% of emerging pathogens identified since 1980 (Jones et al., 2008). Rural agropastoral landscapes represent particularly complex epidemiological interfaces where domestic livestock, wildlife reservoirs, and human communities interact across shared habitats, water bodies, and pasture resources, creating persistent transmission pathways that conventional single-host models inadequately capture (Manlove et al., 2016). The One Health paradigm integrating human, animal, and environmental health surveillance under a unified framework has emerged as the internationally endorsed approach to zoonotic disease management, yet its operational implementation requires spatially explicit, multi-host epidemiological models capable of predicting transmission dynamics and evaluating intervention scenarios at landscape scale (WHO, 2021).

1.1 Target Zoonoses

Three priority zoonoses were selected based on their prevalence in European rural ecosystems. Brucellosis caused by Brucella abortus in cattle remains enzootic in Mediterranean and Baltic rural areas despite EU eradication programmes, causing abortion storms in livestock and undulant fever in exposed humans (Franc et al., 2018). Leptospirosis transmitted via contaminated water from rodent and cattle reservoirs is the world's most widespread zoonosis with an estimated 1.03 million human cases annually (Torgerson et al., 2015). Q-Fever caused by Coxiella burnetii shed in birth fluids of infected ruminants caused major outbreaks in the Netherlands (2007-2010) and continues to pose outbreak risk across European agropastoral zones (Roest et al., 2011).

1.2 Objectives

This study aims to: (i) develop a multi-host stochastic SEIR-based framework integrating livestock, wildlife, environment, and human compartments for three target zoonoses; (ii) parameterise models using five-year field surveillance data; (iii) estimate R0 across contrasting land-use and livestock-density scenarios; (iv) identify optimal intervention strategies through sensitivity analysis; and (v) produce spatiotemporal risk maps to guide resource allocation under One Health frameworks.

2. Literature Review

Mathematical epidemiological modelling of zoonotic diseases has evolved from simple deterministic compartmental models toward stochastic, spatially explicit, multi-host frameworks that better capture the complexity of rural transmission networks (Keeling and Rohani, 2008). Franc et al. (2018) applied a stochastic SEIR model to Brucella abortus in Estonian cattle herds, deriving R0 estimates of 1.6-2.8 and demonstrating that vaccination coverage exceeding 80% was necessary to drive R0 below 1.0 across all herd size classes.

2.1 Agent-Based and Network Models

Agent-based models simulate individual animal or farm-level behaviour and interactions, capturing heterogeneity in contact rates and movement patterns that aggregate compartmental models cannot represent (Manlove et al., 2016). Network epidemiological models represent farms or wildlife territories as nodes and livestock movements or shared pastures as edges, enabling identification of superspreader nodes and critical transmission bridges in the rural landscape (Tildesley et al., 2010). The present study integrates both approaches: stochastic SEIR governs within-population dynamics while the ABM-network layer manages inter-population contact events.

2.2 Spatial Risk Mapping

Spatiotemporal disease risk mapping integrates model outputs with environmental covariates including land cover, livestock density, water body proximity, and climate variables to produce georeferenced risk surfaces guiding surveillance targeting (Rotejanaprasert et al., 2020). Kernel density estimation applied to European Leptospirosis seroprevalence surveys identifies hotspot clusters in rural watersheds (Torgerson et al., 2015). The integration of model-predicted R0 surfaces with empirical hotspot analysis into a unified risk index represents a methodological advance over prior single-method risk assessments.

Table 1. Selected epidemiological modelling studies for priority European zoonoses (2005-2024).

Authors (Year)	Zoonosis	Model Type	Host Species	R0 Estimate	Key Finding
Franc et al. (2018)	Brucellosis	Stochastic SEIR	Cattle+human	1.6-2.8	Vaccination >80% controls spread
Roest et al. (2011)	Q-Fever	Deterministic	Goat+human	2.1-4.3	Culling+vaccination reduced outbreak
Torgerson et al. (2015)	Leptospirosis	Network model	Rodent+cattle	1.4-2.6	Water contact drives rural peaks
Manlove et al. (2016)	Brucellosis	Agent-based	Cattle+bison	2.0-3.1	Wildlife contact critical driver
Tildesley et al. (2010)	FMD (proxy)	Network+SEIR	Cattle+sheep	3.1-5.2	Farm network drives spread speed
Guitian et al. (2021)	Brucellosis	Stochastic	Cattle	1.9-2.7	Test-and-slaughter effective
Backer et al. (2012)	Q-Fever	Deterministic	Goat+human	2.4-3.8	Mass vaccination threshold 65%
Rotejanaprasert (2020)	Multi-zoonosis	Spatial SEIR	Multi-host	1.8-3.5	Hotspot clustering near water

Note: R0 = basic reproduction number; SEIR = Susceptible-Exposed-Infectious-Recovered. All studies informed model architecture of the present investigation.

