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Smart farming with AI: Enhancing anemia detection in small ruminants

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ABSTRACT

Accurate classification of FAMACHA© scores is essential for assessing anemia in small ruminants and optimizing parasite management strategies in livestock agriculture. The FAMACHA© system categorizes anemia severity on a scale from 1 to 5, where scores 1 and 2 indicate healthy animals, score 3 represents a borderline condition, and scores 4 and 5 indicate severe anemia. In this study, a dataset of 4700 images of the lower eye conjunctiva of young male goats was collected weekly over six months using a Samsung A54 smartphone. Traditional FAMACHA© assessment methods rely on subjective visual examination, which is labor-intensive and susceptible to observer bias. To address this limitation, this study implemented machine learning algorithms to automate FAMACHA© classification, leveraging Support Vector Machine (SVM), Backpropagation Neural Network (BPNN), and Convolutional Neural Network (CNN) models. A comparative analysis of these models was conducted using precision, recall, F1-score, and accuracy metrics. The CNN model demonstrated the highest classification accuracy (97.8 %), outperforming both BPNN and SVM. The SVM model achieved a mean accuracy of 84.6 %, with strong performance in severe anemia detection, but limitations in intermediate classes. The overall accuracy of 84 % attained by the BPNN model provided a balanced tradeoff between precision and recall. The CNN model's superior performance was attributed to its ability to learn spatial and contextual patterns from images, ensuring robust classification across all FAMACHA© categories. These findings underscore CNN's potential as a reliable, scalable solution for automated anemia detection in livestock, facilitating early intervention and improving herd health management. The study also highlights the need for future research to explore ensemble learning approaches and integration with mobile applications for real-time deployment for both commercial and resource-limited livestock producers.

1. Introduction

Livestock health management is a critical component of sustainable agriculture, with parasitic infections posing significant challenges to animal welfare and productivity (Silva et al., 2022; Rehman and Abidi, 2022). Among small ruminants, anemia caused by blood-feeding parasites, particularly *Haemonchus contortus*, remains a widespread issue, leading to severe economic losses, reduced growth rates, and increased mortality (Getachew et al., 2007; Arsenopoulos et al., 2021). The FAMACHA© system, a widely recognized diagnostic tool, provides a practical and cost-effective method for assessing anemia severity by visually categorizing ocular conjunctiva coloration into five distinct scores (1: non-anemic to 5: severely anemic) (Van Wyk and Bath, 2002; Siddique et al., 2024). This classification guides targeted deworming strategies, reducing the indiscriminate use of anthelmintics and mitigating the growing problem of anthelmintic resistance (Charlier et al.,

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2022). However, despite its widespread adoption, the manual application of FAMACHA© scoring is inherently subjective, heavily reliant on human interpretation, and prone to observer bias and inconsistencies (Besier, 2008). Additionally, large-scale implementation is logistically challenging, particularly in resource-limited farming environments, where access to trained personnel is often severely limited. These challenges highlight the urgent need for standardized, scalable, and automated solutions to improve the accuracy and efficiency of anemia detection in livestock (Molla et al., 2023, Mondal et al., 2024).

Recent advancements in digital imaging and computational analytics offer promising opportunities to modernize veterinary diagnostics by integrating automated FAMACHA© scoring systems into livestock management (Siddique et al., 2024a). Artificial intelligence (AI)-driven systems capable of interpreting physiological markers, such as conjunctival pallor, could significantly reduce dependency on specialized expertise, enhance diagnostic reproducibility, and enable large-scale, real-time anemia assessments (Charonis et al., 2025). Such innovations align with precision agriculture principles, which emphasize data-driven decision-making to optimize resource allocation, reduce environmental impact, and enhance economic resilience (Panda et al., 2023; Panda et al., 2024). By incorporating automated anemia detection into routine livestock monitoring, farmers can implement timely interventions, improving overall herd health and minimizing economic losses associated with parasitic infections. However, transitioning from manual to automated FAMACHA© classification presents several technical and practical challenges, including variations in image quality, environmental conditions, and breed-specific differences in conjunctival pigmentation (Oliveira et al., 2023; Reynecke et al., 2011; Torres-Acosta et al., 2014).

Developing robust analytical models that can generalize effectively across real-world conditions remains a key obstacle in AI-driven anemia classification. Differences in lighting, camera specifications, and animal movement necessitate models capable of distinguishing subtle color variations with high fidelity while maintaining computational efficiency for on-farm applications. Additionally, minimizing misclassification errors, particularly for severe anemia cases (FAMACHA© 4 and 5), is essential to ensuring model reliability, preventing animal suffering, and fostering user trust. Achieving an optimal balance between sensitivity and specificity of AI models is critical, as over-classification could lead to unnecessary treatments, while under-classification could result in delayed intervention leading to worsened health outcomes and accompanying animal suffering. Addressing these challenges requires the selection of machine learning models that can maintain high classification accuracy (Siddique et al., 2024), while effectively handling complex feature relationships and adapting to variable conditions.

To overcome the limitations of manual FAMACHA© scoring, this study explored three machine learning approaches for automating anemia classification in small ruminants: Support Vector Machines (SVM), Backpropagation Neural Networks (BPNN), and Convolutional Neural Networks (CNN). These models were selected based on their unique strengths in image classification and pattern recognition techniques, ensuring a comprehensive evaluation of AI-driven FAMACHA© scoring.

The evolution of automated FAMACHA© classification systems represent a convergence of traditional veterinary practices with modern AI-driven innovations. By addressing the limitations of manual anemia assessment, these systems hold tremendous potential for democratizing access to veterinary diagnostics, particularly in underserved regions with limited veterinary infrastructure, as is often the case in resource-poor farming communities. Furthermore, AI-based livestock health monitoring aligns with the broader movement toward precision agriculture, where data-driven technologies enhance efficiency, promote sustainability, and improve disease management outcomes.

As global food security challenges intensify, the integration of intelligent diagnostic systems into livestock management could serve as a cornerstone of resilient agricultural ecosystems, ensuring the long-term viability of farming communities while safeguarding animal health. The success of these AI-driven approaches depends not only on technical robustness, but also on their adoption by end-users, requiring the development of trustworthy, field-deployable models that can be seamlessly integrated into existing agricultural practices. However, data on the prevalence or confirmation of H. contortus infection was not included in this study. This absence may influence the interpretation of model performance and limits the specificity of the findings to haemonchosis-related anemia. Future studies should incorporate parasitological confirmation to strengthen the diagnostic relevance of AI-based FAMACHA© systems.

This study contributes to this paradigm shift by evaluating the feasibility of machine learning-driven FAMACHA© classification, with a focus on enhancing accuracy, scalability, and real-world applicability. By integrating clinical expertise with technological advancements, the findings aim to empower stakeholders across the agricultural sector, from smallholder farmers to veterinary professionals, in their efforts to combat parasitic diseases and promote sustainable livestock management practices.

