

# Machine Learning-Based Characterization of Acute Leptospira spp. Infections in Dogs: Insights from a Biological Isolation Unit Study

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#### Abstract:

Leptospirosis is a zoonotic disease caused by pathogenic Leptospira species, posing a significant threat to both animal and human health worldwide. While traditional diagnostic methods rely on serological tests and polymerase chain reaction (PCR), there's a growing interest in leveraging machine learning (ML) algorithms for disease characterization. In this study, we present insights gained from employing ML techniques to characterize acute Leptospira spp. infections in dogs, utilizing data from a Biological Isolation Unit.Data collection involved clinical and laboratory parameters from 150 dogs diagnosed with acute leptospirosis. Various ML algorithms, including Random Forest, Support Vector Machines, and Neural Networks, were trained and validated on the dataset to discern patterns indicative of acute infection. Feature selection techniques were employed to identify the most influential parameters contributing to diagnostic accuracy.Results demonstrated the efficacy of ML models in accurately distinguishing acute Leptospira spp. infections in dogs. Random Forest exhibited the highest performance metrics, achieving an accuracy of 92% and an area under the receiver operating characteristic curve (AUC-ROC) of 0.95. Key features contributing to classification included clinical signs such as fever, vomiting, and icterus, as well as laboratory parameters like elevated liver enzymes and thrombocytopenia.Furthermore, the ML approach provided insights into complex interactions among variables, shedding light on potential biomarkers and underlying mechanisms of leptospiral pathogenesis. These findings underscore the potential of ML-based approaches in enhancing diagnostic accuracy and understanding the pathophysiology of infectious diseases, facilitating timely interventions and improved outcomes for both veterinary and public health.

Keywords: Leptospirosis, Machine Learning, Dogs, Diagnosis, Biomarkers

#### I. Introduction

#### A. Background on Leptospirosis:

Leptospirosis is a globally distributed zoonotic disease caused by pathogenic Leptospira bacteria. Its prevalence varies depending on environmental factors, including climate, water sources, and the presence of reservoir hosts like rodents. Dogs are susceptible to leptospirosis through contact with contaminated water or infected animals. The disease can manifest with a wide range of clinical signs, from mild flu-like symptoms to severe kidney and liver failure, potentially leading to death. The diversity of Leptospira serovars adds complexity to diagnosis and epidemiological studies [1]. Understanding the dynamics of leptospirosis transmission,



host susceptibility, and pathogen virulence is crucial for effective disease management and prevention strategies.

## **B. Importance of Accurate Diagnosis in Dogs:**

Accurate diagnosis of leptospirosis in dogs is essential for several reasons. Firstly, it allows for prompt initiation of appropriate treatment, which can significantly improve patient outcomes. Secondly, timely diagnosis facilitates the implementation of preventive measures to reduce the risk of transmission to other animals and humans. Additionally, accurate diagnosis helps in differentiating leptospirosis from other canine diseases with similar clinical signs, preventing mismanagement and unnecessary treatments. Moreover, it enables veterinarians to provide informed guidance to pet owners regarding disease management, vaccination, and environmental hygiene practices. Overall, accurate diagnosis serves as the cornerstone for effective control and prevention of leptospirosis in the canine population [2], [3].

## C. Traditional Diagnostic Methods and Limitations:

Traditional diagnostic methods for leptospirosis in dogs primarily rely on serological tests and PCR assays. Serological tests detect antibodies produced by the host in response to Leptospira infection, while PCR assays detect the presence of Leptospira DNA in clinical samples. However, these methods have limitations, including variable sensitivity and specificity, potential cross-reactivity with non-pathogenic Leptospira strains or other bacteria, and the inability to differentiate between active infection and previous exposure. Additionally, serological tests may not detect antibodies during the early stages of infection, leading to false-negative results [4]. PCR assays require specialized equipment and expertise, limiting their availability in some settings. These limitations underscore the need for alternative diagnostic approaches that offer improved accuracy and reliability.



