p-ISSN 2615-787X e-ISSN 2615-790X
Accredited by Directorate General of Higher Education, Research, and Technology, Republic of Indonesia, No. 225/E/KPT/2022

Tropical Animal Science Journal, December 2024, 47(4):503-509
DOI: https://doi.org/10.5398/tasj.2024.47.4.503
Available online at https://journal.ipb.ac.id/index.php/tasj

The Prediction of Somatic Cell Count Through Multilayer Perceptron of Deep Machine Learning

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(Received 21-04-2024; Revised 26-07-2024; Accepted 06-08-2024)

ABSTRACT

The main objective of the research is to generate an alternative approach to classical techniques in the prediction of the somatic cell count (SCC), which is the gold standard indicator of subclinical mastitis. This approach involves using the physical properties of milk such as density, the temperature at fore milking (TFM), pH, and electrical conductivity (EC) with a feed-forward backpropagation multilayer perceptron (MLP) artificial neural networks (ANN) model, which is one of the widely used machine learning techniques. The performance of the model was assessed by test with cross-validation on data that was not introduced to the model before and compared to the classical linear model (multiple linear regression) as the control model. The findings showed that the model has satisfactory results in terms of loss and performance criteria (R^2=0.95, RMSE=0.01; AIC=-338). The test model (ANN) had a higher performance (AIC=-338) than the control model (AIC=-240) created with the classical linear model despite using more parameters (81). Using big data from automated milking information—like estrus cycle, lactation stage, and milk yield—on supercomputers can improve the accuracy of performance assessments in dairy farming.

Keywords: artificial neural networks (ANN); deep learning; mastitis; milk; somatic cell count (SCC)

INTRODUCTION

One of the major problems of the livestock industry is udder health and follow-up. Especially in the dairy sector, subclinical mastitis diagnosis and tracking udder health are essential for qualified milk production. The need for alternative methods continues due to the difficulties (high cost, qualified labor, and laboratory requirements) in the determination of the somatic cell count (SCC), which is accepted as the gold-standard indicator in the international literature for monitoring udder health.

People use their intelligence to act in situations that require perception and foresight. Various artificial intelligence applications allow machines to imitate human intelligence. The main purpose of bringing human intelligence to computers up to a certain level is to develop methods and machine intelligence to create computer-based mechanisms that will solve problems, communicate with humans, perceive and interact with the physical environment by understanding the basic principles of humans. Artificial neural networks (ANN), which is based on the working principle of the biological nervous system, is based on the fact that many nerve cells (neurons) work together in the learning process to solve the problem. The ability to generalize, akin to human learning, allows it to learn from past data or examples and to make decisions by using the knowledge gained from experience on new data that has not been encountered before in the future. ANNs can be configured on subjects in the field of dairy and livestock science, e.g., prediction, quality classification, disease detection, temperature measurement, etc. It is known that research has been conducted on disease diagnosis (Zülkadir & Coşkun, 2018;), breed classification (Yeşil & Göncü, 2023; Weber *et al.*, 2020), lameness diagnosis (Coşkun *et al.*, 2023), prediction of live weight (Aytekin *et al.*, 2018), and individual recognition (Zhang *et al.*, 2018; Zhao & He, 2015) with different machine learning models in animal sciences.