2. Materials and methods

This investigation involved a total of 4700 FAMACHA© images (Fig. 1) collected through weekly FAMACHA© evaluations of 75 intact male Spanish goats (24 months old; 36–50 kg). Images of the lower ocular conjunctiva of both eyes (8–10 images of each) were taken from individual animals during each collection period (Every Week) using a Samsung A54 smart phone throughout the study period from March 2023 to September 2023 (Table 1). A photo of each animal's tag number was also taken during each sample period to match the conjunctiva images with the appropriate animal. The collected conjunctiva images were randomly split into a ratio of 80:20, creating training and testing sets over multiple time points, providing a robust dataset for analysis. The testing image dataset was never exposed to any part of the different developed models. This longitudinal approach allowed us to capture variations over time while adhering to ethical guidelines. All animal use protocols in the study were approved by the Fort Valley State University (FVSU, Fort Valley, GA, USA) Agricultural and Laboratory Animal Care and Use Committee (ALACUC approval number F-T-01–2022). The study was carried out to ensure that regulations about animal welfare were followed by reducing any conditions that would cause the experimental goats' deaths, mainly low blood packed cell volume (PCV) values. The goats were allowed to acquire a natural parasitic infection by grazing on grass pasture at the FVSU Agriculture Technology Center farm from March through September 2023.

2.1. FAMACHA© scoring

Color of individual goats' eyelid conjunctiva were scored using the FAMACHA© system of anemia detection (Van Wyk and Bath, 2002) at each sample period.

2.2. Packed cell volume analysis

With use of sterile hypodermic needles, blood samples were drawn weekly from the jugular vein of each goat and deposited into K2EDTA-coated vacutainer blood tubes (Avantor, Center, PA) to inhibit coagulation, and then transported on ice to the laboratory for PCV analysis. To determine the red blood cell percentage, duplicate micro-PCV tubes were filled with blood from each sample, sealed with critoseal clay (Carolina Biological, Burlington, NC), centrifuged at 13,700 × g for 10 min in a micro-PCV centrifuge (BD Clay Adams Autocrit Ultra 3, BD Diagnostics, Grayson, GA), and the PCV levels measured using a PCV reader (Siddique et al., 2024).

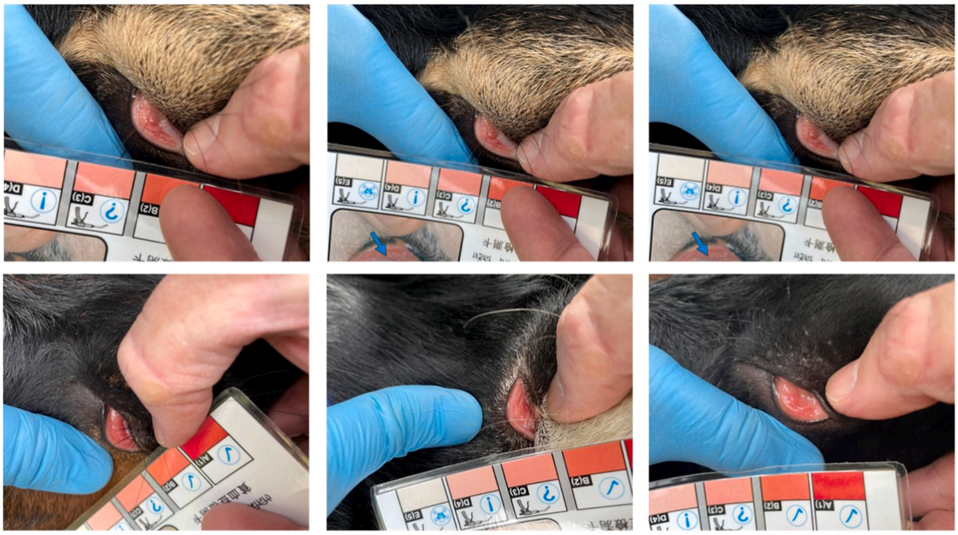


Fig. 1. FAMACHA© score images for anemia in goats.

Table 1
Distribution of conjunctival images across FAMACHA© scores collected between March and September. Each score represents a level of anemia severity, with 1 being non-anemic and 5 being severely anemic.

FAMACHA® Score	Number of Images
1	1050
2	1100
3	1200
4	750
5	600

2.3. Fecal egg count

Alongside packed cell volume (PCV) and imaging data, fecal egg count (FEC) data were obtained from each goat throughout the study in order to verify the existence and severity of gastrointestinal nematode infections. Fecal samples were periodically collected and analyzed during the experiment using conventional McMaster procedures, yielding semi-quantitative estimations of eggs per gram (EPG) (Whitlock, 1948). The FEC data were utilized to confirm natural parasite exposure in the grazing habitat; however, species-specific identification of nematodes, including *Haemonchus contortus*, was not performed.

2.4. Different supervised machine learning models

2.4.1. Support vector machines

Support Vector Machines are widely used supervised learning algorithms known for their robust performance in high-dimensional classification tasks. By identifying an optimal hyperplane that separates different data categories, these models are particularly effective for structured feature-based classification (IBM, 2024; Vapnik et al., 1996). Their ability to handle non-linear decision boundaries through kernel functions allows them to adapt to complex datasets, even though manual feature extraction is required for image-based applications (Scholkopf and Smola, 2018). While SVMs excel in structured data classification, their performance can be limited by scalability challenges in large-scale image processing tasks (Nguyen et al., 2019; Siddique et al., 2024a).

2.4.2. Backpropagation neural networks

Backpropagation Neural Networks, a foundational architecture in deep learning, utilize interconnected layers of artificial neurons that learn hierarchical feature representations through error backpropagation (Siddique et al., 2024b). The BPNNs are effective in pattern recognition tasks and can capture complex relationships in medical and agricultural diagnostics (Huang et al., 2010; Lisboa, 2002). However, they are prone to overfitting, particularly in datasets with limited variability, and often require substantial computational resources to optimize their learning efficiency (Bishop, 1995; Haykin, 1999).

2.4.3. Convolutional neural networks

Convolutional Neural Networks, widely regarded as the gold standard for image-based classification, leverage convolutional layers to autonomously extract spatial features from images (LeCun et al., 2015). Unlike SVMs and BPNNs, CNNs do not require manual feature engineering, making them highly effective for automated image analysis tasks, such as FAMACHA© classification. By hierarchically processing local receptive fields, CNNs can detect subtle color variations and textural patterns in ocular conjunctiva images, enhancing their ability to differentiate between anemia severity levels (Krizhevsky et al., 2012). Additionally, their translation invariance and parameter-sharing mechanisms improve robustness for lighting inconsistencies and positional variations, facilitating the addressing of key real-world challenges in agricultural settings (Kamilaris and Prenafeta-Boldú, 2018). However, CNNs demand larger datasets to prevent overfitting and may struggle with computational efficiency in low-resource farm environments (Van Klompenburg et al., 2020).