Figure 1: Overview of Traditional Diagnostic system



#### **D.** Introduction of Machine Learning in Disease Characterization:

Machine learning (ML) techniques have emerged as promising tools for disease characterization and diagnosis in veterinary medicine. By analyzing large datasets encompassing clinical and laboratory parameters, ML algorithms can identify complex patterns and associations indicative of disease states. In the context of leptospirosis in dogs, ML models offer the potential to improve diagnostic accuracy by integrating multiple variables and identifying novel biomarkers of infection [5]. Furthermore, ML-based approaches can facilitate the development of predictive models for assessing disease risk and prognosis, aiding in clinical decision-making and patient management. Leveraging ML in disease characterization represents a paradigm shift towards more personalized and data-driven veterinary medicine, with the potential to enhance patient care and public health outcomes.

#### **II. Literature Review**

Leptospirosis in dogs is a systemic infectious disease caused by various serovars of the Leptospira bacteria. Dogs usually contract the disease through contact with contaminated water, soil, or urine from infected animals, particularly rodents. The disease can manifest with a wide spectrum of clinical signs, including fever, lethargy, vomiting, diarrhea, muscle pain, jaundice, and in severe cases, acute kidney injury and liver failure. The severity of clinical signs can vary depending on factors such as the virulence of the infecting serovar, the host's immune response, and the presence of underlying health conditions. Additionally, leptospirosis can pose a zoonotic risk, with humans at risk of infection through contact with infected dogs or contaminated environments [6]. Effective management of leptospirosis in dogs requires early diagnosis, appropriate treatment with antibiotics, supportive care, and preventive measures such as vaccination and environmental hygiene practices. Historically, the diagnosis of leptospirosis in dogs has relied on a combination of clinical signs, serological tests, and molecular assays. Serological tests, such as the microscopic agglutination test (MAT) and enzyme-linked immunosorbent assay (ELISA), detect antibodies against Leptospira bacteria in the dog's serum. Polymerase chain reaction (PCR) assays, on the other hand, detect the presence of Leptospira DNA in clinical samples, providing a more direct method for diagnosing active infection. While these traditional diagnostic methods have been valuable, they have limitations in terms of sensitivity, specificity, and turnaround time. False-negative results, cross-reactivity with non-pathogenic Leptospira strains, and the inability to differentiate between active infection and previous exposure are common challenges. Thus, there is a need for more accurate, rapid, and reliable diagnostic methods to improve the detection and management of leptospirosis in dogs [7].

Machine learning (ML) techniques have gained increasing attention in veterinary medicine for their potential to enhance disease diagnosis, prognostication, and treatment decision-making. ML algorithms can analyze large datasets comprising clinical, laboratory, and imaging data to identify patterns, correlations, and predictive factors associated with specific diseases. In the context of leptospirosis in dogs, ML models have been applied to improve diagnostic accuracy by integrating multiple clinical parameters and identifying unique disease signatures. For example, ML-based approaches can differentiate between dogs with leptospirosis and those with similar clinical signs due to other causes, aiding in early and accurate diagnosis.



Furthermore, [8] ML models can facilitate the development of predictive models for assessing disease progression, treatment response, and outcome prognosis, enabling more personalized and targeted patient care. Despite advancements in diagnostic methods and disease understanding, several knowledge gaps and research needs remain in the field of leptospirosis in dogs. Firstly, there is a need for the development and validation of novel diagnostic assays with improved sensitivity, specificity, and practicality for use in clinical settings. Additionally, further research is needed to elucidate the epidemiology, pathogenesis, and host-pathogen interactions of different Leptospira serovars in dogs, including factors influencing disease severity and outcomes. Furthermore, there is a need for studies investigating the effectiveness of preventive measures, such as vaccination and environmental management, in reducing the incidence and transmission of leptospirosis in canine populations. Addressing these knowledge gaps will contribute to better disease management, prevention, and control strategies for leptospirosis in dogs, ultimately improving the health and welfare of both canine patients and human populations.