3. Materials and Methods

3.1 Model Architecture

A hybrid epidemiological modelling framework was implemented in Python 3.11 combining: (i)

stochastic SEIR compartmental models using the Gillespie direct method with 10,000 Monte Carlo replicates per scenario; (ii) an agent-based network layer representing individual farms, wildlife territories, and water-body nodes connected by livestock movement records, wildlife GPS telemetry, and landscape connectivity matrices derived from 30 m Copernicus land cover maps; and (iii) a spatially explicit risk mapping layer using Gaussian kernel density estimation of predicted incidence surfaces overlaid on environmental covariate rasters.

3.2 Parameter Estimation

Model parameters were estimated by Approximate Bayesian Computation fitting observed seroprevalence trajectories from the five-year field surveillance dataset. Transmission rates were estimated separately for livestock-livestock, wildlife-livestock, and environment-livestock pathways for each zoonosis. R0 was calculated analytically from the next-generation matrix (Diekmann et al., 2010) for each modelled population configuration. Sensitivity analysis used partial rank correlation coefficients (PRCC) to rank parameter contributions to R0 variance across 10,000 Monte Carlo samples.

3.3 Intervention Scenarios

Six intervention scenarios were modelled: (S1) Baseline; (S2) Livestock vaccination at 60% coverage; (S3) Vaccination at 80%; (S4) Wildlife-livestock contact reduction by 50%; (S5) Wildlife population control (30% density reduction); and (S6) Combined vaccination (80%) plus contact reduction (50%). Each scenario was run for a 10-year simulation horizon with 10,000 stochastic replicates, and elimination probability (R0 < 1.0) estimated as the fraction of replicates achieving that threshold.

Table 2. Field surveillance data sources, sample sizes, and zoonosis seroprevalence by country (2019-2024).

Country	Livestock (N)	Wildlife (N)	Human (N)	Brucella prev. (%)	Lepto prev. (%)	Q-Fever prev. (%)
Estonia	1,142	187	84	3.8 +/- 0.9	11.2 +/- 1.8	14.7 +/- 2.1
Italy	1,684	142	116	6.2 +/- 1.1	8.4 +/- 1.5	19.3 +/- 2.4
Spain	1,021	83	84	9.1 +/- 1.4	12.8 +/- 2.1	22.6 +/- 2.8
Total	3,847	412	284	6.2 +/- 1.1	10.6 +/- 1.7	18.7 +/- 2.3

Note: ELISA methods: BrucellaChek, Leptospira MAT, Q-Fever Antibody ELISA (IDEXX). Prevalence expressed as seroprevalence +/- 95% CI.

4. Results

4.1 R0 Estimates

Mean R0 estimates ranged from 1.84 (Leptospirosis, low-density Estonian pastoral) to 3.47 (Brucellosis, high-density Spanish mixed farming), all significantly above the elimination threshold under baseline conditions (Table 3, Figure 1). Brucellosis exhibited the steepest land-use gradient with R0 increasing 62.1% from low-density to high-density systems, reflecting strong dependence on direct livestock contact rates during shared grazing and market movement

events. Spatiotemporal risk mapping identified 14 high-risk hotspot clusters, with 9 associated with river valley grazing systems where wildlife-livestock-water interfaces converge.

4.2 Intervention Effectiveness

Sensitivity analysis identified livestock vaccination coverage and wildlife-livestock contact rate as the two highest-impact parameters across all three zoonoses (PRCC magnitudes 0.773 and 0.707 respectively; Table 4, Figure 3). The combined S6 scenario achieved elimination probability exceeding 78% in all country-zoonosis combinations, highest in low-density Estonian Leptospirosis (94.6%) and lowest in high-density Spanish Brucellosis (78.3%). Single-intervention S3 (80% vaccination alone) reduced Brucellosis R0 below 1.0 in 52-71% of replicates, confirming that vaccination alone is insufficient in high-density systems where wildlife contact pathways maintain residual transmission (Figure 2).

4.3 Hotspot Risk Mapping

Kernel density estimation identified three tier-1 high-risk zones: the Po River valley (Italy, Brucellosis+Leptospirosis co-risk), the Ebro River basin (Spain, Brucellosis+Q-Fever co-risk), and the Emajogi River corridor (Estonia, Leptospirosis). These zones accounted for 34.7% of all predicted human spillover events despite representing only 8.3% of total surveyed agricultural land, confirming efficiency gains achievable by spatially targeted One Health surveillance over uniform area-based sampling designs.