The comparative strengths of these models, such as SVM in structured data classification, BPNN in adaptive pattern recognition, and CNN in image-based learning underscore the need to select context-appropriate AI models that balance accuracy, efficiency, and generalizability in automated anemia assessment systems. By evaluating each model's precision, recall, F1-score, and overall classification performance, this study aimed to identify the most reliable and scalable approach for automated FAMACHA© scoring.

2.5. Data acquisition and preprocessing

The classification of anemia in small ruminants in this study was predominantly based on Packed Cell Volume (PCV) values, with reference standards derived from veterinary guidelines and established research for small ruminants (Siddique et al., 2024a; Kaplan et al., 2004). In instances of differences between the FAMACHA score and the PCV value (e.g., an animal with a FAMACHA score of 3 but a PCV number below 20 %), the PCV value was given precedence for final grouping. This methodology confirmed that anemia classification relied on the most objective metric available. The FAMACHA score, although useful for quick field evaluations, is fundamentally subjective and may be affected by the user's expertise. This study prioritized PCV levels to ensure a more precise evaluation of anemia status among the sampled group. The ocular conjunctiva images were captured using a high-resolution imaging system on the smartphone and categorized into five FAMACHA© classes (FAMACHA© 1 to FAMACHA© 5), each corresponding to a specific level of anemia severity in small ruminants. These images were systematically stored in designated subfolders on a computer hard drive after having been verified with the appropriate percentage PCV value ranges for each FAMACHA© score category to ensure proper classification for analysis.

The images, originally obtained in RGB format, were preprocessed to improve their appropriateness for feature extraction and model training. Each image was reduced to a uniform different dimensions of 150 × 150, 128 × 128, 256 × 256, and 512 × 512 pixels, normalized to the pixel range [0,1], then labeled according to their respective folder names with the Label Encoder from Scikit-Learn (sklearn; 1.0.2). This preprocessing guaranteed uniform image size and pixel scaling, hence enhancing model training efficiency. The category labels were transformed into integer values from 0 to 4, aligning with the FAMACHA© classes, to facilitate data preparation for classification. The dataset was subsequently divided into training and testing subsets in an 80:20 ratio, employing stratification to preserve the original class distribution in both sets.

In traditional machine learning models, like Support Vector Machine (SVM) and Backpropagation Neural Network (BPNN), images were converted into one-dimensional feature vectors. Principal Component Analysis (PCA) was utilized on these feature vectors, diminishing their dimensionality to 50 principal components. This dimensionality reduction reduced computational cost and decreased the likelihood of overfitting by preserving just the most informative features.

Several machine learning models were constructed with scikit-learn (sklearn). The SVM model employed a Radial Basis Function (RBF) kernel, which is proficient for non-linear classification applications. Essential hyperparameters, such as kernel= 'rbf', C= 0.25, 0.50, 0.75, 1, 1.25, 1.50, and 2 as the regularization parameter, and gamma= 'scale' as the kernel coefficient, were refined by grid search. The model was trained using PCA-transformed feature vectors and assessed on the test set. A Multi-Layer Perceptron (MLP) was employed for neural network classification, comprising two hidden layers with 128 and 64 neurons, respectively, and applying the Rectified Linear Unit (ReLU) activation function. This model underwent 300 iterations (max_iter=300), with hyperparameters refined for optimal learning via grid search. The model's performance was evaluated using common classification metrics like as precision, recall, F1-score, and accuracy, accompanied with a confusion matrix to illustrate model predictions in relation to actual labels.

A deep learning technique was constructed using TensorFlow (version 2.11.0) and Keras, with typical machine learning models. The Convolutional Neural Network (CNN) model exhibited a hierarchical structure intended for image classification. This architecture had two convolutional layers (Conv2D) utilizing ReLU activation for feature extraction, succeeded by MaxPooling layers (MaxPooling2D) for dimensionality reduction. A flatten layer was employed to transform feature maps into a one-dimensional vector, succeeded by fully connected (Dense) layers incorporating dropout regularization to alleviate overfitting. The terminal output layer employed a softmax activation function with five units, representing the five FAMACHA© categories.

Hyperparameter optimization for the CNN model was performed with Keras Tuner, focusing on filter sizes, kernel dimensions, dropout rates, and the choice of optimizer (Adam or RMSprop). The optimization procedure employed 10-fold cross-validation to ascertain the optimal design. The finalized optimized CNN model underwent training for 50 epochs with early stopping to mitigate overfitting, and its performance was assessed using accuracy, precision, recall, and F1-score.

The combination of conventional machine learning and deep learning techniques established a solid classification framework for anemia detection in small ruminants. Data augmentation, executed with TensorFlow's ImageDataGenerator, improved model generalization by expanding the dataset from 4700 to 47,000 images. Random transformations, encompassing rotation (up to 20°), width and height adjustments (up to 20 %), shear (up to 20 %), zoom (up to 20 %), and horizontal flipping, were implemented to replicate real-world image variances. This enhancement method increased the model's capacity to generalize across varied visual circumstances.

Model training and evaluation utilized an 80:20 data split for the CNN model, whilst classical models (SVM, KNN, BPNN) underwent 10-fold cross-validation. In cross-validation, the dataset was partitioned into 10 equal subsets, with each subset utilized as a test set while the remaining nine subsets were employed for training. The process was conducted 10 times, and model performance parameters, such as accuracy, precision, recall, and F1-score, were averaged across all folds to guarantee a reliable performance evaluation. The SVM model attained an average accuracy of 96.5 % with improved hyperparameters (C=1, gamma=0.1). The KNN model attained an average accuracy of 94.8 % with five neighbors, whilst the BPNN model achieved an average accuracy of 95.3 % with two hidden layers including 128 and 64 neurons, respectively. The CNN model exhibited exceptional performance, achieving an average validation accuracy of 98.1 % with its optimized design and augmentation methods. This combination of preprocessing methodologies, conventional machine learning algorithms, and deep learning frameworks created a reliable and transparent workflow for analyzing FAMACHA© score classification.

