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Relative Risk Estimation for Brucella Abortus in Malaysia: Comparison of SMR and Poisson-Gamma Disease Mapping Models

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Abstract Brucellosis, primarily caused by *Brucella abortus*, is a significant zoonotic disease that negatively impacts both public health and the livestock economy, especially in regions dependent on animal husbandry. This study evaluated the spatial distribution and estimated the relative risk (RR) of *B. abortus* infections in Malaysia from 2018 to 2024, using two statistical methods: the Standardized Mortality Ratio (SMR) method and the Bayesian Poisson-Gamma model. Disease incidence data were obtained from the World Organization for Animal Health (WOAH), and analyses were performed using R Programming and ArcGIS software to generate risk estimates and create spatial disease maps for 14 Malaysian states. The SMR method provided initial risk estimates but showed limitations in regions with zero reported cases, often underestimating potential disease burden. In contrast, the Poisson-Gamma model produced more nuanced and robust risk estimates, identifying additional high-risk areas such as Kuala Lumpur and Sarawak, where the SMR method indicated no observed risk. This discrepancy highlights the Bayesian model's strength in addressing data sparsity and underreporting. Both models consistently identified Perlis, Perak, and Johor as very high-risk states. The study concludes that the Poisson-Gamma model offers superior performance in detecting spatial risk patterns of *B. abortus*, particularly in areas with incomplete surveillance data. However, its limitations include reduced flexibility in adjusting for covariates and spatial dependencies. These findings also highlight the importance of using advanced spatial modeling techniques in disease surveillance to inform targeted interventions, optimize resource allocation, and support evidence-based policy development for managing brucellosis and similar zoonotic diseases.

Keywords: *Brucella Abortus*, Relative Risk Estimation, Disease Mapping, Classical Approach, Bayesian Approach.

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Introduction

Brucellosis, primarily caused by *Brucella abortus*, remains one of the most significant zoonotic diseases, severely impacting public health and the global economy [1, 2]. The disease is transmitted between animals and humans through direct contact with infected animals or their products, such as unpasteurized milk [3, 4]. In livestock, *B. abortus* causes reproductive failures, including abortions, infertility, and decreased milk production, which are directly linked to substantial economic losses for farmers [5, 1, 6]. The zoonotic nature of the disease further increases its impact, as it can be transmitted to humans, resulting in Malta fever, which leads to long-term health complications [7, 2].

Globally, the annual human burden of brucellosis is estimated to exceed 2.1 million cases, with rural and agriculture-dependent regions disproportionately affected due to their proximity to livestock farming [8].

Approximately 500,000 new cases occur each year in developing countries, with Southeast Asia accounting for a significant portion of this burden [9, 10]. In this region, Malaysia has reported increasing case numbers in recent years, consistent with broader trends in developing nations [10]. Studies have confirmed significant geographical variation in the distribution of *B. abortus* worldwide, highlighting the need for region-specific risk assessments [11-13].

In Malaysia, brucellosis remains a significant challenge despite substantial efforts to manage and control the disease, particularly infections caused by *B. abortus*. The livestock sector is vital to the national economy, with cattle farming serving as a primary source of livelihood in many rural areas. Effective brucellosis control is therefore essential for safeguarding both public health and economic stability [5, 9]. *B. abortus* infections cause serious reproductive issues in cattle, leading to economic losses and posing zoonotic risks to humans [14, 7, 15]. Data from 2018 to 2024 show considerable year-to-year variability in prevalence (Figures 2 and 3), with periodic resurgences highlighting gaps in surveillance and control measures [9, 16, 17].

Despite these challenges, previous studies in Malaysia have largely relied on descriptive epidemiology or basic spatial analyses, which often have limitations in handling small-area data, underreporting, and instability in risk estimation [18]. Specifically, conventional methods such as crude rates or Standardized Mortality Ratios (SMR) method can produce unstable estimates in regions with sparse or zero cases [19-20], while more advanced Bayesian smoothing approaches such as the Poisson-Gamma model [21-22] remain underexplored in the context of brucellosis mapping in Malaysia.

To address these methodological gaps, this study aims to compare the performance of SMR and Poisson-Gamma models in estimating the Relative Risk (RR) of *B. abortus* across Malaysian cattle populations and to assess their usefulness in identifying high-risk areas through disease mapping. These methods were selected for their established utility in disease mapping [23-24]: SMR method is widely used for initial risk assessment but is limited by high variance in small areas [20, 19, 18], while the Poisson-Gamma model incorporates Bayesian smoothing to stabilize estimates and improve accuracy in low-count settings [21, 22, 25], a common issue in veterinary surveillance data [26]. Disease mapping displays the geographical distribution of disease occurrence using noisy observed data on disease rates [27]. In other words, disease mapping displays the geographical variability of the disease on maps using different colours or shading. With advancements in computational tools, disease mapping has become widely used in descriptive epidemiology [28]. Disease maps can help government agencies allocate resources effectively and evaluate the performance of public health interventions [24]. In any case, maps must be designed to communicate effectively with the public, health researchers, and decision makers [29, 28, 30, 31]. The use of disease mapping and advanced statistical models in this study offers a promising approach to enhancing disease surveillance and control, ensuring that resources are directed to high-risk areas and contributing to a reduce the economic burden of brucellosis in Malaysia.

Materials and Methods

Data Source and Study Area

In this study, all observed *B. abortus* incidence data and data on the exposed livestock population in Malaysia from 2018 to 2024 were obtained from the World Organization for Animal Health (WOAH). This dataset provides the annual number of reported cases during the study period. The study area includes 13 states in Malaysia: Perlis, Kedah, Pulau Pinang, Perak, Selangor, Negeri Sembilan, Melaka, Johor, Kelantan, Terengganu, Pahang, Sabah, and Sarawak, as well as one Federal Territory, Kuala Lumpur. To reduce complexity, both the states and the Federal Territory are collectively referred to as states in this study.

Software

Data analysis and visualization were conducted using R version 4.3.1 for statistical computation and graphing [32-33], and ArcGIS Pro version 3.1 for spatial mapping and risk visualization [34-35]. The study's overall findings are presented in tables and figures, with risk maps for *B. abortus* generated from computed data.