To the best of our knowledge from the previous literature, due to both high test costs and direct-indirect costs and time loss caused by the high workload during SCC tests, the need for more efficient, easy, and low-cost prediction methods continues. Furthermore, comparing performances of different ML techniques based on only accuracy or coefficient of determination (R2) and loss criteria (error) regardless of the number of parameters has become a common evaluation approach. In this study, however, we compared the performance of ANN not only based on the classical performance criteria (multiple logistic regression model -MLRM-) but also the number of parameters (AIC score). Although attempts to satisfy the existing gap in literature are insufficient, it is understood that no study shows high performance in SCC detection. This study aims to contribute to the removal of the current gap among the literature. Our motivation was to search for an alternative method to SCC detection with variables that are more practical to measure and easily adapted to automation systems in terms of cost and ease of use. This study aims to develop an alternative method model for SCC detection, which is the gold-standard indicator of subclinical mastitis in cows with deep ANN over the physical properties of milk, pH, temperature at fore milking (TFM), electrical conductivity (EC), and milk density. Therefore, our research makes numerous contributions to the literature. First, the prediction techniques used up to date with variables acquired only from milking information limit the performance of the model. Second, despite network-based models using high parameters increasing the success in terms of error and accuracy, there is no knowledge about whether they provide more benefit than the additional increase in processor load they create. Additionally, there is no study that considers the milk's physical features directly related to SCC to solve the practical problem, promising sensitive, precise, and efficient results. Therefore, it is unclear how improvement can be achieved using the milk's physical properties to detect SCC via deep machine learning. Unlike previous studies, this study also discusses the model performances in terms of processor workload since energy concerns are gaining more importance in artificial intelligence. Over and above, this is the first research study to determine SCC with deep ANN based on the physical properties of milk and evaluate the model efficiency by considering energy consumption concerns and the number of parameters. Finally, this study emerges several avenues for further research to investigate in more depth whether SCC detection models over physical properties with a high number of parameters provide more benefit than processor load and energy consumption via enlightening the impact of the number of parameters on the model's efficiency.

MATERIALS AND METHODS

The current study has been generated by improving and expanding the project titled "Relationships Between Some Traits Related to Mastitis in Holstein Friesian Cows' Milk". The research was supported by Cukurova University Research Unit Projects (Project No: FDK-2021-13656) and approved by the Local Ethics Board of Animal Research of Cukurova University (28.11.2017 – 10/2.).

Experimental Material, Sampling, and Measurements

The animal material used in the present study consists of 160 Holstein Friesian dairy cows of similar age and lactation in the Çukurova University Experimental Farm, Adana/Turkey. Milking is done twice a day with the automatic 10x2 fishbone milking system. The company employs a full-time expert zootechnician and veterinarian. Milk samples were taken twice a week between November 2021 and June 2022, at both milking times, from cows of similar age and lactation. Samples were taken daily from those with mastitis during the treatment period. Right before the milking heads are attached to the cows entering the milking system, the foremilk accumulated at the teat was taken into the milking cups, and then the analysis samples were taken into the 250 mL sample tubes, and the milk TFM, EC, and pH were determined with the AZ-86505. The milk density is determined via a pycnometer. Afterward, milk SCC measurements were performed with a Delaval DCC SCC, which was developed to detect SCC-induced change in cow-specific milk and operated based on DNA-specific fluorescent staining in the somatic cell nucleus.

Data Analysis and Modelling

Although the herd projection size in the enterprise is based on 160 lactating cows per year, a total of 2500 data points were obtained from 500 observations of 250 different cows in the enterprise between 2018 and 2023. A total of 2281 remaining data points after data preprocessing were used for research.

Analyses were executed on a PC with a 12th Gen i3 12100 CPU model and 64 GB DDR5 4800 Mhz RAM, and a CUDA-supported RTX 3060 GPU model with 12 GB VRAM. The data analyses of the current study were performed in the R environment, a free, open-source, and accessible programming language developed prior for statistical purposes (R for Statistical Computing, 2022). For this purpose, after applying homogeneity and normality tests to the data set, analysis and modeling were carried out by applying a logarithmic transformation to the SCC since it shows right-skewed distribution. (Appendix A.) (Kayaalp, 2017; Kayaalp *et al.*, 2015; Cebeci, 2020). However, actual values were retained in the charts and descriptive statistics.

Descriptive statistics. Basic core packages embedded in the R environment were used to calculate the descriptive statistics of the variables. The GGally package was used for the analysis and display of the summary graphs and charts (Appendix A).

Compilation, fitting, and training of ANN model. Modelling of ANN was performed with the Keras package (library) using the TensorFlow GPU version as a backend. It consists of 4 neurons (ec, pH, density, and milk temperature during milking) in the input layer, 8 neurons in the first hidden layer, 4 neurons in the second hidden layer, and a single neuron in the output layer. The model architecture and elements of the artificial neural network used in the learning process are given in Figure 1 and Table 1, respectively.