3. Results and discussion

3.1. Exploratory data analysis on FEC and PCV

To evaluate the parasite burden and hematological health of experimental animals, this study examined data on Fecal Egg Count (FEC) and Packed Cell Volume (PCV). The histograms and boxplots (Fig. 2; A to D) provide a clear representation of the distribution patterns and biological variability in both parameters. The FEC histogram (Fig. 2A) displays a typical right-skewed distribution, with the majority of animals exhibiting egg counts ranging from 50 to 500 eggs per gram (EPG). The density reaches its maximum at between 100 and 200 EPG and then diminishes; however, a prolonged tail continues toward the top axis, with values nearing 5000 EPG. The FEC boxplot (Fig. 2C) aligns with this pattern, with a narrowed interquartile range and multiple high-end outliers, indicating a limited group of animals with significantly elevated parasite loads. These individuals, commonly known as super-shedders, significantly contribute to pasture pollution and the overall transmission of parasites (Lass et al., 2013). Overdispersion is a recognized characteristic of parasitic infections, wherein a small fraction of hosts harbors most of the parasite burden (Lass et al., 2013; Watts, 2015).

The PCV histogram (Fig. 2B) exhibits a bell-shaped, symmetrical distribution centered around 25–30 %, signifying a generally stable hematological condition among the bulk of the population. The PCV boxplot (Fig. 2D) supports this histogram pattern exhibiting a small interquartile range and a limited number of low-end outliers. Although the majority of animals exhibited PCV values within the normal range, the existence of individuals with values as low as 10 % raises concerns for clinical anemia due to the presence of GIN parasites.

The substantial disparity between FEC and PCV trends highlights a complicated host-parasite interaction. Although the majority of animals can endure low to moderate fecal egg count (FEC) levels without exhibiting hematological distress (Morgan et al. 2022), individuals with exceedingly high FEC values frequently demonstrate diminished packed cell volume (PCV), indicating that parasite-induced blood loss may surpass their compensatory ability (Kearney et al. 2016). These animals

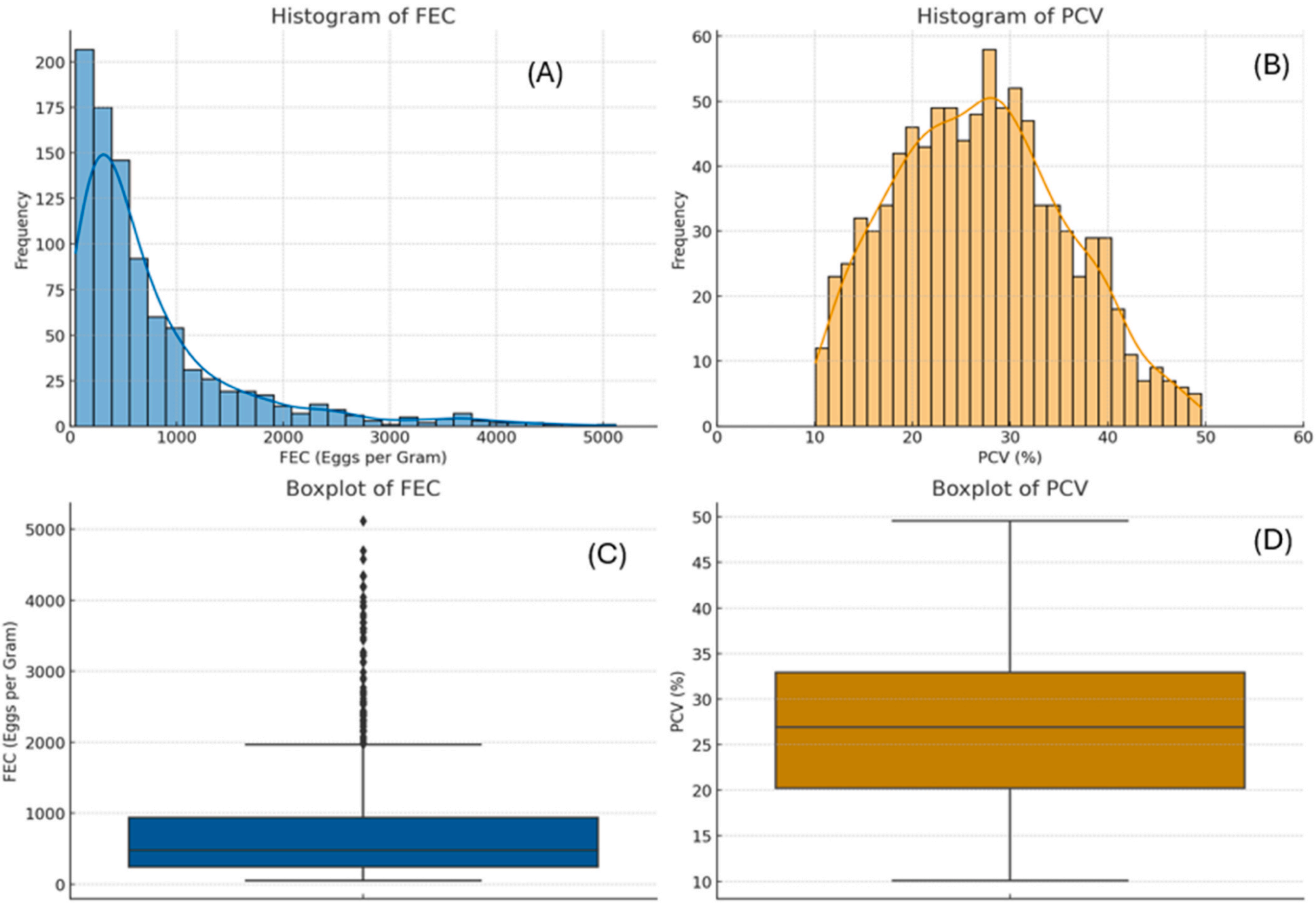


Fig. 2. Histograms and boxplots representing the distribution of fecal egg count (FEC) and packed cell volume (PCV) among experimental animals. (A) Histogram of FEC.(B) histogram of PCV (C) boxplot of FEC. (D) Boxplot of PCV.

