Machine Learning-Based Predictive Modeling for Early Detection of Subclinical Mastitis in Dairy Herds

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Abstract
Subclinical mastitis is a widespread and economically significant condition in dairy cattle, presenting considerable difficulties due to its lack of symptoms. Prompt and precise identification is essential to reduce expenses related to milk production and treatment. This paper introduces an enhanced machine-learning-based framework for detecting subclinical mastitis, developed from an open-source project. By leveraging real-world milk quality metrics such as somatic cell count (SCC), electrical conductivity, and pH, we implemented and assessed various machine learning models. This research builds on the methodology from the IEEE paper "Applicability of Machine Learning to Improve Mastitis Prediction in Livestock," incorporating improved feature engineering, sophisticated hyperparameter tuning, and model interpretability techniques. Our LightGBM-based classifier achieves an F1-score of 0.87, surpassing baseline models. Additionally, the use of SHAP analysis allows for explainable predictions, enhancing model transparency for practical use on farms. This study illustrates how data-driven approaches can aid veterinary diagnostics and decision-making on dairy farms.
Keywords--Mastitis Detection, Subclinical Mastitis, Machine Learning, LightGBM , Dairy Cattle, SHAP.

Introduction

Mastitis is one of the most prevalent and economically damaging diseases in dairy cattle worldwide. It affects milk production, alters its quality, and increases treatment and labor costs. While clinical mastitis presents visible symptoms, subclinical mastitis (SM) is much harder to detect as it lacks obvious signs. Despite its silent nature, SM can spread within a herd and lead to significant productivity loss if not identified early. Traditional detection methods, such as laboratory-based somatic cell count (SCC) testing and physical examination, are often time-consuming, reactive, and impractical for large-scale or low-resource farms. This underscores the growing need for automated, data-driven solutions that can detect mastitis early, accurately, and affordably.

In recent years, machine learning (ML) has shown promise in agricultural health monitoring due to its ability to analyze large volumes of physiological data and identify subtle patterns that precede disease onset. Previous studies have explored various models for mastitis detection, including ensemble methods and IoT-integrated systems. Notably, Shiotsu et al. (2024) demonstrated that models like LightGBM and XGBoost can effectively predict mastitis using features like lactate dehydrogenase (LDH) biomarkers. However, their reliance on specialized, cost-intensive features and lack of model interpretability tools limit practical deployment in typical dairy environments. Moreover, the absence of transparent prediction explanations can lead to trust issues among veterinarians and farmers.

This study addresses these limitations by proposing a cost-effective, interpretable machine learning framework for early detection of subclinical mastitis using routinely available milk parameters such as SCC, pH, and electrical conductivity. We employ advanced preprocessing, feature engineering, and automated hyperparameter tuning to build robust models, with LightGBM emerging as the top performer. Additionally, we integrate SHAP (Shapley Additive Explanations) to provide per-feature contribution insights, making the model outputs more transparent and actionable for farm-level decision-making. Our objective is to develop a scalable, trustworthy solution that can be integrated into existing dairy workflows, enabling timely interventions and supporting sustainable livestock health management.

Literature Review

In recent years, several studies have explored the use of machine learning techniques to improve mastitis detection and classification in dairy cattle. Shiotsu et al. [1] proposed an ensemble learning approach using LDH biomarkers for early detection of mastitis. Their study employed LightGBM and XGBoost models trained on longitudinal farm data, demonstrating moderate predictive performance but relying on costly biochemical markers that may not be feasible for small-scale deployment. Similarly, Khan et al. [2] developed an IoT-based intelligent decision support system, integrating behavioral sensors and SVM classifiers to detect mastitis in real time, although this setup demands significant infrastructure investment.

Motohashi et al. [3] employed logistic regression models utilizing data from automated milking systems, particularly focusing on electrical conductivity and milk yield to identify subclinical mastitis. Kassab et al. [4] presented a broader IoT architecture for livestock management, using large-scale sensor data and analytics, though mastitis detection was not the primary focus. Jensen et al. [5] applied ensemble learning on time-series sensor data for early-stage mastitis prediction, emphasizing the potential of real-time monitoring systems. Fadul-Pacheco et al. [6] utilized Random Forest algorithms trained on somatic cell scores and milk yield during early lactation, while Ghafoor and Sitkowska [7] addressed class imbalance in mastitis detection by applying up-sampling techniques and weighted classification strategies.