The training or learning process is basically the process of optimizing performance and loss values using a trial and error method. The performance values are desired to converge to 1 (one), while the loss values are expected to converge to 0 (zero) (Soydaner, 2020). The sequential model was used in modeling the network, and the "ReLU" (Rectified Linear Unit) function was preferred in the activation process of hidden layers, as reported by Asadi & Jiang (2020). The ReLU layer is the layer where the activation function is applied (İnik & Ülker, 2017). RMSProp (Root Mean Squared Propagation) algorithm was used as the optimization function, as reported by Soydaner (2020). Accordingly, the loss functions Mean Squared Error (MSE) and Mean Absolute Error (MAE) are used to validate the model. During training, the hyperparameters of ephocs, learning rate and batch size were 1000, 0.16, and 0.015, respectively. Over-fitting was prevented by regularizing the model, increasing the number of observations, reducing the complexity of the network, early stopping during training and dropping out in between hidden layers.

Evaluation and comparison of the models. While creating models, 75% was reserved as a training set of the total data set, and 25% was the test in terms of evaluating model performances on previously unknown data. In the training of ANN, the validation split rate for cross-validation was also preferred as 25%, where the dataset is more than 1000 observations, the validation split rate should be 10%; otherwise, 20-25% would be sufficient for the validation process. Cross-validation is used to determine which of the models outperforms in model selection by determining the prediction error and performance values of the model on previously unknown data (Fushiki, 2011). In order to compare the performance of the ANN model, which uses a large number of parameters, the Multiple Linear Regression Model (MLRM), one of the classical methods, was preferred because it uses few parameters (Kayaalp *et al.*, 2015). Core packages of the R programming language were used in the MLRM analysis. The root mean squared of error (RMSE), coefficient of determination (R^2), and Akaike Information Criteria (AIC score) were computed as loss and performance criteria. It is reported that using the AIC score will give positive results in evaluating model performance if the number of inputs and outputs is large. In terms of the AIC score, the performance of the model with a lower value is higher (Panchal *et al.*, 2010). The packages of the R environment used in the analysis and modeling are given in Table 2.

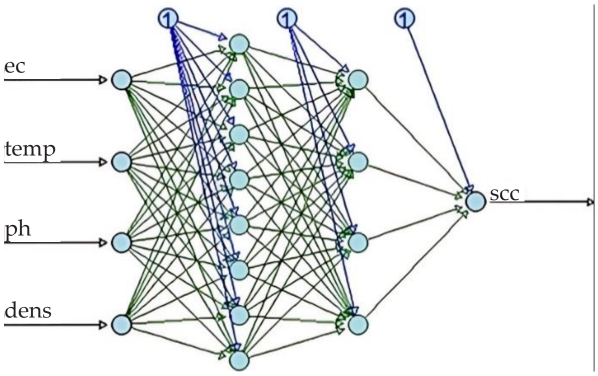

Figure 1. The model architecture of the test model used in the research (fully connected ANN with feedforward backpropagation multilayer perceptron). "scc" stands for milk somatic cell count; "ec" for "electrical conductivity"; "temp" for the temperature at foremilking; "ph" for pH (negative logarithm of hydrogen concentration); "dens" for density of milk. The meaning of the number "1" in the figure stands for each bias per node.

Table 1. Elements of the fully connected ANN model architecture with feedforward backpropagation multilayer perceptron

Layers	Layer type	Output shape	NoP	NoM
Input	Input	4		4
1. Hidden	3. dense	(None, 8)	40 (4x8+8)	8
1. Dropout	2. dropout	(None, 8)	0	
2. Hidden	2. dense	(None, 4)	36 (8x4+4)	4
2. Dropout	1. dropout	(None, 4)	0	
Output	1. dense	(None, 1)	5 (4x1+1)	1

Note: Total number of parameters= 81; Total number of trainable parameters= 81; Total number of non-trainable parameters= 0. NoP stands for the number of parameters; NoM stands for the number of multipliers.

Execution time was also observed for the whole model training to make inferences about both the processor load of the model in the case of working with big data and the cost-effectiveness of the TensorFlow GPU version executed on a CUDA-supported graphics card. Execution time refers to the time between the start and end of the training process and is important in terms of hardware (material) and model (method) performance in research (İnik & Ülker, 2017).