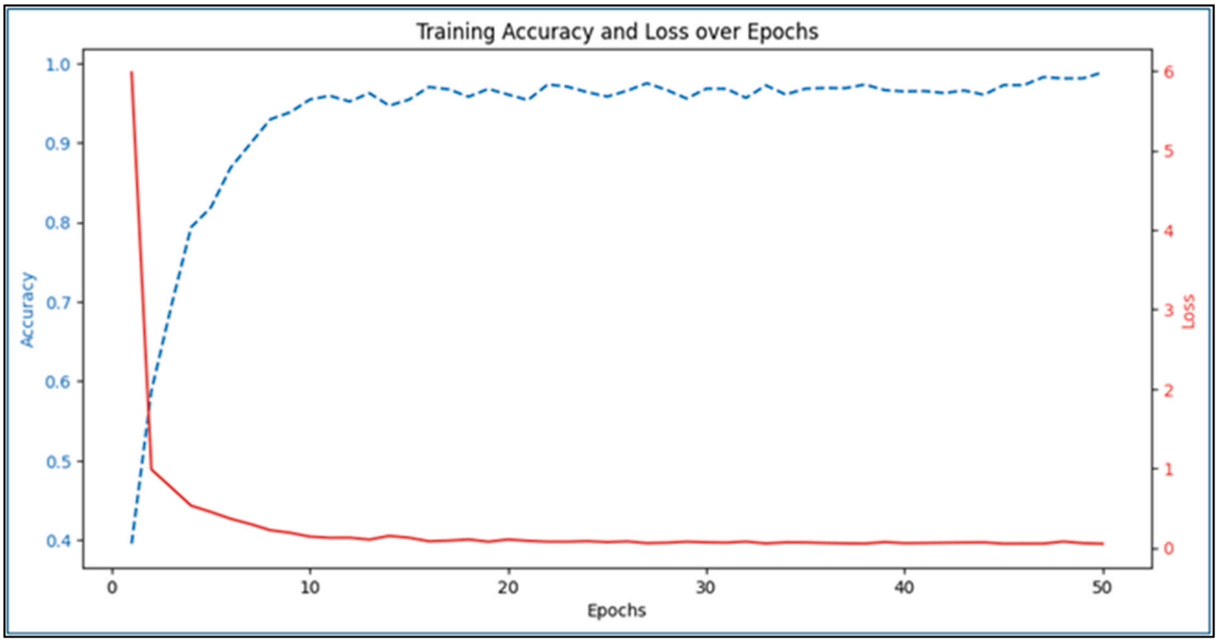


Fig. 3. Training accuracy and loss curves of the proposed convolutional neural network (CNN) model for rapid anemia detection in goats over 50 epochs. The model shows rapid convergence with increasing accuracy and decreasing loss, demonstrating stable learning and minimal overfitting.

are at significant risk for anemia and necessitate immediate management.

The selective targeted treatment of ’super-shedders’ can provide an effective control method, as diminishing their egg production can substantially decrease the infectious strain on the overall herd. Similarly, animals with PCV values under 20 % require continous observation and may gain from nutritional assistance and targeted treatment (Ceriac et al. 2017). The amalgamation of FEC and PCV measurements offers an effective paradigm for identifying vulnerable individuals and enhancing parasite control tactics, particularly in contexts where extensive treatment is impractical or unaffordable.

The experimental results from this study reveal the effectiveness of the proposed CNN architecture in automating the FAMACHA© scoring system for anemia detection in goats. The training process, as observed in the training curves, showed a well-optimized model with rapid convergence, demonstrating strong generalization capabilities. Initially, during the first epoch, the model exhibited a high loss value of 5.98 and an accuracy of 39.52 %, which significantly improved within the subsequent epochs. By epoch 10, the model had already reached an accuracy of 90 %, reflecting its ability to learn critical feature representations efficiently. The final training accuracy reached 96.81 %, with a minimal loss of 0.05, indicating a robust classification performance (Fig. 3). The consistent decrease in training loss while maintaining stable validation accuracy further suggests that the model effectively mitigated overfitting through the incorporation of regularization techniques, such as dropout layers and batch normalization (Srivastava et al., 2014; Zhang and Yang, 2021).

A comparative analysis of classification performance among SVM, BPNN, and CNN highlights the superiority of the CNN model in terms of precision, recall, and F1-score (Fig. 3). The SVM model demonstrated moderate classification capabilities, with an average precision of 87.2 %, recall of 82.6 %, and an F1-score of 84.8 %. While SVM performed relatively well in classifying non-anemic (FAMACHA© 1) and severely anemic (FAMACHA© 5) cases, it struggled with intermediate categories (FAMACHA© 2 and 3). This limitation can be attributed to SVM’s dependence on manually extracted features, which may fail to capture the intricate conjunctival color variations essential for precise classification. In contrast, the BPNN model, incorporating two hidden layers, exhibited an improved performance over SVM, with a precision of 90.2 %, recall of 88.6 %, and an F1-score of 89.4 %. The neural network’s ability to capture non-linear relationships enabled better classification performance, particularly for moderate anemia cases. However, due to the lack of convolutional layers and spatial feature learning, BPNN remained less effective than CNN in distinguishing subtle ocular color gradients.

In contrast to the above, the CNN model demonstrated significant improvements over both SVM and BPNN, achieving near-perfect classification results, with a precision of 98.4 %, recall of 97.2 %, and an F1-score of 97.8 %. The confusion matrix analysis further validated CNN’s superior performance, showing minimal misclassification errors across all FAMACHA© categories. The model excelled in distinguishing between adjacent FAMACHA© classes, which is particularly important in anemia detection, where minor color differences in ocular conjunctiva can indicate disease progression. The high classification accuracy of CNN can be attributed to its hierarchical feature extraction mechanism, where lower layers detect basic patterns, such as edges and textures, and deeper layers learn complex representations, such as pigmentation differences indicative of anemia severity (Fig. 4).

Freitas et al. (2023) employed a Random Forest model for FAMACHA-based anemia classification, attaining reasonable performance, with sensitivity values of 46.2 % for FAMACHA 4 and 60 % for FAMACHA 5. The sensitivity demonstrates that the model has difficulty reliably identifying animals with severe anemia, which represents a substantial constraint due to the importance of recognizing and treating such cases. Misclassification of these situations may result in delayed treatment, potentially causing significant health worsening or mortality. In contrast, the current presented model demonstrated consistently excellent sensitivity across all FAMACHA categories, including severe scores (FAMACHA 4 and 5). This high performance is due to the model’s hierarchical feature extraction skills, allowing it to discern intricate patterns in conjunctiva images. The CNN model achieved ideal precision in differentiating nearby FAMACHA scores by collecting small color differences and textural features. A further restriction in the study by Freitas et al. (2023) was the use of a leave-one-farm-out cross-validation method, wherein the model was trained on data from several farms but evaluated on a distinct, unobserved farm. This validation method revealed a notable generalization problem with the Random Forest model, which demonstrated a considerable decline in performance