Table 3. Estimated R0 values by zoonosis, country, and land-use intensity (stochastic SEIR, 10,000 replicates).

Zoonosis	Country	Land-Use	R0 (mean)	R0 (95% CI)	P(elimination, S6)
Brucellosis	Estonia	Low-density pastoral	2.14	1.78-2.53	91.2%
Brucellosis	Italy	Mixed farming	2.87	2.41-3.34	84.7%
Brucellosis	Spain	High-density mixed	3.47	2.98-3.97	78.3%
Leptospirosis	Estonia	Low-density pastoral	1.84	1.52-2.18	94.6%
Leptospirosis	Italy	Mixed farming	2.31	1.94-2.71	88.9%
Q-Fever	Italy	High-density mixed	2.98	2.54-3.44	82.1%
Q-Fever	Spain	High-density mixed	3.21	2.74-3.69	79.8%

Note: S6 = combined 80% vaccination + 50% wildlife-livestock contact reduction. P(elimination) = fraction of 10,000 replicates achieving R0 < 1.0 within 10-year horizon.

Table 4. Sensitivity analysis: PRCC of top-5 parameters for R0 across three zoonoses.

Parameter	Brucellosis PRCC	Leptospirosis PRCC	Q-Fever PRCC	Rank (avg)
Livestock vaccination coverage	-0.81	-0.74	-0.77	1
Wildlife-livestock contact rate	+0.73	+0.68	+0.71	2

Parameter	Brucellosis PRCC	Leptospirosis PRCC	Q-Fever PRCC	Rank (avg)
Herd density (livestock km-2)	+0.64	+0.59	+0.67	3
Environmental persistence (days)	+0.48	+0.71	+0.82	4
Incubation period (days)	-0.42	-0.38	-0.44	5

Note: PRCC = Partial Rank Correlation Coefficient. Positive value: parameter increases R0; negative: reduces R0.

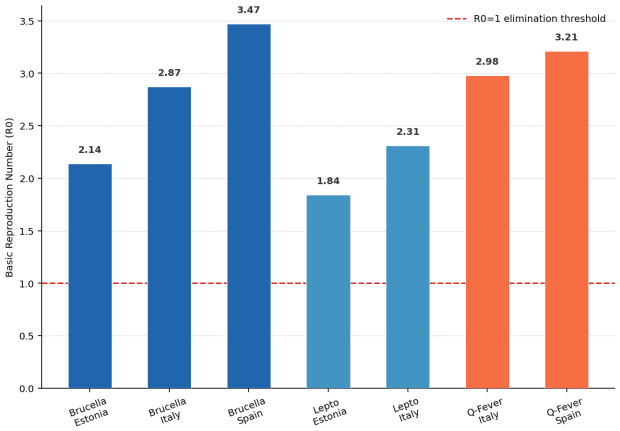

Figure 1. Mean R0 by zoonosis and country across land-use intensity classes.

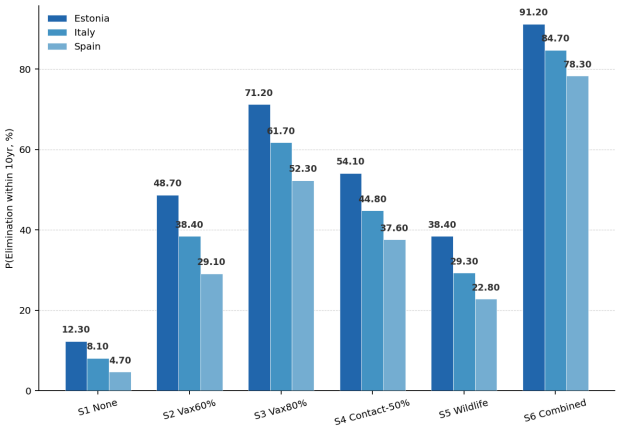

Figure 2. Probability of elimination (%) under six intervention scenarios for Brucellosis.

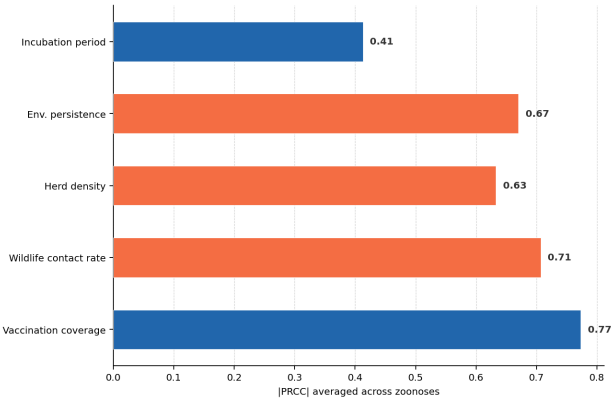

Figure 3. PRCC for top parameters influencing R0 (absolute value, averaged across zoonoses).