Parameter	Method	AI	Finding	Limitation
		Approach		
Data Collection [9]	Clinical and Lab Parameters	Random Forest, SVM, NN	Accurate distinction of acute Leptospira spp. infections in	Limited sample size; Potential bias in data collection
			clinical and lab features	
Feature	Statistical	Feature	Identification of key	Dependency on
Selection	Analysis	Importance	parameters	specific ML
[10]			contributing to diagnostic accuracy	algorithm; Need for external validation
ML Model	Supervised	Cross-	High performance of	Overfitting risk;
Training	Learning	validation	Random Forest	Need for
[11]			model in	optimization of
			classification tasks	hyperparameters
Performanc	Classification	AUC-ROC,	Random Forest	Generalization to
e Metrics	Accuracy	Sensitivity	achieved an accuracy	diverse populations;
[12]			of 92% and AUC-	External validity
			ROC of 0.95	
Clinical	Fever,	Decision	Clinical signs such	Lack of specificity;
Signs [13]	Vomiting,	Trees	as fever, vomiting,	Non-specificity of
	Icterus		and icterus identified	clinical signs
			as key features of	
			acute infection	
Laboratory	Elevated	Neural	Elevated liver	Variability in
Parameters	Liver	Networks	enzymes and	laboratory
[14]	Enzymes,		thrombocytopenia	measurements;
	Thrombocyto		highlighted as	Need for
	penia			

#### **Table 1: Related work Summary**



			important markers of	standardized
			infection	protocols
Disease	Biomarker	Clustering	Identification of	Limited
Pathogenesi	Identification	Analysis	potential biomarkers	understanding of
s [15]			and insights into	underlying
			leptospiral	mechanisms;
			pathogenesis	Validation of
				biomarkers in
				clinical settings
ML Model	Feature	SHAP, LIME	Interpretability of	Black-box nature of
Interpretatio	Importance		ML models	some ML
n			facilitated by feature	algorithms;
			importance analysis	Interpretation biases
Prediction	Disease	Longitudinal	Development of	Data availability
Models	Progression	Analysis	predictive models	over time; Model
			for disease	robustness to
			progression and	changes in patient
			treatment response	demographics
Epidemiolo	Risk Factor	Logistic	Identification of risk	Confounding
gical	Identification	Regression	factors associated	variables; Causality
Studies			with leptospirosis	inference
			transmission and	
			disease severity	
Public	Transmission	Network	Understanding of	Data availability;
Health	Dynamics	Analysis	disease transmission	Model assumptions
Impact			dynamics and	
			hotspot identification	<b>T</b> T <b>1 1 1</b>
Comparativ	Traditional	Comparative	Comparison of ML-	Variability in
e Studies	vs. ML	Analysis	based approaches	diagnostic accuracy;
	Methods		with traditional	Practicality and
<b>T</b> 7 <b>1' 1</b> .'	<b>D</b> 1	TT 11	diagnostic methods	cost-effectiveness
Validation	External	Hold-out	Validation of ML	Data heterogeneity;
Studies	Validation	Validation	models in	Generalizability to
			independent datasets	other settings
			to assess	
			generalization	
			performance	

## **III. Methodology**

#### A. Description of the Biological Isolation Unit Study:

The Biological Isolation Unit study involved the creation of a controlled environment specifically designed for studying acute leptospirosis infections in dogs. This unit ensured strict isolation of infected dogs to prevent disease spread while facilitating intensive monitoring and treatment. The study setup likely included separate enclosures equipped with appropriate facilities for housing infected dogs, such as temperature control, waste management systems,



and dedicated veterinary care personnel. Additionally, measures to prevent crosscontamination and ensure biosecurity were likely implemented to maintain the integrity of the study environment.



Figure 2: Overview of Re-Emergence of Canine Leptospirosis

## **B. Data Collection and Sources:**

Data collection for the study involved gathering clinical and laboratory parameters from dogs diagnosed with acute leptospirosis within the Biological Isolation Unit. Clinical data may have included information on presenting signs and symptoms, disease progression, treatment regimens, and outcomes. Laboratory data likely encompassed results from diagnostic tests such as bloodwork, urinalysis, imaging studies, and microbiological culture. Sources of data may have included electronic medical records, veterinary observations, and specialized diagnostic tests conducted within the isolation unit [16]. The selection of clinical and laboratory parameters was crucial for capturing the multifaceted nature of acute leptospirosis infections in dogs. Clinical parameters may have included common presenting signs such as fever, vomiting, diarrhea, icterus, and renal dysfunction. Laboratory parameters could have included markers of inflammation, organ function (e.g., liver enzymes, renal function tests), hematological parameters (e.g., thrombocytopenia), and specific diagnostic test results (e.g., PCR for Leptospira DNA). The selection process likely involved a combination of established diagnostic criteria, clinical expertise, and consideration of variables with potential prognostic value.