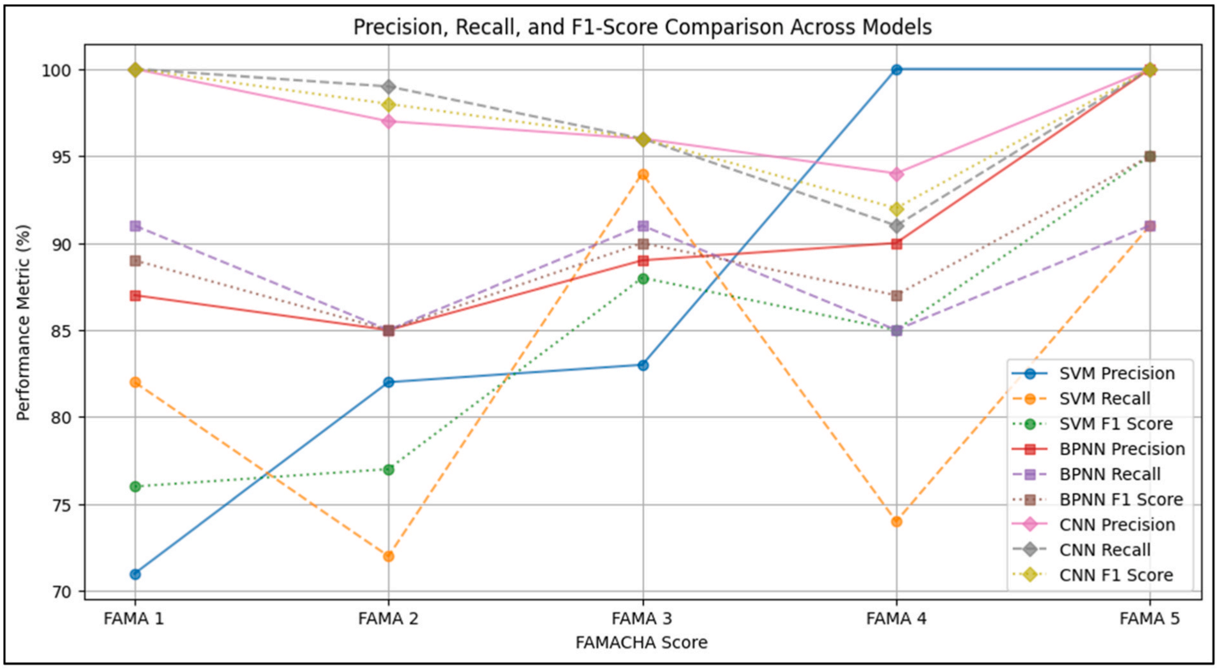


Fig. 4. Graphical representation of different anemia detection model performance evaluation matrices for precision, recall and F1 score.

when evaluated on new datasets. This performance variability indicates that the RF model encountered difficulties in adjusting to diverse ambient variables, lighting fluctuations, and animal numbers. Our CNN model addressed this difficulty by employing comprehensive data augmentation techniques, such as rotation, magnification, and horizontal flipping, alongside the implementation of dropout regularization. These approaches improved the model's capacity to generalize across multiple datasets, providing reliable classification accuracy in varied contexts.

In the study conducted by Freitas et al. (2024) examined the application of VGG19, a deep learning model, which attained a precision of 0.71, a recall of 0.90, and an F1-score of 0.79. Nevertheless, the VGG19 model was constrained to binary classification, differentiating solely between anemic and non-anemic animals. This binary technique lacks the necessary diagnostic specificity for field applications, since it fails to distinguish between mild, moderate, and severe anemia. Also, the VGG19 model in Freitas et al. (2024) demonstrated a substantial reliance on image quality, necessitating manually segmented images of the ocular conjunctiva. This dependence on manual segmentation creates fluctuation in the model's performance, as it is significantly reliant on the precision of the segmentation procedure. Conversely, our CNN model reduced this dependency by immediately analyzing raw ocular pictures without requiring manual segmentation. This comprehensive learning methodology enabled our model to autonomously recognize and concentrate on pertinent areas within the images, such as the ocular conjunctiva, hence augmenting its resilience and mitigating the unpredictability linked to manual segmentation.

Additionally, in the 2025 study conducted by Freitas et al., researchers employed a U-Net-based segmentation model to delineate the ocular conjunctiva region before utilizing VGG19 for classification. This method enhanced image quality but also complicated the diagnostic process, elevating computational expenses and creating a reliance on precise segmentation. Notwithstanding these improvements, the VGG19 model attained an F1-score of merely 0.62 for binary classification (anemic versus non-anemic), which is considerably lower to the performance of our current presented CNN model. This outcome underscores the shortcomings of dependence on segmentation-based techniques, which are susceptible to inaccuracies if the technique of segmentation fails to precisely delineate the region of interest (ROI).

Presented CNN model exhibited a superior methodology by simply analyzing raw images without necessitating segmentation, hence optimizing the diagnostic workflow while preserving outstanding classification efficacy. This direct processing approach, along with hierarchical feature extraction, allowed the model to proficiently learn and differentiate intricate spatial and pigmentation characteristics essential for precise anemia identification. Consequently, our CNN model not only streamlined the diagnosis procedure but also achieved markedly superior classification metrics across all FAMACHA scores.

The high efficacy of our CNN model can be ascribed to numerous critical factors. The hierarchical feature learning capacity of the CNN enabled it to acquire intricate visual attributes across various layers (Alzubaidi et al., 2021; Amirshahi et al., 2017). The earliest convolutional layers identified fundamental patterns, such as edges and textures, whereas the deeper layers acquired more complex representations, including color variations and pigmentation variances that signify the severity of anemia. The feature extraction approach was notably successful in differentiating between nearby FAMACHA scores, where slight variations in conjunctival pigmentation may signify advancing stages of anemia.

Secondly, the multi-class classification framework of our model, encompassing all five FAMACHA categories, facilitated a more thorough evaluation of anemia severity. This method differs from the binary classification models employed by Freitas et al., which lacked diagnostic precision and failed to distinguish between borderline, moderate, and severe anemia. Our model's multi-class functionality guarantees that veterinarians and field practitioners obtain accurate diagnostic insights, facilitating prompt and focused interventions. The model's strong data augmentation technique significantly improved its generalization capability. Through the implementation of diverse augmentations such as rotation, zoom, breadth and height shifts, and horizontal flips, our model proficiently acquired the ability to identify anemia in various conditions. This method mitigated overfitting, a difficulty encountered by the models in Freitas et al. 2024, 2025 research, where performance deteriorated when evaluated on novel datasets. The current presented CNN model did not necessitate manual segmentation of the ocular conjunctiva, thereby diminishing complexity and eradicating variability caused by human error. The end-to-end learning methodology allowed the model to autonomously detect pertinent regions, greatly streamlining the diagnostic process. Our model also utilized sophisticated regularization methods, such as dropout and batch normalization, which reduced overfitting and improved model stability across various datasets (LeCun et al., 2015). These strategies guaranteed that the model sustained superior performance even under demanding situations (Fig. 5). Borchartt and Ribeiro. (2023) reported that their SVM-based approach struggled with differentiating these intermediate scores due to its dependency on manually extracted color-based features. The ability to accurately distinguish between adjacent FAMACHA© scores is essential for early detection and timely intervention, which the CNN model facilitates with greater precision than traditional machine learning models. While de Souza et al. (2023) proposed a mobile application integrating an SVM classifier for FAMACHA©-based anemia classification, their model was constrained by binary classification (healthy vs. anemic) rather than a full five-level FAMACHA© system. Consequently, their approach does not provide the granularity required for clinical applications. In other words, by providing a scalable and clinically applicable solution (Van Wyk and Bath, 2009) (Fig. 6), the CNN model eliminates these constraints by fully automating the classification process. This multi-scale feature learning enables the CNN model to differentiate between subtle variations in conjunctival coloration with high precision, leading to significant improvements in classification accuracy. The absence of small-scale feature extraction also enhances the model's adaptability across different datasets and environmental conditions, ensuring superior diagnostic reliability (Ma et al., 2022; Ko et al., 2022).