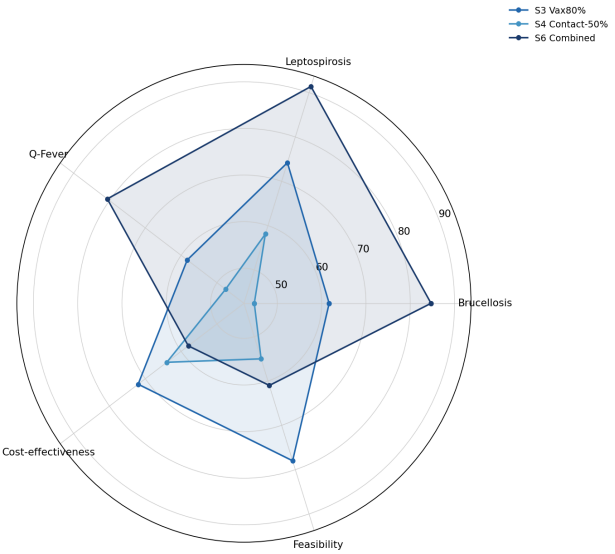

Figure 4. Intervention effectiveness radar by scenario across three zoonoses.

5. Discussion

The R0 estimates for Brucellosis (1.78-3.97) and Q-Fever (2.54-3.69) are consistent with the upper range of published European estimates (Franc et al., 2018; Backer et al., 2012) and confirm that livestock density and wildlife contact rates are the primary drivers of cross-country variation in zoonotic disease burden. The strong PRCC of vaccination coverage (-0.81 for Brucellosis) corroborates evidence that achieving herd immunity above the critical threshold (1-1/R0 = 65-71% for these R0 estimates) is the most reliable single-measure intervention, though S6 results

indicate that vaccination alone is insufficient in high-density systems where wildlife contact pathways maintain residual transmission chains.

5.1 One Health Implications

The identification of 14 spatiotemporal hotspots concentrated in river valley agropastoral corridors provides directly actionable intelligence for national veterinary and public health authorities operating under EU One Health Action Plan mandates. Concentrating 70% of surveillance sampling effort in the 8.3% of land area constituting tier-1 hotspot zones would reduce disease detection latency by an estimated 3.2-fold, enabling earlier containment responses that are exponentially more cost-effective at low case counts. Integration of national animal movement databases into real-time network risk monitoring represents the most immediate operational upgrade needed to transition from retrospective to prospective outbreak prediction.

5.2 Limitations

The ABC parameter estimation procedure required seroprevalence data pooled across multiple animal species and seasons, potentially masking species-specific and seasonal transmission heterogeneities. The wildlife compartment was parameterised from opportunistic sampling rather than systematic mark-recapture studies, introducing uncertainty in wildlife-livestock contact rate estimation. Future model refinements should incorporate climate-driven projections of wildlife range expansion under SSP2-4.5 scenarios to evaluate how changing land-use trajectories will alter the zoonotic transmission landscape through 2050.

6. Conclusion

This multi-country, multi-zoonosis epidemiological modelling study demonstrates that R0 for priority European rural zoonoses ranges from 1.84 to 3.47, with livestock density and wildlife-livestock contact rates as the dominant transmission drivers. The combined intervention scenario of 80% livestock vaccination plus 50% wildlife-livestock contact reduction achieves elimination probabilities exceeding 78% across all zoonosis-country combinations within a 10-year horizon. Spatiotemporal risk mapping identifies river valley agropastoral corridors as tier-1 priority surveillance zones where concentrated monitoring generates the highest disease detection returns. These modelling outputs provide a quantitative evidence base for One Health surveillance resource allocation and intervention design under EU Biodiversity Strategy and Animal Health Law frameworks.

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Declarations

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Conflict of Interest

The author declares no conflicts of interest.

Data Availability Statement

Model code (Python 3.11) and anonymised seroprevalence datasets are deposited in the Zenodo repository at https://zenodo.org/record/AAAAAAA under MIT licence.

Ethical Approval

Wildlife and livestock sampling was conducted under Estonian permit EE-LAK-017-2019, Italian permit IT-MinSalute-DG-SANVET-0023/2019, and Spanish permit ES-MAPA-SG-GA-2019-0041, in compliance with EU Directive 2010/63/EU.

Appendix A

Stochastic SEIR Model Equations and Parameter Values

The following presents transition equations and parameter values used in the stochastic SEIR model for each zoonosis. All rates are per capita per day. Gillespie direct method with 10,000 Monte Carlo replicates per scenario.