Rationale for Model Selection

Disease mapping is a strategic tool for risk assessment that the Department of Veterinary Services (DVS) Malaysia can use to identify high-risk areas. It is also importance in research, particularly in public health and epidemiology [36, 2]. For *B. abortus*, disease mapping generated with ArcGIS software can help

DVS Malaysia in pinpoint regions with a high concentration of infection cases. Identifying these high-risk areas is essential for supporting DVS Malaysia's control intervention strategies, including culling and slaughtering measures, to manage *B. abortus* outbreaks in cattle herds nationwide [37-39]. In this section, the existing models used in disease mapping studies are described and applied. Commonly used models in such studies include non-spatial models, spatial models, and space-time models [40-42]. For this study, the Standardized Mortality Ratio (SMR) method and the Poisson-Gamma model were selected to address specific methodological gaps in *B. abortus* risk estimation in Malaysia. The SMR method provides a straightforward, non-spatial baseline estimate of relative risk (RR), which is useful for initial identification of high-risk areas [23]. However, SMR method estimates can be unstable in regions with small or zero case counts, potentially leading to misleading risk interpretations [20, 19]. To address this limitation, the Poisson-Gamma model, a Bayesian hierarchical approach was applied [21, 25]. This model incorporates prior information and smooths risk estimates, improving stability and accuracy in low-count settings [22], which is particularly relevant for underreported diseases such as brucellosis [26, 24]. Comparing these two methods allows for an evaluation of their respective strengths and limitations in the context of veterinary disease surveillance [18]. The analysis of RR estimation begins with the SMR method, which is widely used in disease mapping studies to assess disease incidence in a particular area. This is followed by the application of the Poisson-Gamma model to estimate the RR of *B. abortus* infection in Malaysia.

Standardized Mortality Ratio (SMR) Method

The SMR method is a widely used epidemiological measure employed for initial disease mapping to estimate relative risk (RR) [43, 20]. In this study, the SMR method is calculated by comparing the observed number of *B. abortus* cases (O_i) within a specific region to the expected number of *B. abortus* (E_i), derived from a reference population. This method has traditionally been used for analyzing case counts within tracts, as described by Lawson [23]. In disease mapping, the study area is assumed to be divided into Z mutually exclusive regions $(i = 1,2, \dots, Z)$, where each region has its own observed number of *B. abortus* cases (O_i) and expected number of *B. abortus* cases (E_i). Based on the values of O_i and E_i obtained from the World Organization for Animal Health (WOAH) data, the RR δ_i, which is the SMR method for region i, can be calculated using the following equation:

$$\delta_i = \frac{O_i}{E_i}, i = 1,2, \dots, Z. \tag{1}$$

In general, the SMR method strategy offers a straightforward risk comparison tool through the application of equation (1) for Malaysian regions, highlighting both high-risk and low-risk areas for *B. abortus* infection. This ratio serves as a fundamental indicator for the Department of Veterinary Services (DVS) Malaysia to identify regions that require policy improvements and enhanced control measures. However, the SMR method approach has limitations, particularly in areas with no observed cases, as it inherently assigns a risk value of zero, which may misrepresent the actual disease burden [44-46]. Therefore, the application of Bayesian methods is necessary, as they improve the accuracy of detecting disease patterns [47, 48, 19, 49].

Poisson-Gamma Model

Considering the shortcomings of the SMR method approach, the Poisson-Gamma model has emerged as a preferred Bayesian method recommended by numerous scholars [21, 22, 50]. This study employs the Poisson distribution due to its suitability for modeling count-based data. Within this framework, it is assumed that the number of newly reported infections, denoted as z_{ij}, follows a Poisson distribution across a specific time interval, where both the mean and variance are defined as $e_{ij}\theta_{ij}$. In this context, $i = 1,2, \dots, P$ indicates the geographical areas under investigation, while $j = 1,2, \dots, Q$ refers to the respective periods. The term e_{ij} represents the expected count of new infections, and θ_{ij} denotes the estimated relative risk (RR):

$$z_{ij} |\, e_{ij}, \theta_{ij} \sim Poisson(e_{ij}\theta_{ij}). \tag{2}$$

The RR parameter follows a gamma prior distribution, with parameters α and β:

$$\theta_{ij} \sim Gamma(\alpha, \beta). \tag{3}$$

According to Lawson ***et al***. [25], the prior parameter values α and β in the Poisson-Gamma model are unknown, and the hyperparameter values are assumed to be 0.1. In this study, the model-based prior estimates for RR are set at 0.5 for α and 0.0001 for β.

Risk Visualization

For Malaysian *B. abortus* data, relative risk (RR) estimates from the traditional Standardized Mortality Ratio (SMR) method and Poisson-Gamma model were visualized as thematic maps in ArcGIS, with risk categories defined by quartiles of the estimated RR [18]. An RR value close to one (RR=1) indicates that individuals in a particular group are not significantly different from the overall population in their likelihood of contracting the disease. An RR value below one (RR<1) indicates that the population in the area has a lower probability of contracting the disease compared to the general population. Conversely, an area with an RR value greater than one (RR>1) indicates that its inhabitants have a higher likelihood of contracting the disease compared to the overall population [51-53].

Analytical Workflow

The analytical process followed a structured sequence, as summarized in Figure 1. The first phase involved data acquisition and preparation. Observed case counts and exposed cattle population data at the state level for 2018 to 2024 were obtained from the World Organization for Animal Health (WOAH). After cleaning and validation, these data were aggregated into 14 administrative regions. For each region-year unit, expected case counts were calculated using indirect standardization, with national incidence rates as the reference population. The second phase focused on estimating relative risk (RR). Using the prepared observed and expected counts, RR was calculated independently through two methodological frameworks: the classical Standardized Mortality Ratio (SMR) method and a Bayesian Poisson-Gamma model. This dual approach enabled direct comparison between frequentist and hierarchical Bayesian estimators.

In the third phase, results from the two models were systematically compared. A quantitative comparison of the RR values was performed, followed by a reclassification analysis to examine how risk categories (e.g., low, moderate, high) assigned by the SMR method differed from those assigned by the Poisson-Gamma model, thereby assessing model performance and consistency. The final phase included visualization, interpretation, and output generation. Results were visualized using R and ArcGIS Pro to create comparative graphs and detailed risk maps. This synthesis enabled the identification of persistent high-risk regions and the assessment of model performance. The workflow was designed to provide actionable insights, including targeted policy recommendations for intervention and priority areas for improving epidemiological surveillance.

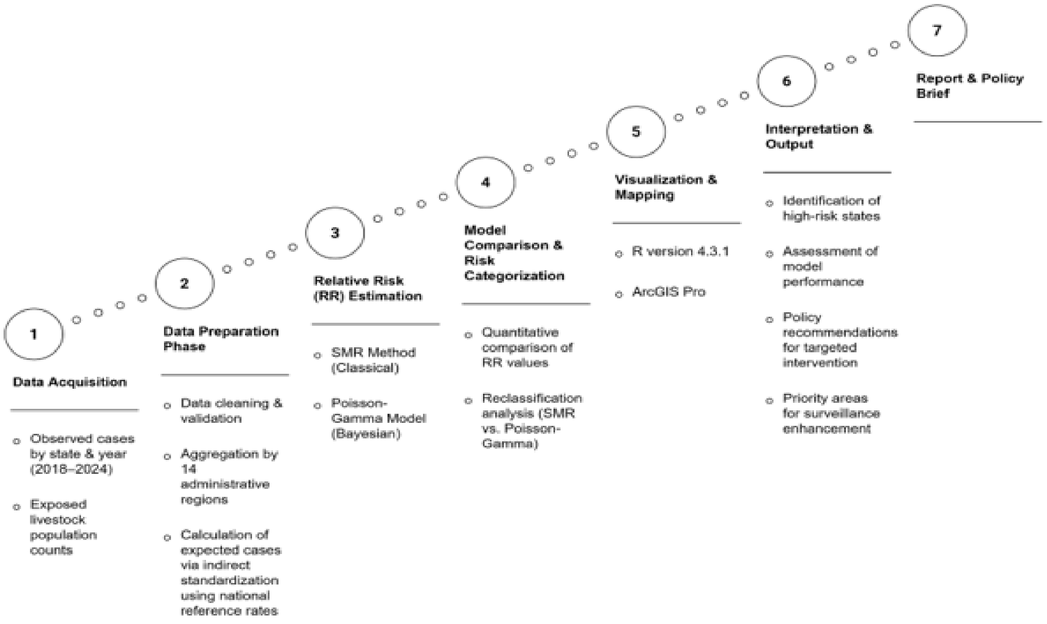

Figure 1. Analytical Workflow for Estimating and Visualizing Regional Disease Risk

