Original Paper

A Computerized mastitis classification aid using a dairy herd-based records: Multi-Layer Perceptron (MLP) neural network with backpropagation approach

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ARTICLE INFO

ABSTRACT

The main objective of this study is to develop an efficient machine learning-based model for the early prediction of clinical mastitis in Holstein Friesian dairy cattle where automatic milking system (AMS) data is used. The model aims to offer a costless opportunity for mastitis control and reduce its negative impact on livestock production. Different forward multilayer perceptron (MLP) neural networks with backpropagation (BP) learning algorithms using various numbers of hidden neurons and epochs have been introduced. The results of the established models are evaluated based on different metrics such as the accuracy, the F1 core, the precision, the recall, and the area under the receiver operating characteristic curve (ROC-AUC). Out of the established twelve models, the optimal neural network consisted of a single hidden layer of 15 hidden neurons, Relu hidden activation function, and a sigmoid activation function at the output layer. After training the model for 100 epochs, it achieved a high classification accuracy of 86%, an F1-score of 78%, precision of 93%, recall of 67%, and an excellent ROC-AUC of 82%. The study demonstrated that the total milk this lactation (TOTM), days in milk (DIM), days open, milk peak (MPEAK), 305-day mature equivalent milk production (305 ME), and daily milk yield (DMY) are important inputs for the model training. The results show that the forward neural network (FNN) with a backpropagation algorithm can offer opportunities to integrate clinical mastitis prediction within a computerized decision support tool.

1. INTRODUCTION

Bovine mastitis, a mammary gland inflammation that results in abnormal milk composition (Dhoble et al., 2019), is one of the costliest endemic disorders of dairy farms and is thought to account for 38% of all direct production disease costs (Hyde et al., 2017). In addition to the high economic loss, mastitis is a painful condition that hinders animal welfare and reduces its production. It is also considered one of the most important causes of extensive antimicrobial usage in the worldwide dairy industry (Hyde et al., 2020). The early detection, diagnosis, and control of such health problems, which have clinical and subclinical forms, is a challenge for dairy farms to minimize the resulting negative impacts early (Zhou et al., 2022).

In the dairy field, large quantities of data are generated daily and stored in databases. Such data involves valuable information to improve farm management and the decision-making process. However, as a result of the large flow of records and the large number of features, pattern visualization and discovering abnormalities in this multidimensional data are challenging and require advanced software tools to be explained (Pietersma et al., 2005). It has been demonstrated that the application of advanced processing and analytics tools to such multidimensional dairy data can have a positive impact on livestock production systems and the decision-making process (Fadul-Pacheco et al., 2022).

In the last decade, there has been great interest in Artificial Neural Networks (ANNs), and they have been successfully integrated into many domains such as medicine, molecular biology, image recognition, and environmental, and ecological sciences (Mas et al., 2004).

In the livestock field, ANN has various applications such as forecasting milk production, estrous detection, lameness detection, mastitis prediction, and bull breeding soundness assessment (Dongre and Gandhi, 2016).

ANNs, a deep learning computing technique, are non-linear mapping structures that mimic the human brain in the way it learns. During the learning process, it acquires knowledge by responding to new environments and stores it in interneuron synapses (Shaikhina and Khovanova, 2017). They have been successfully used to build accurate predictive models as they are effective since they accommodate a wide range of uncertainty and are flexible to accommodate noisy, incomplete, fuzzy, and probabilistic data. So, now they are utilized as alternative statistical analytical tools (Parthasarathy and Narayanan, 2014).

The multi-layer feed-forward neural network, or multi-layer perceptron (MLP), is one of the most widely used ANNs and consists basically of three layers: the input, hidden, and output layers. It can model complex, non-linearly separable problems (Pijanowski et al., 2002). In MLP, the information flows unidirectionally forward through the consecutive fully connected layers from the input layer to the output layer, passing by the hidden layer, the output of one layer introduced as input to the next layer, and so on. Each union between processing units (neurons) has its weight vector and

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neurons of the same layer (hidden and output layers) have the same activation function (Mas et al., 2014).

Backpropagation (BP) is an iterative gradient learning algorithm that is commonly used in MLP to minimize the mean square error between the predicted output of ANN and the actual output (Paegelow, 2018). During the learning or training process of the neural network, the calculations are carried out starting from the input layer passing towards the output layer. The final ANN output values are then compared with the true output values; any error obtained is then propagated back through the network and weights are adjusted after many iterations of forward and backpropagation steps (epochs). The approximate expected output is obtained once the error converges to a minimum value (Shreyas et al., 2023).