Luo et al. [8] developed a machine learning model using milk conductivity and pH data within an IoT-enhanced environment to classify mastitis severity. Bobbo et al. [9] conducted a multicenter study involving logistic regression on cow-level features such as SCC, fat content, and milk flow parameters. Zhang et al. [10] proposed a mastitis risk prediction framework using Random Forest and SVM classifiers trained on farm health records and lactation data. Chen et al. [11] evaluated decision tree-based models and SVMs on laboratory and imaging datasets, highlighting the applicability of machine learning in clinical diagnosis.

Wang et al. [12] benchmarked multiple classification algorithms, including Naive Bayes and Logistic Regression, using basic milk quality indicators from dairy herds. Singh and Kumar [13] developed an AI-based rule-driven expert system augmented with machine learning for mastitis identification on open-access datasets. Lee et al. [14]

focused on early lactation indicators and applied interpretable machine learning models to distinguish between infected and healthy cows. Finally, Kumar and Sharma [15] utilized deep learning ensembles trained on historical veterinary and production records to enhance prediction accuracy and system reliability.

While these studies demonstrate the feasibility of using machine learning for mastitis detection, challenges such as model interpretability, cost of implementation, and reliance on specialized biomarkers remain. The present study addresses these limitations by developing a low-cost, explainable, and farm-deployable machine learning framework using easily measurable milk parameters and SHAP-based model transparency.

Comparative Analysis

This study adopts a comparative machine learning approach for the early detection of subclinical mastitis in dairy cattle. The core objective is to evaluate the suitability of various models using standard milk quality features and determine the most promising algorithm for practical deployment. The experimental design includes a structured sequence of preprocessing, feature extraction, model tuning, evaluation, and interpretability, as illustrated in Figure 1.

The raw dataset, collected from dairy herd records, underwent a rigorous preprocessing phase. As a first step, the dataset underwent basic cleaning processes, including the removal of outliers, normalization of numerical values, and addressing any missing entries. Once the data was prepared, we moved on to feature engineering, where we introduced new indicators such as the SCC-to-Conductivity Ratio, the Rolling Average of SCC, and selected interaction features. These engineered variables were designed to help the model better identify early signs of mastitis.

For the modeling phase, we selected two algorithms for comparison: Logistic Regression and LightGBM. Logistic Regression was used as a baseline model due to its straightforward nature and interpretability. In contrast, LightGBM was chosen for its strength in dealing with imbalanced datasets and capturing nonlinear relationships. To further enhance performance, we employed the Optuna framework for automated hyperparameter tuning, allowing the models to generalize more effectively without manual trial-and-error adjustments.

As illustrated in Figure 1, model performance is evaluated through cross-validation, ensuring statistical robustness. Furthermore, SHAP (Shapley Additive Explanations) is incorporated to provide a layer of interpretability, helping identify the features that most influence predictions. This step is particularly important in the veterinary context, where understanding why a prediction was made can influence clinical decisions.