Results and Discussion

Temporal Trend

The epidemiological trend of *B. abortus* incidence in Malaysia from 2018 to 2024, as shown in Figure 2, reveals a complex temporal pattern with significant year-to-year variation, reflecting possible changes in both disease transmission and national surveillance efforts. The annual case count, reported through national surveillance, started at 196 in 2018 and declined steadily to a low of 53 in 2021. A marked resurgence to 158 cases occurred in 2022, followed by decreases to 66 in 2023 and 52 in 2024. This pattern of decline, resurgence, and subsequent decline suggests a non-stationary epidemic process, potentially influenced by external factors.

The notable resurgence in 2022 may indicate a decline in the long-term effectiveness of control measures such as livestock vaccination or movement restrictions, or changes in local transmission dynamics influenced by environmental, demographic, or husbandry factors [9, 16, 54, 55]. Similar post-suppression resurgences in brucellosis epidemiology are well documented, studies often associate such rebounds with gaps in sustained vaccination coverage [9], reductions in surveillance intensity [26], or the introduction of infection through livestock trade [27-28]. These recurring patterns highlight the challenge of maintaining durable disease control and underscore the need for adaptive, resilient public health and veterinary strategies that can respond to shifting risk landscapes.

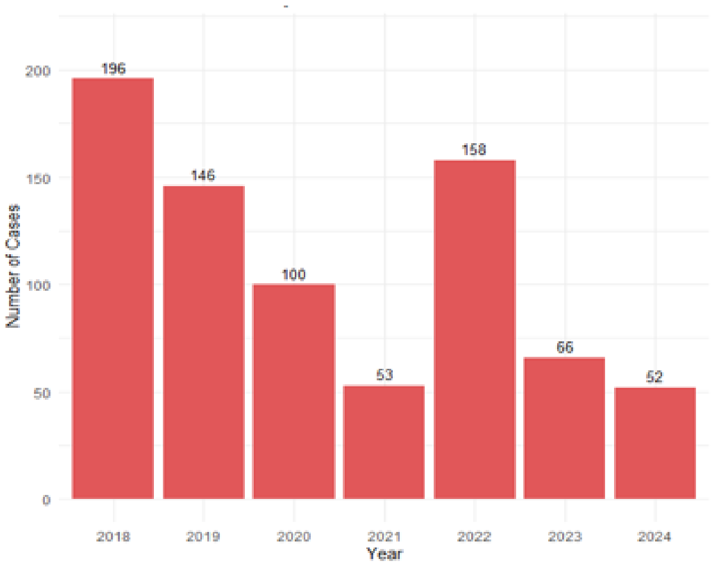

Figure 2. Incidence of *Brucella Abortus* Cases from 2018 to 2024

Spatial Distribution

Figure 3 shows the spatial distribution of *B. abortus* cases across Malaysian states from 2018 to 2024. The highest cumulative case counts were in Pahang (134 cases), Negeri Sembilan (129 cases), and Melaka (126 cases), followed by Selangor (110 cases) and Johor (105 cases). Terengganu and Pulau Pinang consistently reported lower incidence throughout the period, while all other states recorded between 0 and 19 cases.

This marked geographical heterogeneity may be influenced by several factors, including differences in livestock density, regional animal husbandry and management practices, environmental conditions, and proximity to cross-border livestock trade routes [27, 56]. Previous studies in similar settings have linked higher brucellosis incidence to intensive dairy farming and less stringent biosecurity measures [57, 6]. Additionally, differences in surveillance intensity and reporting completeness across states could contribute to the observed pattern, as noted in prior research on zoonotic disease surveillance in Malaysia [58]. These factors collectively highlight the need for targeted, state-specific interventions and strengthened surveillance systems to address the underlying drivers of disease persistence.

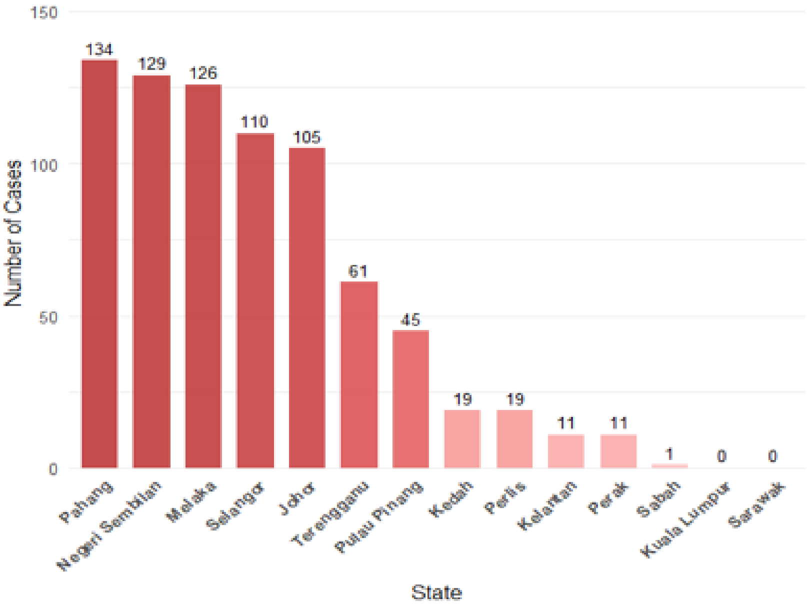

Figure 3. Total Number of *Brucella Abortus* Cases Reported for each State in Malaysia from 2018 to 2024

Relative Risk Estimation of Brucella Abortus

This study presents the estimated relative risk (RR) outcomes using the existing models, namely the Standardized Mortality Ratio (SMR) method and the Poisson-Gamma model, for all 14 states in Malaysia over seven years from 2018 to 2024, as shown in Table 1. Table 1 displays the numerical RR values derived from both models. During the study period, several states recorded RR values less than one (RR<1), indicating that the observed number of *B. abortus* cases (O_i) was lower than the expected number of cases (E_i) in those states according to both models. Five states in Malaysia recorded RR values less than one (RR<1), namely Negeri Sembilan, Kedah, Selangor, Terengganu, and Sabah under both models.