The milk features associated with bovine mastitis could be used to establish robust ANN models and the integration of such models in in-line automated milking systems may raise the efficiency and accuracy of the early pathogens causing mastitis detection in milk even before the onset of any clinical signs (Dongre and Gandhi, 2016). Therefore, this paper aims to develop different backpropagation-based ANN models for mastitis classification in purebred Holstein Friesian cattle based on production, reproduction, and some health parameters obtained from the automatic dairy records. The classifying ability of the ANN models is evaluated and compared using the models' performance metrics, to obtain the optimal prediction model. The performance metrics include the accuracy, the F1 score, the precision, the recall, and the area under the receiver operating characteristic curve (ROC-AUC).

2. MATERIAL AND METHODS

The Animal Care and Welfare Committee, Faculty of Veterinary Medicine, Benha University, Egypt approved the current study with the reference ethical approval number (BUFVTM:17-04-23).

2.1.Data collection and variables identification

The current investigation material included information on purebred Holstein-Friesian dairy cows. A random sample of 3880 retrospective milk, reproduction, and some health computerized records was collected from a commercial production farm in Egypt. All cows included in the study had a freshening date between 2016 and 2019 and they are of different age groups and at different numbers and stages of lactation. The process of milk information recording is carried out by an automatic sensor installed in the automated milking parlor and then monitored in the dairy herd management system (Dairy Comp 305 software). The variables used to develop the current study are outlined in Table 1.

2.2.Herd management and mastitis detection

Cows are housed in a shaded open yard with free stalls, lined with a sand floor, and equipped with a cool spraying system in the summer thus relieving heat stress in the summer months. The farm applies the total mixed ration method with computerized calculating systems that control feeding portions according to the productivity and the reproductive demand of animals. Water was supplied freely all day long. Pre-milking and post-milking udder hygiene measures were practiced through udder washing and dipping the teats in an iodine solution. The milking process takes place on a herringbone with a rapid exit automatic milking parlor three times a day using machine milking, and milk parameters for each cow are recorded in a computerized database. Detection of CM depends on the presence of clinical signs on the udder such as hotness, redness, swelling, painful reaction, and hardness of udder tissues, and then the infection is confirmed by the California Mastitis Test (CMT).

2.3. Data preprocessing

Before the model building, data was visualized against the missing values and outliers. No missing value was detected. However, outliers were detected in almost all the numerical predictor features including age at the last season, lactation order, daily milk yield (DMY), milk peak (MPEAK), total milk yield this lactation (TOTM), 305-days mature equivalent milk production (305ME), and days open, and they have been replaced with these features' percentiles. Dependent (mastitis) and independent features (lactation order, age at last season, DMY, TOTM, MPEAK, 305ME, days in milk (DIM), days open, reproductive status, calving season, lameness, abortion, metritis, milk fever, and retained placenta) were identified. Data was scaled using the Z-score standardization method. All the categorical features were labeled using the label-encoder which assigns a unique numerical value to each category of the categorical variable.

Table 1: The input and output model features description.

Features	Description	Type
• Input features:		
1) Lactation order	How many lactation season/cattle? (Min=1 and Max= 9)	Numerical
2) Age at last season	Animal age at the time of data collection. (Mean = 3.55 year)	Numerical
3) DMY	Average milk production/cow/day = 29.6 kg/day	Numerical
4) TOTM	The cumulative milk production/cow of the last lactation. (Mean = 7028.9 kg)	Numerical
5) MPEAK	The peak milk yield/cow in the last season. (Mean = 42.18 kg)	Numerical
6) 305ME	305ME = 305 x TOTM / DIM. (Mean = 10987.6 kg)	Numerical
7) DIM	(Mean = 242.18 days)	Numerical
8) Days Open	(Mean = 180.68 days from calving to conception)	Numerical
9) Reproductive status	Pregnant, non-pregnant, and bred	Categorical
10) Calving season	Summer and winter	Categorical
11) Lameness	Yes / No	Categorical
12) Abortion	Yes / No	Categorical
13) Metritis	Yes / No	Categorical
14) Milk fever	Yes / No	Categorical
15) Retained placenta	Yes / No	Categorical
• Output feature:		
Mastitis	Healthy / Mastitis	Categorical

DMY: daily milk yield, TOTM: total milk this lactation, MPEAK: milk peak, 305ME: 305-days mature equivalent milk production, DIM: days in milk.