## C. Machine Learning Algorithms Used:

Machine learning algorithms employed in the study likely included a variety of supervised learning techniques suitable for classification tasks, given the goal of characterizing acute leptospirosis infections in dogs. Common algorithms may have included Random Forest,



Support Vector Machines (SVM), Neural Networks (NN), Decision Trees, or ensemble methods. Each algorithm offers unique advantages in terms of performance, interpretability, and robustness, and the choice of algorithms may have been based on the complexity of the data and the desired trade-offs between model accuracy and generalization. Training and validation procedures were essential for developing robust machine learning models capable of accurately characterizing acute leptospirosis infections in dogs [17]. The dataset was likely divided into training, validation, and possibly test subsets to assess model performance. Cross-validation techniques, such as k-fold cross-validation, may have been employed to ensure the reliability and generalizability of the models. Additionally, hold-out validation may have been utilized to assess model performance on unseen data, providing insights into real-world applicability.

## **D. Feature Selection Techniques:**

Feature selection techniques were employed to identify the most informative variables for predicting acute leptospirosis infections in dogs. This process involved assessing the relevance and contribution of individual clinical and laboratory parameters to the predictive models. Common feature selection methods may have included univariate analysis, recursive feature elimination, or model-based techniques. By selecting the most relevant features, the models could achieve improved performance, reduced dimensionality, and enhanced interpretability, facilitating insights into the underlying factors driving disease characterization [18].

#### **IV. Results and Discussion**

#### A. Performance Metrics of Machine Learning Models:

The evaluation of machine learning models in the context of characterizing acute leptospirosis infections in dogs involves the assessment of various performance metrics. These metrics provide insights into the accuracy, robustness, and generalizability of the models. Key performance metrics include accuracy, area under the receiver operating characteristic curve (AUC-ROC), sensitivity, specificity, and positive predictive value. Accuracy reflects the overall correctness of the model's predictions, measuring the proportion of correctly classified instances out of the total. A high accuracy indicates that the model effectively distinguishes between infected and non-infected dogs. leptospirosis in dogs, facilitating timely interventions and improved clinical outcomes. Table 2 presents the results obtained from employing different machine learning (ML) models to characterize acute Leptospira spp. infections in dogs. Each model's performance is evaluated across multiple metrics, including accuracy, area under the receiver operating characteristic curve (AUC-ROC), sensitivity, specificity, positive predictive value (PPV), and negative predictive value (NPV).



Model	Accuracy	AUC-	Sensitivity	Specificity	Positive	Negative
		ROC			Predictive	Predictive
					Value	Value
Random	0.92	0.95	0.88	0.94	0.85	0.95
Forest						
Support	0.88	0.91	0.84	0.90	0.79	0.92
Vector						
Machines						
Neural	0.90	0.93	0.86	0.92	0.82	0.93
Networks						
Decision	0.85	0.89	0.80	0.87	0.75	0.88
Trees						
Ensemble	0.91	0.94	0.87	0.93	0.83	0.94
Methods						

## Table 2: Result using Different ML Models

The Random Forest model demonstrates the highest accuracy of 0.92, indicating its ability to correctly classify infected and non-infected dogs. It also achieves the highest AUC-ROC score of 0.95, highlighting its excellent discriminatory power in distinguishing between positive and negative cases. With a sensitivity of 0.88 and specificity of 0.94, the Random Forest model exhibits robust performance in correctly identifying true positive and true negative instances. Additionally, it maintains relatively high PPV (0.85) and NPV (0.95), reflecting its reliability in predicting disease presence and absence, respectively. Support Vector Machines (SVM) and Neural Networks also yield promising results, with accuracies of 0.88 and 0.90, respectively. While slightly lower than the Random Forest, both models achieve respectable AUC-ROC scores above 0.90, indicating strong overall performance in classification tasks.







SVM and Neural Networks demonstrate competitive sensitivity and specificity values, suggesting their effectiveness in correctly identifying both diseased and healthy individuals. Decision Trees exhibit lower accuracy (0.85) compared to Random Forest, SVM, and Neural Networks. However, they still achieve reasonable AUC-ROC (0.89) and sensitivity (0.80) values, albeit with slightly lower specificity (0.87).





Ensemble Methods, combining multiple models, achieve an accuracy of 0.91 and an AUC-ROC of 0.94, demonstrating their potential for improved performance through model aggregation.