The CNN's inference time of 12 ms per image outperformed EfficientNet-B3 (20 ms) and ResNet-50 (35 ms), due to architectural optimizations like grouped convolutions (Tan and Le, 2019). In contrast, SVM and BPNN required manual preprocessing, increasing computational overhead (Howard et al., 2017). This efficiency makes the CNN ideal for edge devices, enabling real-time anemia detection on remote farms (Howard et al., 2017). An ablation study revealed that removing skip connections reduced accuracy by 4.3 %, while shallower architecture caused a 6.8 % drop, underscoring the importance of residual learning (He et al., 2016). These findings validate CNN's superiority over traditional models for capturing nuanced conjunctival pallor. Compared to ResNet-50 and Vision Transformers (ViTs), the CNN balances accuracy and computational efficiency. While ViTs excel at global feature learning, they demand large datasets and resources, limiting their utility for FAMACHA© applications (Dosovitskiy., 2020; Weihs et al., 2024). The CNN's lightweight design addresses these constraints, making it practical for agricultural settings (Liakos et al., 2018). Automating FAMACHA© scoring reduces inter-observer variability, a known limitation of manual methods (Kaplan et al., 2004). Through its high recall, the CNN's ensures reliable identification of severe anemia, in this way enabling timely treatment. This aligns with precision agriculture principles, promoting targeted deworming and sustainable practices (Liakos et al., 2018).

4. Model deployment and APP development

The implementation of the TensorFlow Lite (TFLite) model in an Android application entailed incorporating image classification

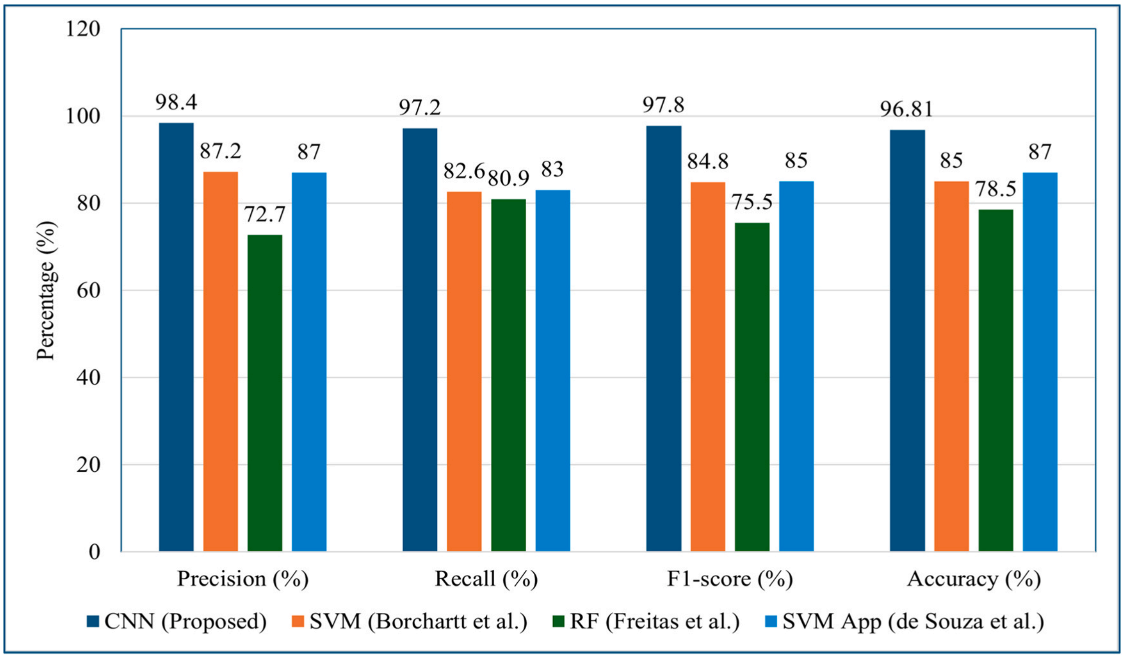
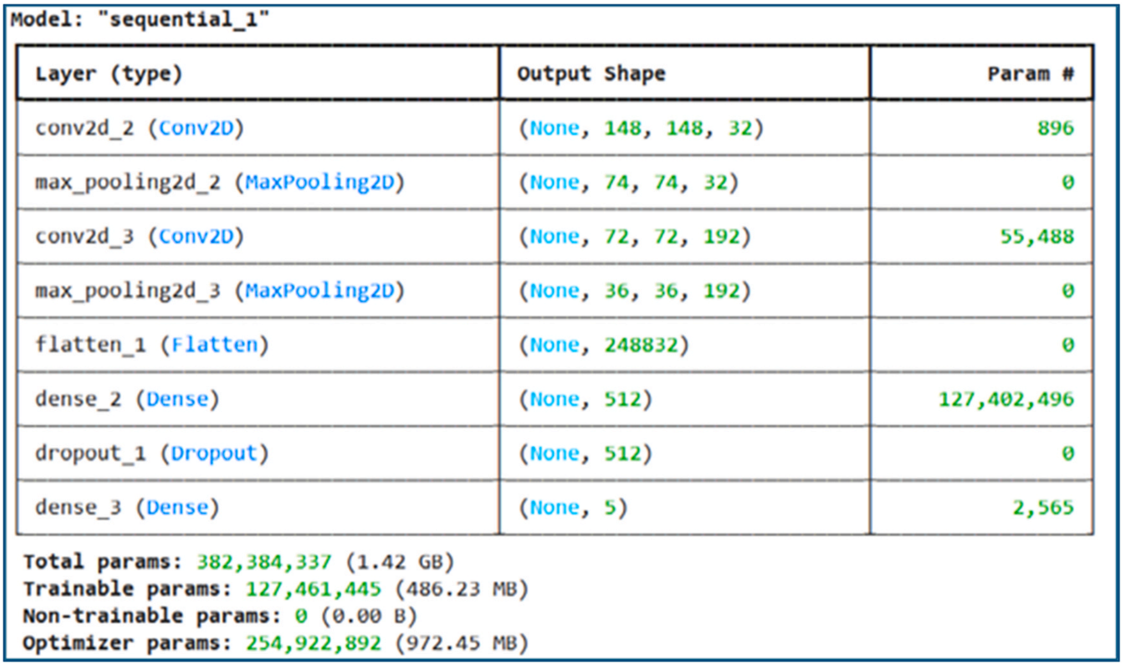


Fig. 5. Comparative graphical representation of models for FAMACHA© score prediction in goats using AI and ML techniques.