2.4 Multi-layer perceptron (MLP) neural network with backpropagation (BP) learning algorithm

MLP is a widely used neural network with a BP-supervised learning method for error backpropagation through weight adjustment. It is very suitable for modeling non-linearly separable issues and finding non-linear functions that describe the complex interacting relationships between the inputs (Paegelow, 2018).

The weighting step is the initial step of MLP learning that involves multiplying each input variable by its weight $(X_i W_i)$. Then the sum of product S_i is calculated by adding the product of the subsequent step together as in Equation (1):

$$S_i = \sum_{i=1}^{n} X_i W_i + \beta_0 \qquad (1)$$

Where X_i is the input feature i, n is the total number of inputs, W_i is the weight of each i input feature, and β_0 is the bias.

The second transfer step involves passing the sum of product through the activation function therefore a predicted output y is produced as shown in Equation (2):

$$y = f\left(\sum_{i=1}^{n} X_i W_i + \beta_0\right) \qquad (2)$$

Then the error is calculated by comparing the predicted and the actual outputs using the following Equation (3):

$$E = \sum_{i=1}^{N} (d - y)^2 \qquad (3)$$

Where E is the error, N is the total number of training samples, d is the actual output, and y is the model output.

Any error detected returns backward again and the weights are adjusted using the adaptive moment estimation algorithm (*Adam*) as shown in Fig (1). The *Adam* optimizer is a new extension of the stochastic gradient descent algorithm. It combines the benefits of 2 algorithms: momentum gradient descent and root mean square propagation algorithms to rapidly and efficiently update weights during the learning process (Kingma and Ba, 2015). The *Adam* mathematical formula is explained as in Equation (4):

$$m_t = \beta_1 m_{t-1} + (1 - \beta_1)\left[\frac{\delta L}{\delta w_t}\right],$$

$$v_t = \beta_2 v_{t-1} + (1 - \beta_2)\left[\frac{\delta L}{\delta w_t}\right]^2 \qquad (4)$$

Where m_t is the aggregate of gradients at time (t), β is the moving average parameter, m_{t-1} is the aggregate of gradients at time $(t-1)$, δL is the derivative of the Loss Function, δw_t is the derivative of weights at time (t), and v_t *is* the sum of the square of past gradients.
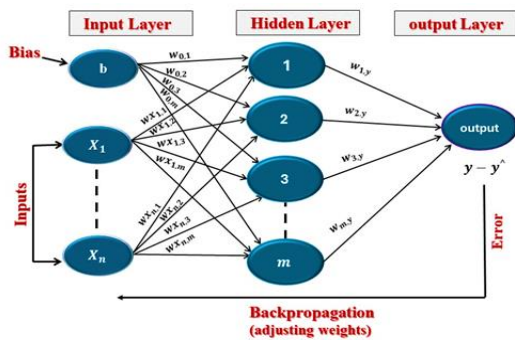

Fig. 1. Architecture of the multilayer perceptron with backpropagation algorithm.

2.5 Model building and hyperparameters tuning

To build the model, of the 3880 records, 2716 records were attributed to the train data set (70%). The remaining 1164 records were divided between the validation and the test data sets, 582 records for each set representing (15%) of the total data set. A 10-fold cross-validation technique was used to validate the results to avoid overfitting. MLPs with a BP algorithm of only one hidden layer were computed using a rectified linear activation function (Relu) at the hidden layer and a non-linear activation function (sigmoid) at the output layer.

$$\text{Relu function} = f(z) = \begin{cases} 0 \; for \; z < 0 \\ z \; for \; z \geq 1 \end{cases} \qquad (5)$$

$$\text{Sigmoid function} = f(z) = \frac{1}{1+e^{-z}} = \begin{cases} 0 \; for \; z < 0 \\ 1 \; for \; z \geq 0 \end{cases} \qquad (6)$$

(Popescu et al., 2009).

Different setups of MLP with different numbers of hidden neurons (8, 10, 15) in combination with different numbers of epochs (50, 75, 100, 125) were run with the empirically tuned learning rate = 0.001, and batch size = 32. The algorithm was programmed to stop learning when 10 successive rounds didn't show any decrease in the loss error (early stopping).