Table 1. Relative Risk Based on the SMR Method and Posterior Expected Relative Risks Based on the Existing Model (Poisson-Gamma Model) for *Brucella Abortus* Cases from 2018 to 2024

State	SMR Method	Poisson-Gamma Model
Perlis	18.96	19.47
Kedah	0.88	0.90
Pulau Pinang	1.55	1.57
Perak	6.95	7.27
Kuala Lumpur	0.00	9.48
Selangor	0.77	0.78
Negeri Sembilan	0.98	0.98
Melaka	1.29	1.30
Johor	3.71	3.73
Pahang	1.02	1.02
Terengganu	0.40	0.40
Kelantan	1.01	1.06
Sabah	0.05	0.07
Sarawak	0.00	9.48

Standardized Mortality Ratio (SMR) Method

Based on the SMR method (Table 1, Figure 4), seven states had a relative risk (RR) greater than one (RR>1), indicating that the observed number of *B. abortus* cases exceeded the expected number from 2018 to 2024: Perlis (18.96), Perak (6.95), Johor (3.71), Penang (1.55), Melaka (1.29), Pahang (1.02), and Kelantan (1.01). Five states had an RR less than one (RR<1): Negeri Sembilan (0.98), Kedah (0.88), Selangor (0.77), Terengganu (0.40), and Sabah (0.05). Kuala Lumpur and Sarawak were assigned an RR of 0 because no cases were reported. These results differ from estimates obtained using the Poisson-Gamma model.

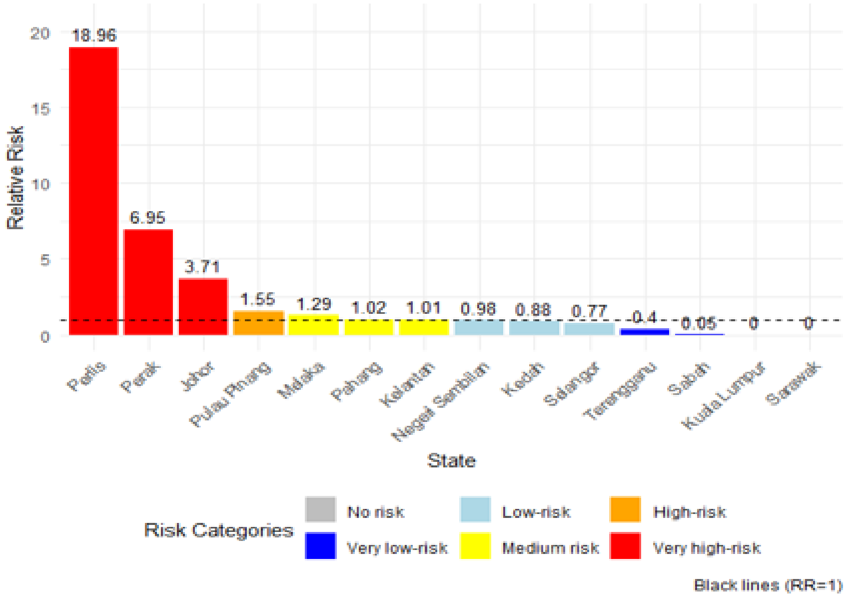

Figure 4. Plot of Estimated *Brucella Abortus* Relative Risk using the Standardized Mortality Ratio (SMR) Method from 2018 to 2024

Poisson-Gamma Model

The Poisson-Gamma model produced notably different results, generating non-zero relative risk (RR) estimates for all states and smoothing extreme values (Table 1, Figure 5). Under this model, nine states showed an RR greater than one (RR>1), indicating that observed *B. abortus* cases exceeded expectations from 2018 to 2024. These include the seven states identified by the SMR method (Perlis, Perak, Johor, Penang, Melaka, Pahang, and Kelantan), as well as Kuala Lumpur and Sarawak (RR=9.48 for both). This contrasts sharply with the SMR method, which assigned an RR of 0 to Kuala Lumpur and Sarawak due to zero reported cases. The model's ability to assign elevated risk in areas with no observed cases highlights a key limitation of the SMR approach.

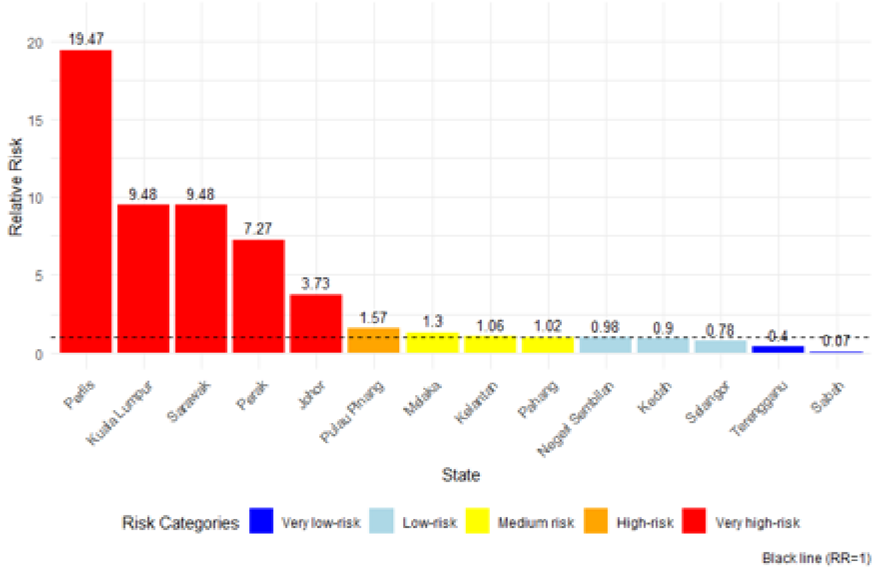

Figure 5. Plot of Estimated *Brucella Abortus* Relative Risk using the Poisson-Gamma Model from 2018 to 2024

Model Comparison and Interpretation

The Poisson-Gamma model consistently produced higher and more stable relative risk (RR) estimates than the Standardized Mortality Ratio (SMR) method, especially in states with low or zero case counts [21, 20]. This difference occurs because the Bayesian approach incorporates prior information and shrinks estimates toward the mean, reducing the influence of sampling variability [19, 25, 23] and better accounting for underreporting [26, 24]. A notable example is Kuala Lumpur and Sarawak, which shifted from RR=0 under SMR method to RR ≈ 9.48 under the Poisson-Gamma model. This quantitative reclassification of two states from zero-risk to very high-risk changed the status of 2 out of 14 states, representing a 14.3% change in high-risk designations. This shift demonstrates the model's utility in settings with sparse or unreliable surveillance data. Overall, Table 1 shows significant discrepancies in identifying high- and low-incidence regions for *B. abortus* across Malaysian states, depending on the model used. Therefore, RR estimation using the Poisson-Gamma model addresses a key shortcoming of the SMR method, particularly in areas with no observed cases. This suggests that cattle populations in states such as Kuala Lumpur and Sarawak may have a higher likelihood of *B. abortus* exposure than raw surveillance data indicate. The elevated risk in these states is likely due to underreporting and underdiagnosis, as noted in studies of zoonotic disease surveillance in Malaysia and similar settings [58], along with the persistent demand for raw dairy products in potential brucellosis hotspots [4, 59, 60]. Additionally, cross-border livestock trade, particularly in Borneo, may further contribute to the increased risk [61, 62, 63, 57].