RESULTS

The ANN model was used to predict SCC over the model variables of EC, pH, TFM, and milk density, which are the factors affecting SCC as a numerical response variable. Descriptive statistics belonging to variables used in the training and compilation of the model are presented in Table 3, and summary graphics are given in Appendix A.

Means ± standard errors of the variables used in the model were EC (mS) 7.23±0.10, TFM (°C) 35.71±0.06, Density (gr/mL) 1.03±0.00, pH 6.86±0.01, SCC (*1000 pcs/mL) 790.43±49.87. Similar to the present study Norberg *et al.* (2004), when they tried to predict healthy or clinical mastitis individuals with EC, mean EC values were 5.30 in healthy, 5.75 for subclinical, and 6.75 for clinical mastitis cows, respectively.

It is seen from Figure 2 that the MAE and loss (MSE) values converge to 0 and become stable by the 50th iteration in the learning (training) process of the model. While it is expected that the loss values, such as mean absolute error and mean squared error will converge to 0 (zero) in the training process. In addition, it is understood that the training and validation curves de-

Table 2. The packages of R environment used in the prediction of somatic cell count through multilayer perceptron

Packages	Use purpose	Reference
ehaGoF	calculation of performance metrics	(Eyduran & Gulbe, 2022)
GGally	summarise and visualization	(Schloerke *et al.*, 2022)
Keras	modeling MLP	(Kalinowski *et al.*, 2022)
Core packages	modeling MLRM and descriptive statistics	(R for Statistical Computing, 2022)

Table 3. Descriptive statistics of the variables used in the prediction of somatic cell count through multilayer perceptron

Parameters	N	Mean ± Std. error	Min.	Max.
SCC (*1000/mL)	500	790.43±49.87	6	4588
EC (mS)	500	7.23±0.10	4.91	12.65
pH	500	6.86±0.01	6.55	7.32
Density (gr/mL)	500	1.03±0.00	1.01	1.05
TFM (°C)	500	35.71±0.06	33	38.62

Note: "SCC" stands for milk somatic cell count; "EC" for "electrical conductivity"; "TFM" for temperature at foremilking; "pH" for negative logarithm of hydrogen concentration; "Density" for density of milK; "Std. Error" for standard error; "N" for number of observations; "Min.". and "Max." for minimum and maximum observations respectively.

crease together in parallel during the learning process, and both curves approach each other without diverging. The model is completed successfully without encountering any over-fitting (or memorization) problems during the training process.

The execution time was observed to be executed in 683 seconds. The coefficient of determination (R^2) of the ANN model was determined as 0.95, 0.01, and -338 for the RMSE and AIC scores, respectively, at a satisfactory level, as expected in a successful model (Kayaalp *et al.*, 2015; Cebeci, 2021).

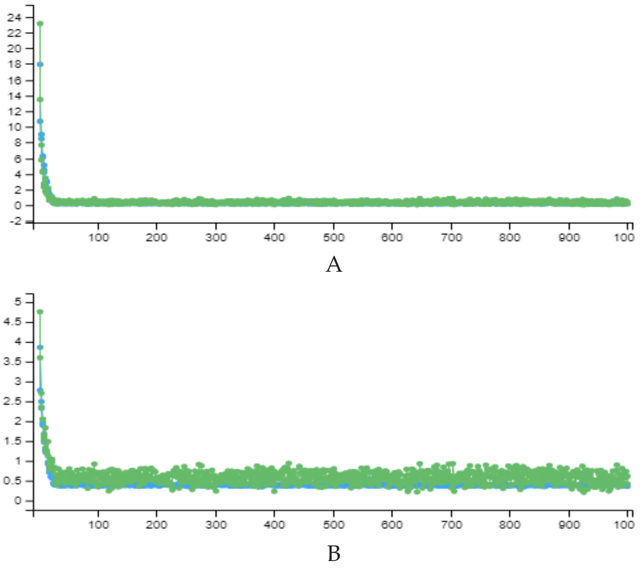

Figure 2. The training (learning) process of the model. A) 🟦 = "loss" stands for "mean squared error" during training, 🟩= "val_loss" during validation; B) 🟦= "mae" for "mean absolute error" during training, 🟩= "val_mae" during validation. The vertical axis indicates the loss values while the horizontal axis indicates the number of ephocs during the learning process. "x" axis shows the number of iterations while training, and the axis "y" shows the degree of errors (SCC/mL) for each iteration.