2.6 Model evaluation

The last step involved the evaluation and comparison of the final achieved models based on accuracy, F1 score, precision, recall, and ROC-AUC (Dalianis, 2018). Accuracy: A measurement that expresses the ratio of the total number of correctly obtained predictions.

$$\text{Accuracy} = \frac{\text{True positive (TP)} + \text{True negative (TN)}}{\text{True positive} + \text{False positive (FP)} + \text{True negative} + \text{False negative (FN)}}$$

Precision: is also called the positive predictive value and it is the proportion of the correctly classified positive instances to all positive predictions.

$$\text{Precision} = \frac{\text{TP}}{\text{TP+FP}}$$

Recall: the ratio of the correctly predictive positive to the total actual positive.

$$\text{Recall} = \frac{\text{TP}}{\text{TP+FN}}$$

$$\text{F1-score} = 2 \times \frac{\text{Precision .Recall}}{\text{Precision+Recall}}$$ (Awoyemi et al., 2017).

The ROC-AUC evaluation criteria calculate the area under the receiver operating characteristic (ROC) curve and present the TPR (sensitivity) against the FPR (1- specificity)

$$= \frac{1}{2} \times (\text{Sensitivity} + \text{Specificity})$$ (Bonestroo et al., 2022).

All procedures were performed using the Python software V.3.7.1.

3. RESULTS

The comparative analysis of the different single hidden layer MLP with BP networks developed in this study by varying the number of hidden neurons (8, 10, and 15) and the number of epochs (50, 75, 100, and 125) has been made in terms of accuracy, F1 score, precision, recall, and AUC on the test data set as presented in Table 2.

The classification accuracy of all models ranged between 78% and 86%. Further, the F1 score, precision, and recall of NN models varied in the ranges of 70–78%, 73–93%, and 67%–79%, respectively, and the ROC-AUC results varied between 76% and 82%. The optimally performed network of 86% accuracy, 78% f1score, 93% precision, 79% recall, and 82% ROC-AUC (underlined in Table 2) was selected based on the accuracy and the ROC-AUC findings. It was obtained from a single hidden layer MLP with a BP neural network established by 15 hidden processing units, 100 epochs, batch size = 32, learning rate = 0.001, a linear transfer function (Relu) in the hidden layer, and a non-linear transfer function (sigmoid) in the output layer.

Table 2. Comparison of different MLP with BP models' performance of various numbers of hidden neurons and epochs

		Epochs	Accuracy	F1 Score	Precision	Recall	ROC AUC
Number of hidden neurons	8	50	0.82	0.76	0.77	0.75	0.81
		75	0.82	0.75	0.77	0.73	0.80
		100	0.82	0.75	0.78	0.71	0.80
		125	0.82	0.77	0.75	0.79	0.81
	10	50	0.83	0.76	0.81	0.72	0.81
		75	0.78	0.70	0.73	0.67	0.76
		100	0.82	0.76	0.76	0.77	0.81
		125	0.82	0.76	0.80	0.71	0.80
	15	50	0.78	0.70	0.73	0.68	0.76
		75	0.82	0.76	0.78	0.74	0.81
		100	<u>0.86</u>	<u>0.78</u>	<u>0.93</u>	<u>0.67</u>	<u>0.82</u>
		125	0.79	0.72	0.75	0.69	0.78

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Fig. 2 shows the AUC under the ROC curve, a graph presenting the model classification performance by plotting the model sensitivity (true positive rate (TPR)) against 1-specificity (false positive rate (FPR)) at all thresholds, for the optimal model on the train and test datasets (80% and 82%, respectively). Fig. 3 shows the training and validation loss and AUC against epochs for the best model of 100 epochs and 15 hidden neurons. The graph indicated reduced loss and improved AUC with successive epochs.
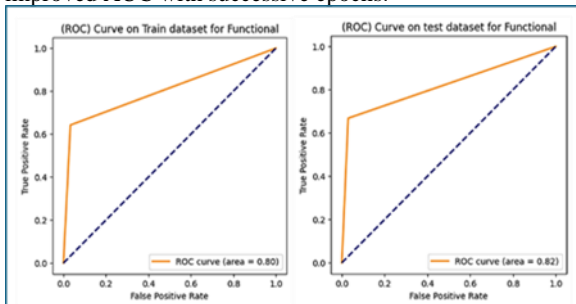