Brucella Abortus Disease Mapping in Malaysia

The geographical distribution of *B. abortus* risk across Malaysian states from 2018 to 2024 was visualized using thematic maps based on relative risk (RR) estimates derived from the Standardized Mortality Ratio (SMR) method and Poisson-Gamma model. A color-graded thematic mapping approach was used to improve interpretability and clearly distinguish different risk levels [27, 43, 33]. This method enables visual identification of high- and low-risk zones, which is essential for guiding targeted interventions [28, 12, 64].

RR values were grouped into five levels: very low risk [0.0, 0.5), low risk [0.5, 1.0), medium risk [1.0, 1.5), high risk [1.5, 2.0), and very high risk [2.0, ∞). This classification was chosen because it aligns with established epidemiological mapping practices and provides a policy-relevant gradient that clearly differentiates regions with below-average (RR<1), moderately elevated (RR 1.0–1.5), and substantially elevated risk (RR≥1.5) [18]. A continuous color scale was applied across the 14 states, ranging from the lightest shade for very low risk to the darkest for very high risk.

Figure 6 shows the SMR-based thematic map for 2018 to 2024. According to this classification, Perlis (RR=18.96), Perak (RR=6.95), and Johor (RR=3.71) were categorized as very high-risk states. Penang (RR=1.55) was classified as high risk, while Melaka, Kelantan, and Pahang (RRs between 1.01 and 1.29) were assigned to the medium-risk category. The remaining states were mapped as low or very low risk. However, this approach does not account for uncertainty in areas with no reported cases, such as Kuala Lumpur and Sarawak, which were assigned an RR of 0 and therefore appeared without observable risk on the map.

Figure 7 shows the corresponding thematic map based on the Poisson-Gamma model, which addresses this limitation by accounting for uncertainty in regions with zero cases. This adjustment resulted in a notable reclassification: Kuala Lumpur and Sarawak shifted from "no observed risk" under SMR method to "very high risk" under the Poisson-Gamma model (RR=9.48 for both). As a result, five states (Perlis, Perak, Johor, Kuala Lumpur, and Sarawak) were classified as very high risk using the Poisson-Gamma model, compared to only three under SMR method. Penang remained high risk, and Melaka, Kelantan, and Pahang remained medium risk. All other states retained their low or very low risk classifications.

Although both models consistently identified Perlis, Perak, and Johor as core high-risk zones, the Poisson-Gamma model provided a more refined spatial assessment, especially for regions with sparse or unreported data. The elevated risk in these areas may be associated with factors such as high livestock density, cross-border animal movement, and surveillance gaps [61, 62, 65, 56]. For Penang, the high-risk status may be due to challenges in managing disease transmission across urban–rural interfaces and intensive dairy farming [62, 66]. In contrast, the medium- to low-risk classifications in other states may reflect stricter veterinary controls, geographical isolation, or more effective regulatory and surveillance systems [61, 62, 56].

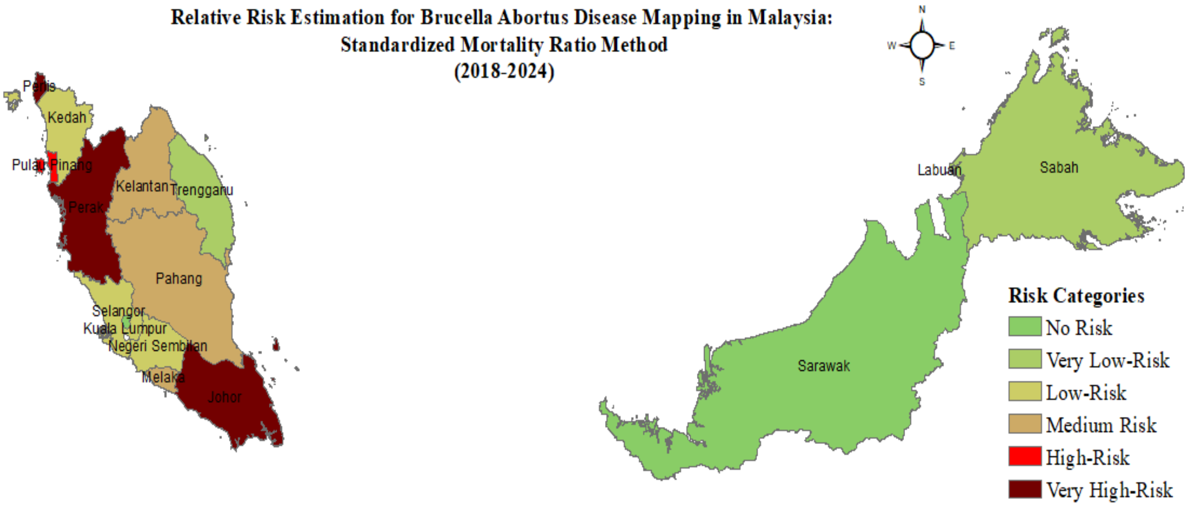

Figure 6. Standardized Mortality Ratio Method Map for Brucella Abortus Cases during the years 2018 to 2024

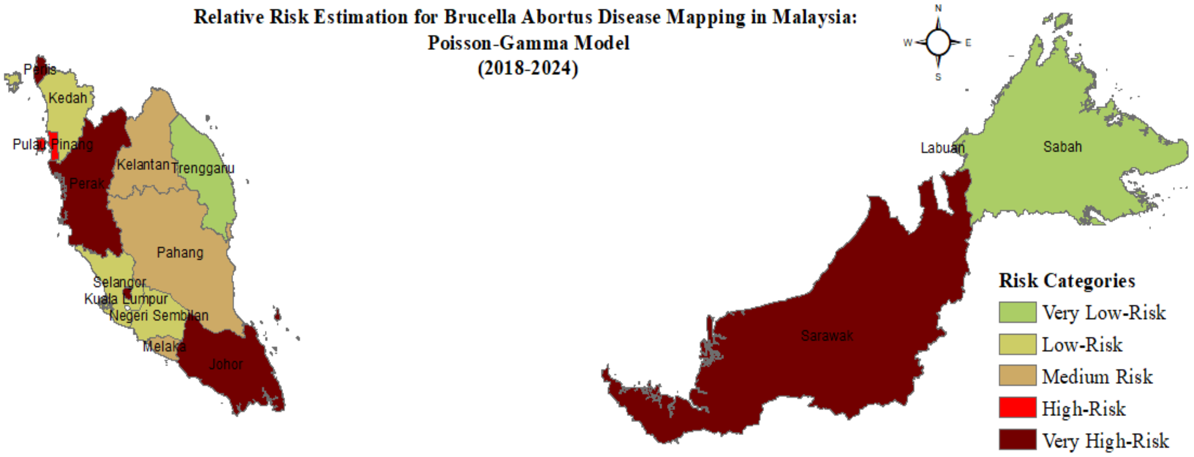

Figure 7. Poisson-Gamma Model Map for *Brucella Abortus* Cases during the years 2018 to 2024