DISCUSSION

Panchal *et al.* (2016) found the EC, pH, and milk temperature values as 6.79, 7.03, and 35.77 for cases with mastitis, 5.16, 6.49, and 33.53 for healthy ones. Since the aim of the present study is not to diagnose healthy animals and animals with mastitis, descriptive statistics are given together without any distinction according to health status. Harmon (1994) reported that the pH of milk varies between 6.6 and 6.9 and can reach higher levels because disease factors such as mastitis cause deterioration in milk structure. Severe clinical signs of mastitis were observed in cases around the maximum pH value of 7.32 attained in our study.

Too *et al.* (2019) found the lowest training period to be 1051 seconds in their study where they estimated plant diseases. It is known that the difference between the training time obtained in the current study is due to several factors, such as data size, the structure of the network used in training the models, the number of neurons in the hidden layers and input layer, and the characteristics of the hardware used in model training.

With lower performance than the current study, Soyeurt *et al.* (2020) compared the 4 different models, and the model using ANN was the most successful, with 0.60 R2 and 162.17 RMSE. This suggests that they developed their prediction model without applying any conversion to the response variable in their study (log(162.17) = 2.29 > 0.01). In addition, it is reported that this is due to the high variation observed in the response variable. For this reason, it is stated that prediction performance will increase in predictions made with different variables directly affecting response variables except for the mid-infrared spectrum. Anglart *et al.* (2020) modeled the cow SCC with logarithmic transformation, as in our study, by using the data of a series of milking information such as milking time, milk yield obtained from the automated milking system and the sensor data of only milk flow rate and conductivity from milk physical properties. In their study, they determined the loss to be 0.09. Bobbo *et al.* (2021) reported an accuracy rate and error values of 80% and 15%, respectively, in the model they used. Lievaart *et al.* (2010), when they tried to estimate the SCC over the sampling interval using the ANN model, stated that the model error values were in the range of 15-40 SCC (*1000/mL) according to different interval values between 4 and 14 days. To be able to compare these values with our current research, when the logarithmic transformation is applied, it is seen that they are in the range of 4.18-4.60 and are higher than the error values obtained in the findings we presented (RMSE= 0.01; MSE=1e-04). Panchal *et al.* (2016) reported that when they estimated SCC using a multiple linear regression model over EC and pH in milk, they found it to be 4.91% of RMSE, which is lower than ours considering that the % RMSE value is less than 1% and 0.01% for MLRM and ANN, respectively. Bai *et al.* (2022) tried to estimate the total udder SCC from the milk obtained from the mammary lobe, and stated that the model they used could only explain 15% of the variation in SCC. Similarly, Wellnitz *et al.* (2009) found 0.25 of R^2 when estimating total udder SCC over anterior milk lobe SCC using random-effect linear regression. They reported that the anterior milk lobe SCC performed poorly in terms of the model for low SCC (<1,000,000) values in estimating the total SCC of the whole udder, and the success of prediction increased at high SCC values. The increase in prediction success at high SCC values is similar to the findings we obtained (Figure 3). This suggests that the SCC has a nonlinear data structure and that at high SCC values, most of the variation is due to a single factor (mastitis). This indicates that the sources of variation that cause high SCC values are decreasing. In other words, it suggests that higher SCC values are caused by major factors such as mastitis

The current study shows that the prediction performance has increased since 4 different input variables are used to predict SCC. Therefore, the higher the number of factors affecting the variation included in the model as a predictive model variable in the prediction of SCC, the better the model explains the variation of the response variable (R^2 of 0.95). This is because the model does not include the physical and chemical properties of milk with a high correlation, which directly affects SCC. The difference is that the EC, pH, TFM, and density parameters used in the prediction of SCC in the current study better represent the factors causing the overall variation in SCC (Kayaalp *et al.*, 2015). It is seen that these previous studies reported lower results than our findings in the current study. This also suggests that model performance increases when the number of input and predictive model variables of milk physical and chemical properties directly affecting the variation in SCC is increased instead of milking information. In addition, it shows the importance of increasing the number of predictive model variables (input) together with the selection of the right predictive model variables, instead of using a large number of inputs that would complicate the model structure of the ANN. On the other hand, considering that mastitis, which is the major factor affecting SCC levels, can develop separately in each udder lobe when the results are evaluated together, it is understood that udder lobe SCC values and SCC measurement interval alone are not sufficient parameters in the prediction of SCC values of the total udder (for 4 lobes).