Fig. 2. The receiver-operator characteristic (ROC) curve for both train and test datasets presenting the area under the curve (AUC) for the best MLP with the BP learning algorithm (hidden neurons = 15, and number of epochs = 100).
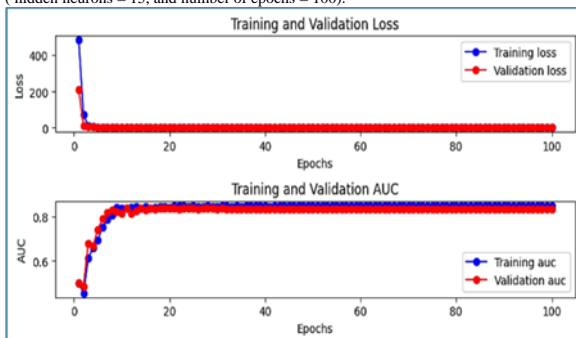

Fig. 3. The epochs versus the loss and the AUC plot of the best MLP with BP model on training and validation datasets (100 epochs and 15 hidden neurons).

The contribution and importance of each input feature for the classification model are displayed in the SHAP value-based graphs (Figs. 4 and 5). The features in Fig. 4 are organized in order from the highest to the lowest impact on classification. It depends on the absolute mean SHAP value for every feature over the 100 examined samples on the x-axis, but it does not indicate whether this has a positive or negative effect on the prediction. TOTM and DIM showed the major impact on the prediction model, followed by Days

Open, DMY, MPEAK, and 305 ME, which were of moderate importance, while lactation order, age at last season, and reproductive status showed low importance, and the other six input features were of no effect on the model.
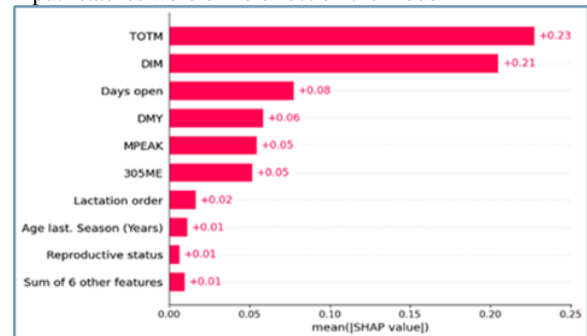

Fig. 4. Bar plot showing the global features importance plot (The average shap values of the important features over all the 100 manipulated samples arranged in descending order).

In Fig. 5, the features are also ordered by their effect on prediction, but we can also see how higher and lower values of the feature will affect the result. The data points are colored according to the observed feature importance values (red: high feature value; blue: low feature value). Red positive SHAP values on the right are indicative of mastitis, while blue negative SHAP values on the left are indicative of healthy cases. The highest values of TOTM and MPEAK have a positive impact on mastitis prediction, while the lower values have a negative impact. In contrast, the lowest values of DIM, Days Open, 305 ME, and DMY have a negative impact on the prediction, and their highest values affect the prediction positively.

Fig. 5. SHAP value-based feature importance visualization plot.
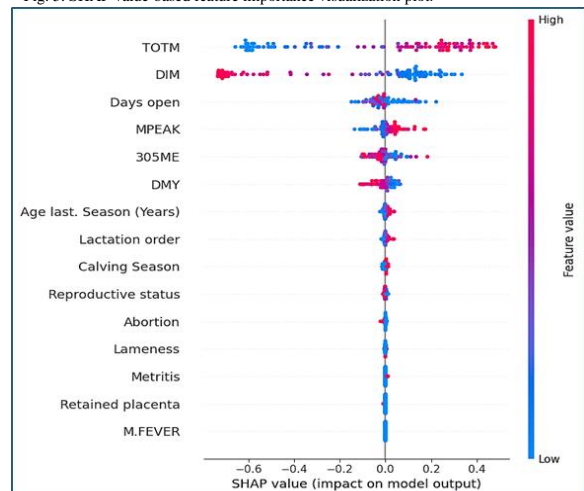
4. DISCUSSION

Two main reasons make the prediction of clinical mastitis by the traditional statistical methods insufficient and inaccurate: The first is the fact that clinical mastitis is a complex multi-factorial disorder that depends on various interactive and

highly correlated factors, such as udder exposure to various types of pathogens, genetic and non-genetic factors, and environmental risk factors (Litwińczuk et al., 2015).