Conclusions

This study compared the Standardized Mortality Ratio (SMR) method and the Poisson-Gamma model for estimating the relative risk (RR) of *B. abortus* in Malaysian cattle populations from 2018 to 2024. The findings indicate that the Poisson-Gamma model provides a more robust estimation of spatial risk, especially in regions with zero or sparse reported cases, such as Kuala Lumpur and Sarawak. By incorporating Bayesian smoothing, this model addresses a key limitation of the SMR method, which inaccurately assigns zero risk to areas with no reported data, and offers a more realistic reflection of the underlying disease burden in the context of likely underreporting.

Applying these models has identified several states, including Perlis, Perak, Johor, Kuala Lumpur, and Sarawak, as priority areas for intensified surveillance and intervention. The spatial patterns revealed through disease mapping highlight the need for a targeted, risk-based approach to brucellosis control in Malaysia. This includes strengthening diagnostic capacity, enforcing livestock movement restrictions, and implementing vaccination programs in high-density farming regions.

In practical terms, the Poisson-Gamma model is recommended for ongoing national surveillance because it produces stable risk estimates even with incomplete data. However, the model's limitations, such as difficulty adjusting for covariates and handling spatial correlation, suggest that future research should explore more advanced spatial Bayesian frameworks. These methodological advancements could further improve the accuracy of risk estimation and support more effective, evidence-based public health and veterinary policies in Malaysia.

Conflicts of Interest

The authors declare that there is no conflict of interest regarding the publication of this paper.

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References

[1] Khurana, S. K., Sehrawat, A., Tiwari, R., Prasad, M., Gulati, B., Shabbir, M. Z., ... & Chaicumpa, W. (2021). Bovine brucellosis–a comprehensive review. *Veterinary Quarterly*, *41*(1), 61-88.

[2] Qureshi, K. A., Parvez, A., Fahmy, N. A., Abdel Hady, B. H., Kumar, S., Ganguly, A., ... & Aspatwar, A. (2023). Brucellosis: epidemiology, pathogenesis, diagnosis and treatment–a comprehensive review. *Annals of medicine*, *55*(2), 2295398.

[3] Al-Afifi, A. H., Almashhadany, D. A., Al-Azazi, A. S., Khalaf, A. M., Odhah, M. N. A., & Al-Gabri, N. A. (2022). Prevalence of Brucella spp. in milk from aborted and non-aborted animals in Dhamar governorate, Yemen. *Italian Journal of Food Safety*, *11*(4), 10370.

[4] Sharma, V., Singh, B. B., & Brookes, V. J. (2025). Risk Assessment of Brucella Exposure Through Raw Milk Consumption in India: One Health Implications and Control Strategies. *Veterinary Sciences*, *12*(5), 465.

[5] Dadar, M., Tiwari, R., Sharun, K., & Dhama, K. (2021). Importance of brucellosis control programs of livestock on the improvement of one health. *Veterinary Quarterly*, *41*(1), 137-151.

[6] Lokamar, P. N., Kutwah, M. A., Atieli, H., Gumo, S., & Ouma, C. (2020). Socio-economic impacts of brucellosis on livestock production and reproduction performance in Koibatek and Marigat regions, Baringo County, Kenya. *BMC veterinary research*, *16*(1), 61.

[7] Ghssein, G., Ezzeddine, Z., Tokajian, S., Al Khoury, C., Kobeissy, H., Ibrahim, J. N., ... & Hassan, H. F. (2025). Brucellosis: Bacteriology, Pathogenesis, Epidemiology and Role of the Metallophores in Virulence: A Review. *Frontiers in Cellular and Infection Microbiology*, *15*, 1621230.

[8] Laine, C. G., Johnson, V. E., Scott, H. M., & Arenas-Gamboa, A. M. (2023). Global estimate of human brucellosis incidence. *Emerging infectious diseases*, *29*(9), 1789.

[9] Samadi, A., Amiri, M., & Hailat, N. (2024). The reasons behind long-term endemicity of brucellosis in low and middle-income countries: challenges and future perspectives. *Current Microbiology*, *81*(3), 82.

[10] Maldonado-García, J. L., Alvarez-Herrera, S., Pérez-Sánchez, G., Becerril-Villanueva, E., Pavón, L., Tesoro-Cruz, E., ... & Moreno-Lafont, M. C. (2024). Concomitant treatment with doxycycline and rifampicin in Balb/c mice infected with Brucella abortus 2308 fails to reduce inflammation and motor disability. *Pharmaceuticals*, *17*(5), 638.

[11] Yang, C., Gao, J., Xian, R., Liu, X., Kuai, W., Yin, C., ... & Ma, J. (2024). Molecular epidemiology of Brucella abortus isolated from the environment in Ningxia Hui autonomous region, China. *Infection, Genetics and Evolution*, *123*, 105635.

[12] Yektay, S., Alimi, R., Attarian, F., Siuki, H. A., Aval, M. G., & Gholizadeh, A. (2025). Brucellosis and associated risk factors, spatial distribution and cluster analysis: Case study in Khorasan Razavi Province, Iran. *Journal of Infection and Public Health*, *18*(6), 102747.

[13] Zhao, Y., Pan, D., Zhang, Y., Ma, L., Li, H., Li, J., ... & Liang, P. (2025). Spatial interpolation and spatiotemporal scanning analysis of human brucellosis in mainland China from 2012 to 2018. *Scientific Reports*, *15*(1), 7403.

[14] Beig, M., Ebrahimi, E., Moradkasani, S., Goodarzi, F., Sholeh, M., & Golab, N. (2024). Unravelling the challenge of cotrimoxazole and rifampin resistance in B. melitensis and B. abortus: A systematic review and meta-analysis. *PLOS Neglected Tropical Diseases*, *18*(12), e0012630.

[15] Semango, G. P., & Buza, J. (2024). Review of the Current Status on Ruminant Abortigenic Pathogen Surveillance in Africa and Asia. *Veterinary Sciences*, *11*(9), 425.

[16] Yang, L., Fan, M., & Wang, Y. (2025). Dynamic Modeling of Prevention and Control of Brucellosis in China: A Systematic Review. *Transboundary and Emerging Diseases*, *2025*(1), 1393722.