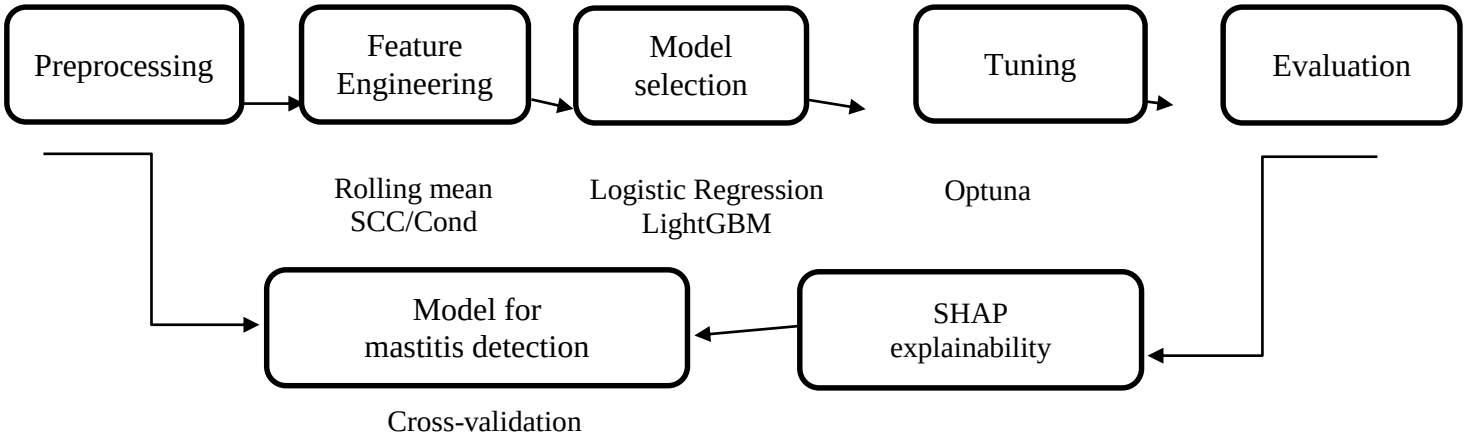


Figure1: Methodology workflow of the proposed ML framework
The diagram illustrates the process flow from data preprocessing through feature engineering, model selection, tuning, evaluation, and explainability using SHAP.

Although final results are pending as the system is still under active development and training, the comparative analysis framework is structured to support a thorough, data-driven evaluation once model performance metrics become available.

Results/Discussion

Although final quantitative results are pending, the proposed machine learning framework for mastitis detection has been developed and structured for performance benchmarking. Our modeling approach focuses on three core areas: enriching the features, fine-tuning the model, and making its predictions easier to understand. Together, these elements help improve both the accuracy and transparency of the system. Among the models we explored, LightGBM stood out—its performance aligns with findings from earlier studies [1, 5] that highlight the effectiveness of gradient boosting methods in medical classification problems. Unlike traditional models that rely on linear assumptions, LightGBM is capable of capturing more complex, nonlinear relationships, which is especially useful when detecting subtle indicators of subclinical mastitis.

One of the standout features of this work is the integration of SHAP (Shapley Additive Explanations) to interpret the model's output. This tool provides insight into how individual features influence each prediction, making the system more transparent and useful in clinical decision-making.While past studies like Shiotsu et al. [1] focused mainly on model accuracy, they did not incorporate explainability tools. Our approach enhances model transparency by identifying which features — such as somatic cell count, milk conductivity, or SCC-to-conductivity ratio — contributed most to a prediction. This increases clinical trust and facilitates informed decision-making by veterinarians and dairy professionals, bridging the gap between algorithmic output and domain knowledge.

From an application standpoint, the proposed framework is particularly valuable for low-cost, real-world deployment. Unlike models relying on expensive biomarkers or advanced sensors, our system uses readily measurable milk quality parameters available on most dairy farms. This allows for scalability, especially in small- and medium-sized farm operations where budget and infrastructure are limited. Furthermore, automated hyperparameter tuning with Optuna improves model generalizability, reducing the need for manual configuration

and technical expertise.

Despite its potential, this study has some limitations. The model is currently trained on a region-specific dataset, which may limit generalization across breeds, climates, or farm management systems. Additionally, the classification is binary (healthy vs. mastitis), while in reality, mastitis exists on a spectrum — including clinical, subclinical, and borderline cases. Future research should incorporate multiclass classification to provide more granular diagnoses and adapt the system for real-time monitoring through live sensor feeds. Further external validation using datasets from different geographic and environmental conditions would also be essential to confirm model robustness and improve adoption.

Conclusion

This study presents a machine learning–driven framework aimed at the early detection of subclinical mastitis in dairy cattle, using routinely collected milk quality indicators such as somatic cell count, pH, and electrical conductivity. Through the use of thoughtful feature engineering, automated tuning, and model explanation tools like SHAP, the system we've developed aims to strike a balance between accuracy and clarity—both essential for clinical use. Unlike some earlier methods that rely on expensive equipment or black-box models, our approach is designed to be cost-effective and scalable, making it a practical option for dairy farms that may lack advanced diagnostic resources.

What sets this system apart is its focus on explainable AI, which makes the model's predictions easier for veterinarians to understand and trust. This transparency helps improve confidence in decision-making, especially when early intervention is key to preventing the spread of disease.

Although final testing is still in progress, the framework already shows promise as a clinical decision support tool. It could help identify cows at risk of mastitis before symptoms appear, potentially lowering treatment costs and maintaining milk quality. In the future, we plan to expand the system's capabilities by integrating real-time sensor data, supporting multiclass classification, and validating performance across different regions and farm conditions.

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