Similar to the present study, Bai *et al.* (2022) and Kusumoto & Yuasa (2019), in their studies on the diagnosis of mastitis with ANN, found the accuracy rates of their most successful models to be 97% and 90%, and error values of 4% and 7%, respectively. Hernández-Ramos *et al.* (2019) achieved 100% success when they tried to predict the SCC of the milk of cheese samples in 3 categories (low, medium, and high) using ANNs with the physicochemical compounds of hard sheep cheeses. This is because they estimate SCC categorically instead of numerically. As the response variable (out-put) SCC is included in the model by dividing it into 3 categories, it can be explained by the decrease in the number of factors that cause variation in intermediate values.

Model Performances

While the RMSE and AIC scores of the ANN model (0.01 and -338), respectively, were lower than the MLRM (0.10 and -240), the coefficient of determination (R^2=0.95) was higher than the MLRM (0.79) (Table 4). It is understood that the ANN model has a lower AIC score, although the AIC score has the advantage of having few numbers of parameters in the MLRM because it penalizes the number of parameters entering the model. This is due to using the likelihood function or MSE in calculating the AIC score (Panchal *et al.*, 2010). The findings show that the ANN model outperforms the control model (MLRM) in terms of prediction accuracy. This is because the control model, MLRM, is highly influenced by the interactions between the independent variables affecting SCC, which is our response variable, and gives misleading results. Interactions between input variables do not cause any change in the performance of our test model, ANN. Ebrahimi *et al.* (2019) compared different machine-learning applications to predict subclinical mastitis based on milk volume, flow rate, EC, milking time, milk fat, protein, and lactose contents. They reported that the deep learning model (%RMSE=15%) performed better in terms of error values. In the current research, the ANN model also performs better than the control model (MLRM). Lievaart *et al.* (2010) reported that they obtained the highest AIC score (3513) in the group with low SCC when they tried to predict SCC for the coming months using a linear mixed-effects model. Similar to our results, it shows that prediction success is reduced at low SCC levels. In addition, the linear model AIC score (-240) obtained in our research is significantly lower than the AIC score (3513) obtained in the aforementioned study, and the predictive model variables (EC, TFM, density, and pH) used in the current study were more accurate in estimating SCC. The technique presented in the current study also saves time compared to the model presented in the other study since it does not require any weekly interval in the prediction of SCC.

Table 4. Performance indicators of the models validated on the test set

Model	N (test)	R^2	MSE	RMSE	AIC	*NoP.
MLRM	125	0.79	0.01	0.1	-240	5
ANN	125	0.95	1.00E-4	0.01	-338	81

Note: *NoP: Number of Parameters; MLRM= multiple logistic regression model; ANN= artificial neural networks.

When compared with the prediction and actual values conducted on the test set for both models, MLRM (Figure 4) shows a higher deviation from the actual ones compared to the ANN (Figure 5). Figures 3 and 5 show that the prediction values made on the test set with ANN are in parallel with the actual observation values and successfully explain the variation of the general -low and high- SCC (R^2=0.95). This shows that the model developed with ANN better represents the factors that cause general variation in SCC. In other words, it shows that ANN better explains the variation occurring in SCC. From Figure 4, it is clarified that the error values belonging to the MLRM predictions validated on the test data observation values show a high deviation, causing the coefficient of determination (R^2) to decrease and the loss values such as RMSE, MSE, MAE to increase. Observing high deviations in the MLRM error values caused the AIC score to increase, although the number of parameters included in the model was low. In addition, when the prediction curves of both the MLRM (Figure 4) and the ANN model are examined