[17] World Organization for Animal Health. (2025). *2025 Report - The state of the world's animal health*. https://www.woah.org/app/uploads/2025/05/woah-the-state-of-the-worlds-animal-health-2025.pdf

[18] Diah, I. M., Aziz, N., & Kasim, M. M. (2017). A comparison of four disease mapping techniques as applied to TB diseases in Malaysia. *Journal of Telecommunication, Electronic and Computer Engineering (JTEC)*, *9*(2-11), 133-137.

[19] Meza, J. L. (2003). Empirical Bayes estimation smoothing of relative risks in disease mapping. *Journal of Statistical Planning and Inference*, *112*(1-2), 43-62.

[20] Perez-Panades, J., Botella-Rocamora, P., & Martinez-Beneito, M. A. (2020). Beyond standardized mortality ratios; some uses of smoothed age-specific mortality rates on small areas studies. *International journal of health geographics*, *19*(1), 54.

[21] Ghanbarnejad, A., Turki, H., Yaseri, M., Raeisi, A., & Rahimi-Foroushani, A. (2021). Spatial modelling of malaria in south of iran in line with the implementation of the malaria elimination program: a Bayesian poisson-gamma random field model. *Journal of Arthropod-Borne Diseases*, *15*(1), 108.

[22] Jaya, I. G. N. M., & Folmer, H. (2020). Bayesian spatiotemporal mapping of relative dengue disease risk in Bandung, Indonesia. *Journal of geographical systems*, *22*(1), 105-142.

[23] Lawson, A. B. (2006). Statistical Methods in Spatial Epidemiology. England: Wiley, pp 1-424.

[24] Di Bari, C., Venkateswaran, N., Bruce, M., Fastl, C., Huntington, B., Patterson, G. T., ... & Devleesschauwer, B. (2022). Methodological choices in brucellosis burden of disease assessments: A systematic review. *PLoS neglected tropical diseases*, *16*(12), e0010468.

[25] Lawson, A. B., Browne, W. J., & Rodeiro, C. L. V. (2003). *Disease mapping with WinBUGS and MLwiN*. John Wiley & Sons.

[26] Worsley-Tonks, K. E., Bender, J. B., Deem, S. L., Ferguson, A. W., Fèvre, E. M., Martins, D. J., ... & Hassell, J. M. (2022). Strengthening global health security by improving disease surveillance in remote rural areas of low-income and middle-income countries. *The Lancet Global Health*, *10*(4), e579-e584.

[27] Akoko, J. M., Mwatondo, A., Muturi, M., Wambua, L., Abkallo, H. M., Nyamota, R., ... & Bett, B. (2023). Mapping brucellosis risk in Kenya and its implications for control strategies in sub-Saharan Africa. *Scientific Reports*, *13*(1), 20192.

[28] Tian, Z., Jiang, S., Yuan, P., Wang, X., Pei, J., Tang, H., ... & Chen, Y. (2025). Mapping risks: A value chain approach to brucellosis introduction in Zhijiang's Cattle Population, China. *Preventive veterinary medicine*, *238*, 106467.

[29] Charypkhan, D., & Rüegg, S. R. (2022). One Health evaluation of brucellosis control in Kazakhstan. *PloS one*, *17*(11), e0277118.

[30] Ziapour, A., Rezaei, F., Jafarzadeh, M., Mirzaei, N., Moradi-Asl, E., & Nejhaddadgar, N. (2025). Practical Steps to Design Brucellosis Preventive Interventions: An Intervention Mapping Approach. *Health Science Reports*, *8*(1), e70369.

[31] Ahmad, A., Alolaiyan, H., Masmali, I. A., Salleh, Z., & Ismail, S. (2021). A descent four-term of Liu and Storey conjugate gradient method for large scale unconstrained optimization problems. *European Journal of Pure and Applied Mathematics*, *14*(4), 1429–1456.

[32] Grembi, J. A., & Rogawski McQuade, E. T. (2022). Introducing risk Communicator: an R package to obtain interpretable effect estimates for public health. *PLoS One*, *17*(7), e0265368.

[33] Ribeiro, M., Azevedo, L., & Pereira, M. J. (2024). EpiGeostats: an R Package to facilitate visualization of Geostatistical Disease Risk maps. *Mathematical Geosciences*, *56*(1), 103-119.

[34] Peterson, E., & Ver Hoef, J. (2014). STARS: An ArcGIS toolset used to calculate the spatial information needed to fit spatial statistical models to stream network data. *Journal of Statistical Software*, *56*(1), 1-17.

[35] Pinatt, J. M., Chicati, M. L., Ildefonso, J. S., & Filetti, C. R. G. D. A. (2020). Evaluation of pavement condition index by different methods: Case study of Maringá, Brazil. *Transportation Research Interdisciplinary Perspectives*, *4*, 100100.

[36] He, Y., Wang, J., Zhang, R., Chen, L., Zhang, H., Qi, X., & Chen, J. (2023). Epidemiology of foodborne diseases caused by Salmonella in Zhejiang Province, China, between 2010 and 2021. *Frontiers in public health*, *11*, 1127925.

[37] Bedir, M., Marouf, S., Sayed, R. H., El-Diasty, M., Hassan, H. M., Shahien, M. A., ... & Eljakee, J. (2025). Development and evaluation of a novel lateral flow immunoassay for rapid diagnosis of brucellosis across different animal species. *Scientific Reports*, *15*(1), 24149.

[38] Loubet, P., Magnan, C., Salipante, F., Pastre, T., Keriel, A., O'callaghan, D., ... & Lavigne, J. P. (2024). Diagnosis of brucellosis: Combining tests to improve performance. *PLoS neglected tropical diseases*, *18*(9), e0012442.

[39] Ni, H., Dai, H., Yang, X., Zhao, J., He, Y., Yi, S., ... & Lv, Y. (2024). Effective intervention of brucellosis prevention in developing countries: A dynamic modelling study. *One Health*, *19*, 100840.

[40] Azuara-García, G., Palacios, E., & Montesinos-Barrios, P. (2022). Embedding sustainable land-use optimization within system dynamics: Bidirectional feedback between spatial and non-spatial drivers. *Environmental Modelling & Software*, *155*, 105463.

[41] Kumari, S., & Upadhyay, R. K. (2020). Dynamics comparison between non-spatial and spatial systems of the plankton–fish interaction model. *Nonlinear Dynamics*, *99*(3), 2479-2503.

[42] Yin, Z., Jin, Z., Ying, S., Li, S., & Liu, Q. (2020). A spatial data model for urban spatial–temporal accessibility analysis. *Journal of geographical systems*, *22*(4), 447-468.

[43] Flórez-Lozano, K., Navarro-Lechuga, E., Llinás-Solano, H., Tuesca-Molina, R., Sisa-Camargo, A., Mercado-Reyes, M., ... & Acosta-Reyes, J. (2020). Spatial distribution of the relative risk of Zika virus disease in Colombia during the 2015–2016 epidemic from a Bayesian approach. *International Journal of Gynecology & Obstetrics*, *148*, 55-60.