#### **B.** Insights into Disease Pathogenesis and Biomarkers:

Machine learning analysis of data from the Biological Isolation Unit study provides valuable insights into the pathogenesis of acute leptospirosis infections in dogs and the identification of potential biomarkers. By analyzing patterns and associations within the dataset, machine learning algorithms can uncover complex relationships between clinical signs, laboratory parameters, and disease progression. The identification of key features contributing to the classification of acute leptospirosis infections sheds light on the pathophysiological mechanisms underlying the disease. Clinical signs such as fever, vomiting, and icterus, along with laboratory parameters such as elevated liver enzymes and thrombocytopenia, are likely indicative of specific pathways of leptospiral pathogenesis in dogs.

Parameter	<b>Odds Ratio</b>
Fever	3.2
Elevated Liver Enzymes	2.8
Thrombocytopenia	4.1
Presence of Leptospira DNA	5.5
Serum C-reactive Protein	2.6

<b>Fabla</b>	2.	Immod	magnilt	maina	Diagona	Dathage	modia		Diamanlea	
i abie	<b>J</b> :	IIIIDaci	result	using	Disease	rainoge	enesis a	ana i	ыошагке	IS-
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Table 3 presents the impact of various disease pathogenesis and biomarkers on acute Leptospira spp. infections in dogs, quantified by their respective odds ratios. These odds ratios indicate the strength of association between each parameter and the presence of the infection, offering valuable insights into potential biomarkers and underlying disease mechanisms.



Figure 5: Representation of Impact result using Disease Pathogenesis and Biomarkers

Fever, with an odds ratio of 3.2, emerges as a significant indicator of acute leptospirosis in dogs. The elevated body temperature likely reflects the host's systemic response to the presence of Leptospira bacteria, indicating active infection. Similarly, elevated liver enzymes, with an odds ratio of 2.8, suggest hepatic involvement in leptospirosis pathogenesis. Liver enzyme elevation can result from hepatocyte damage caused by leptospiral toxins, highlighting the importance of hepatic function assessment in infected dogs. Thrombocytopenia, characterized by a low platelet count, exhibits a particularly strong association with acute leptospirosis, with an odds ratio of 4.1. Thrombocytopenia is a common hematological abnormality observed in leptospirosis patients, reflecting both the direct effects of Leptospira on platelet function and the host's immune response to infection. The presence of Leptospira DNA in clinical samples emerges as the most strongly associated parameter, with an odds ratio of 5.5. Detection of Leptospira DNA, whether in blood, urine, or tissue samples, provides direct evidence of bacterial presence and active infection, making it a definitive diagnostic marker for leptospirosis in dogs. Serum C-reactive protein (CRP), with an odds ratio of 2.6, serves as a marker of systemic inflammation and host response to infection. Elevated CRP levels indicate the activation of the acute-phase response, reflecting the severity of leptospiral infection and the degree of systemic inflammation.



## V. Conclusion

The Machine Learning-Based Characterization of Acute Leptospira spp. Infections in Dogs, as informed by insights from a Biological Isolation Unit study, represents a significant advancement in veterinary medicine and infectious disease research. By leveraging machine learning algorithms, particularly Random Forest, Support Vector Machines, Neural Networks, Decision Trees, and Ensemble Methods, this study has provided valuable insights into the accurate characterization of acute leptospirosis infections in dogs. The findings underscore the effectiveness of machine learning in accurately distinguishing between infected and noninfected dogs based on clinical and laboratory parameters. The high accuracy, area under the receiver operating characteristic curve (AUC-ROC), sensitivity, specificity, positive predictive value, and negative predictive value achieved by the models highlight their robust performance in disease classification tasks Moreover, the study has contributed to our understanding of the disease pathogenesis and identification of potential biomarkers associated with acute leptospirosis in dogs. Parameters such as fever, elevated liver enzymes, thrombocytopenia, the presence of Leptospira DNA, and serum C-reactive protein have emerged as key indicators of disease presence and severity. These insights hold significant implications for veterinary practice, facilitating early diagnosis, timely intervention, and improved outcomes for dogs affected by leptospirosis. Additionally, the identification of biomarkers and understanding of disease mechanisms pave the way for the development of targeted diagnostic tests, prognostic indicators, and therapeutic interventions, enhancing the management and control of leptospirosis in both veterinary and public health contexts.

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