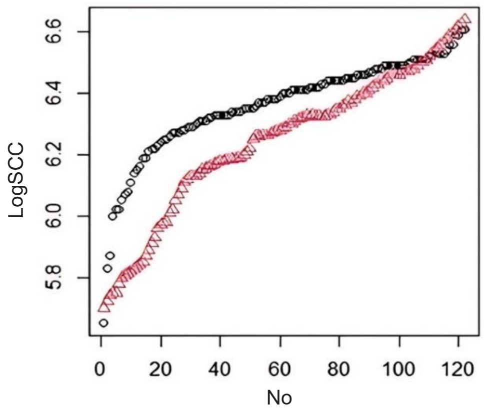

Figure 3. The compatibility between logSCC observations (actual values) and predicted values by the test model (ANN). “logSCC” stands for logarithmic transformed somatic cell count, while “no” stands for the number of predictions and observations. ∆= prediction; ○= actual.

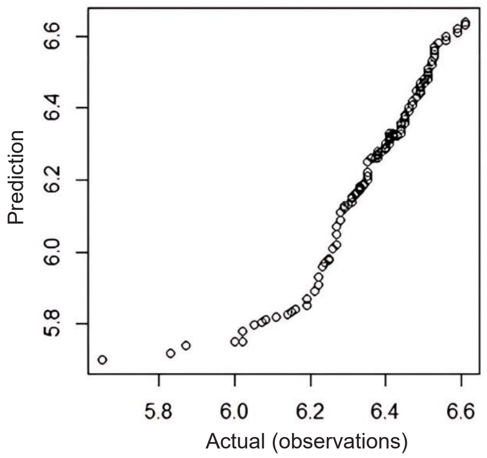

Figure 5. Graph showing actual observations and predicted loggSCC values validated on the test data belong to the multilayer perceptron feedforward backpropagation ANN model. “Actual” axis represents the actual values (observations), while “Prediction” represents the predictions by the model.

(Figure 5), it is seen that the deviation decreases as the SCC values increase. In Figures 4 and 5, it is understood that SCC has a non-linear data structure. For this reason, high deviations are observed in the loss values of the predictions made with linear models.

CONCLUSION

In this study, a deep learning approach (ANN) was compared to a low parameter estimation approach (MLRM) for predicting SCC, the gold-standard indicator of subclinical mastitis. The ANN model showed superior performance with better metrics (AIC=-338; RMSE=0.01; R^2=0.95) compared to MLRM (AIC=-240; R^2=0.79), despite requiring more parameters. The training time was a satisfactory 683 seconds using TensorFlow GPU on a CUDA-supported system, demonstrating an efficient and cost-effective method for handling large datasets. Future research with supercomputers and automated milking data is expected to improve prediction accuracy further. Overall, SCC detection using the deep learning technique proved effective and economical, highlighting the ongoing need for AI-driven solutions in animal health and milk quality.

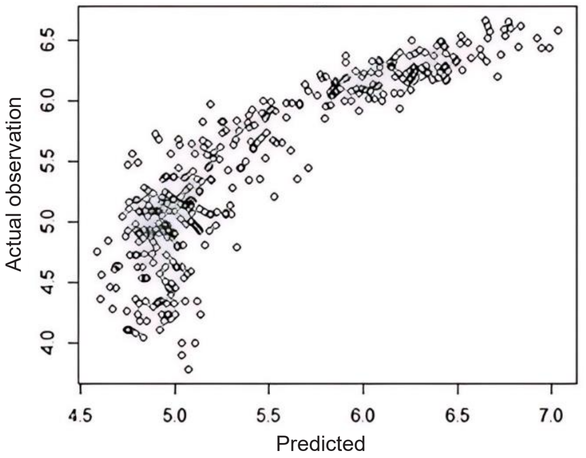

Figure 4. The actual and predicted logSCC observations validated on the test data belong to the MLRM. The “Actual” axis represents the actual values (observations), while the “Predicted” represents the predictions of the model.

CONFLICT OF INTEREST

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

ACKNOWLEDGMENT

The research was supported by Cukurova University Research Unit Projects (Project No: FDK-2021-13656). The authors wish to thank the Cukurova University Research Unit Projects for their support.

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