[44] Hasani, W. S. R., Muhamad, N. A., Hanis, T. M., Maamor, N. H., Chen, X. W., Omar, M. A., ... & Musa, K. I. (2023). The global estimate of premature cardiovascular mortality: a systematic review and meta-analysis of age-standardized mortality rate. *BMC Public Health*, *23*(1), 1561.

[45] Li, X., Cao, X., Guo, M., Xie, M., & Liu, X. (2020). Trends and risk factors of mortality and disability adjusted life years for chronic respiratory diseases from 1990 to 2017: systematic analysis for the Global Burden of Disease Study 2017. *bmj*, *368*.

[46] Pizzato, M., Li, M., Vignat, J., Laversanne, M., Singh, D., La Vecchia, C., & Vaccarella, S. (2022). The epidemiological landscape of thyroid cancer worldwide: GLOBOCAN estimates for incidence and mortality rates in 2020. *The lancet Diabetes & endocrinology*, *10*(4), 264-272.

[47] Haakonsson, S., Rodríguez, M. A., Carballo, C., del Carmen Perez, M., Arocena, R., & Bonilla, S. (2020). Predicting cyanobacterial biovolume from water temperature and conductivity using a Bayesian compound Poisson-Gamma model. *Water Research*, *176*, 115710.

[48] Karim, M. R. (2024). Bayesian hierarchical spatial modeling of covid-19 cases in bangladesh. *Annals of Data Science*, *11*(5), 1581-1607.

[49] Sarker, I., Karim, M. R., E-Barket, S., & Hasan, M. (2024). Dengue fever mapping in Bangladesh: a spatial modeling approach. *Health Science Reports*, *7*(6), e2154.

[50] Katale, R. N., & Gemechu, D. B. (2023). Spatio-temporal analysis of malaria incidence and its risk factors in North Namibia. *Malaria journal*, *22*(1), 149.

[51] Murray, C. J., Aravkin, A. Y., Zheng, P., Abbafati, C., Abbas, K. M., Abbasi-Kangevari, M., ... & Borzouei, S. (2020). Global burden of 87 risk factors in 204 countries and territories, 1990–2019: a systematic analysis for the Global Burden of Disease Study 2019. *The lancet*, *396*(10258), 1223-1249.

[52] Samat, N. A., & Percy, D. F. (2012, September). Dengue disease mapping in Malaysia based on stochastic SIR models in human populations. In *2012 International Conference on Statistics in Science, Business and Engineering (ICSSBE)* (pp. 1-5). IEEE.

[53] Taquet, M., Dercon, Q., Luciano, S., Geddes, J. R., Husain, M., & Harrison, P. J. (2021). Incidence, co-occurrence, and evolution of long-COVID features: A 6-month retrospective cohort study of 273,618 survivors of COVID-19. *PLoS medicine*, *18*(9), e1003773.

[54] Dhawan, S., Muluneh, A. G., Pan-Gnum, W., MacIntyre, C. R., Summermatter, K., & Blacksell, S. D. (2025). Risk factors and mitigation strategies of laboratory-acquired infections in research and clinical laboratories worldwide: a systematic review. *The Lancet Microbe*.

[55] Tschopp, R., & Kidanu, A. G. (2024). Knowledge-attitude and practice of Anthrax and brucellosis: Implications for zoonotic disease surveillance and control in pastoral communities of Afar and Somali region, Ethiopia. *PLOS Neglected Tropical Diseases*, *18*(4), e0012067.

[56] Zamri-Saad, M., & Kamarudin, M. I. (2016). Control of animal brucellosis: The Malaysian experience. *Asian Pacific journal of tropical medicine*, *9*(12), 1136-1140.

[57] Sadiq, M. B., Hamid, N. A., Yusri, U. K., Ramanoon, S. Z., Mansor, R., Affandi, S. A., ... & Syed-Hussain, S. S. (2021). Ruminant farmers' knowledge, attitude and practices towards zoonotic diseases in Selangor, Malaysia. *Preventive veterinary medicine*, *196*, 105489.

[58] Mazlan, S. A. N., Sabri, F. S. A. H., Zahidi, J. A. M., Seman, Z., Ahmad, N., & Ramli, S. R. (2022). Human brucellosis: Six years retrospective study on seropositivity in Malaysia. *The Malaysian Journal of Pathology*, *44*(2), 269-276.

[59] Islam, M. S., Islam, M. A., Rahman, M. M., Islam, K., Islam, M. M., Kamal, M. M., & Islam, M. N. (2023). Presence of Brucella spp. in milk and dairy products: a comprehensive review and its perspectives. *Journal of Food Quality*, *2023*(1), 2932883.

[60] Zeb, S., Yasmin, H., Malik, I. R., Farah, M. A., Arya, V. M., & Hassan, M. N. (2025). Antimicrobial resistant Brucella spp. prevail in raw milk and animal feces of different livestock farms. *BMC microbiology*, *25*(1), 1-9.

[61] Bamaiyi, P., Hassan, L., Khairani-Bejo, S., Zainalabidin, M., & Adzhar, A. (2017). Seroprevalence of Brucellosis among Farmers and Veterinary Technical Staff in the Central States of Peninsular Malaysia. *Sains Malaysiana*, *46*(6), 933-943.

[62] Jimale, Y. A., Jesse, F. F. A., Paul, B. T., Chung, E. L. T., Zakaria, A., Azhar, N. A., & Mohd Lila, M. A. (2024). Seroprevalence and contributing factors of transboundary animal diseases in sheep and goats: a study in Peninsular Malaysia. *Tropical Animal Health and Production*, *56*(6), 212.

[63] Pereira, C. R., Cotrim de Almeida, J. V. F., Cardoso de Oliveira, I. R., Faria de Oliveira, L., Pereira, L. J., Zangeronimo, M. G., ... & Dorneles, E. M. S. (2020). Occupational exposure to Brucella spp.: A systematic review and meta-analysis. *PLoS neglected tropical diseases*, *14*(5), e0008164.

[64] Mwaba, J., Debes, A. K., Shea, P., Mukonka, V., Chewe, O., Chisenga, C., ... & Ali, M. (2020). Identification of cholera hotspots in Zambia: a spatiotemporal analysis of cholera data from 2008 to 2017. *PLoS neglected tropical diseases*, *14*(4), e0008227.

[65] Ola-Fadunsin, S. D., Sharma, R. S. K., Abdullah, D. A., Gimba, F. I., Jesse, F. F. A., & Sani, R. A. (2020). Molecular detection, prevalence and risk factors of Theileria orientalis infection among cattle in Peninsular Malaysia. *Preventive veterinary medicine*, *180*, 105027.

[66] Sadiq, M. B., Ramanoon, S. Z., Mossadeq, W. S., Mansor, R., & Syed-Hussain, S. S. (2021). Prevalence and risk factors for hoof lesions in dairy cows in Peninsular Malaysia. *Livestock Science*, *245*, 104404.