Also, the interactions and multicollinearity among the predictors restrict the prediction capability of traditional statistical analytical techniques based on both univariate and multivariate explanatory variables (Fan and Li, 2001). The second is that mastitis is a nonlinear phenomenon and its prediction with conventional statistical methods may be inappropriate (Tasdemir et al., 2011). A modeling technique provided by the ANNs enables the mapping of highly complex non-linear functional relationships (Bauer and Jagusiak, 2022). In this study, twelve ANNs are introduced (MLP with a BP learning algorithm and Adam optimizer) varying the number of hidden neurons and epochs to determine the optimal model for bovine mastitis prediction in Holstein-Friesian cattle milked by the automatic milking machine. Out of the twelve computed models, the network with 15 hidden neurons and 100 epochs was found to be the best one in terms of accuracy (86%), F1 score (78%), precision (93%), recall (67%), and an excellent ROC-AUC (82%). This is according to Hosmer and Lemeshow (2000), who stated that an AUC of 0.8 to 0.9 indicates excellent classification ability. Similar results were achieved by Wang and Samarasinghe (2005), who compared two different ANN algorithms for the classification of clinical mastitis (MLP and self-organizing map (SOM)). The MLP showed a higher accuracy of 84%. Also, the recurrent NN gained a high accuracy ranging from 78% to 82% for the clinical mastitis prediction 3 days before its diagnosis using all milk and behavioral variables and their daily variance recorded by the farm AMS (Naqvi et al., 2022). TOTM, DIM, Days Open, DMY, MPEAK, and 305 ME were the important features in building such an excellent model with an 82% AUC. Consistent with these findings, Faris et al. (2024) reported that DIM, age at the last season, lactation order, 305ME, and DMY were the important features for the 73% accurate decision tree model of clinical mastitis prediction .

It was shown that TOTM and MPEAK had a positive impact on the onset of mastitis (cows with higher TOTM and MPEAK were classified as having positive mastitis).

This finding can be explained based on the fact that highly lactating exotic and cross-dairy breeds like Holstein Friesian are more susceptible to intra-mammary infection and mastitis than indigenous breeds (Sinha et al., 2021). Also, Shalan et al. (2023) reported that cows with higher milk production (12820.2 kg) were three times more prone to mastitis than others with lower milk production (11421.89 kg) due to the metabolic stress of peak milk yield.

DIM was the second important input that showed a negative effect on the positive classification of mastitis. This was in line with Ankinakatte et al. (2013), who found that including DIM as an input improved the NN's sensitivity by almost 10%. The significant udder tissue changes noticed in the early lactation lead to decreased natural defense ability of the cow udder, resulting in pathogens' invasion of the teat canals causing infection (Tiwari et al., 2013), and also the oxidative stress of the early lactation and the suppressed antioxidant defense mechanism are the important factors of mastitis infection immediately after parturition (Gunay and Gunay, 2008) .

Regarding the days open, it was revealed that the lower values were associated with a mastitis infection. This result agreed with Borş et al. (2023), who revealed that the average number of days open in the mastitic cows (112 days) was significantly lower than in the healthy cows (142 days).

Both DMY and 305ME showed an inverse relationship with mastitis, as it resulted in a significant loss of milk production. Supportive results were obtained by Ameni et al. (2022), who found that the mastitis-infected cows had a significantly ($p <$ 0.001) lower average DMY than healthy cows (18.6 kg and 40.5 kg, respectively). This is due to the pathological changes in the udder tissue due to the inflammatory reaction; hence, the udder becomes unhealthy, and its productive efficiency declines (Hagnestam et al., 2007). As a result of diminished milk production and discarding the milk during the illness period, the 305ME continuously decreases.

Overall, these results prove that MLP neural networks with the BP algorithm are powerful tools for building mastitis detection and prediction models in dairy farms monitored using AMS, which provides accurate decision-making and livestock profitability.

5 . CONCLUSIONS

This study explores the capability of the neural network for intelligent prediction of clinical mastitis in Holstein dairy cattle using the AMS data. The error backpropagation forward neural networks along with various combinations of model hyperparameters as well as the number of hidden neurons and epochs we empirically explored. The optimal model of 86% accuracy and excellent ROC-AUC (82%) was achieved using a single hidden layer MLP with the BP algorithm and Adam optimizer of 15 processing hidden units, 100 epochs, a learning rate =0.001, a batch size = 32, and the Relu activation function at the hidden layer and the sigmoid function at the output layer.

6. CONFLICT OF INTEREST
No conflict of interests.

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