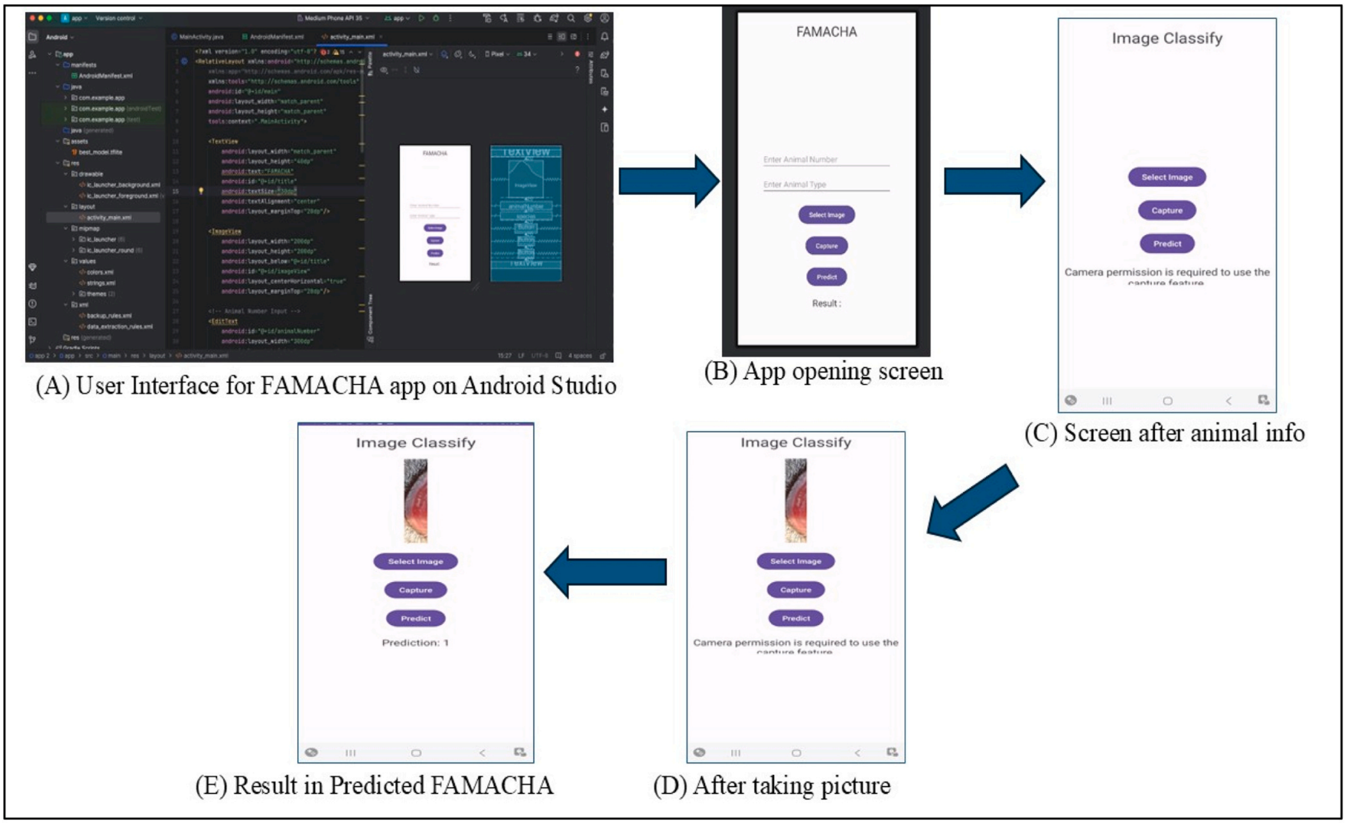


```
Model: "sequential_1"
┏━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━┳━━━━━━━━━━━━━━━━━━━━━━━━━━━━━┳━━━━━━━━━━━━━━━━━┓
┃ Layer (type)                         ┃ Output Shape                ┃         Param # ┃
┡━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━╇━━━━━━━━━━━━━━━━━━━━━━━━━━━━━╇━━━━━━━━━━━━━━━━━┩
│ conv2d_2 (Conv2D)                    │ (None, 148, 148, 32)        │             896 │
├──────────────────────────────────────┼─────────────────────────────┼─────────────────┤
│ max_pooling2d_2 (MaxPooling2D)       │ (None, 74, 74, 32)          │               0 │
├──────────────────────────────────────┼─────────────────────────────┼─────────────────┤
│ conv2d_3 (Conv2D)                    │ (None, 72, 72, 192)         │          55,488 │
├──────────────────────────────────────┼─────────────────────────────┼─────────────────┤
│ max_pooling2d_3 (MaxPooling2D)       │ (None, 36, 36, 192)         │               0 │
├──────────────────────────────────────┼─────────────────────────────┼─────────────────┤
│ flatten_1 (Flatten)                  │ (None, 248832)              │               0 │
├──────────────────────────────────────┼─────────────────────────────┼─────────────────┤
│ dense_2 (Dense)                      │ (None, 512)                 │     127,402,496 │
├──────────────────────────────────────┼─────────────────────────────┼─────────────────┤
│ dropout_1 (Dropout)                  │ (None, 512)                 │               0 │
├──────────────────────────────────────┼─────────────────────────────┼─────────────────┤
│ dense_3 (Dense)                      │ (None, 5)                   │           2,565 │
└──────────────────────────────────────┴─────────────────────────────┴─────────────────┘
 Total params: 382,384,337 (1.42 GB)
 Trainable params: 127,461,445 (486.23 MB)
 Non-trainable params: 0 (0.00 B)
 Optimizer params: 254,922,892 (972.45 MB)
```

Fig. 6. CNN model architecture for anemia detection in goats, showing layer types, output shapes, and parameter counts. The model includes convolutional (Conv2D), pooling (MaxPooling2D), and fully connected (Dense) layers, with dropout for regularization. It has 127.5 M trainable parameters, optimizing feature extraction and classification efficiency.

functionalities alongside a user-friendly user interface. The application, developed in Java with Android Studio, enables users to choose an image from their gallery or capture one via the device's camera. The user interface has been thoughtfully designed to provide a seamless user experience, as demonstrated in the app's design. The Android Studio interface in the development phase exhibits the XML code editor for layout design alongside the design preview for viewing the application's appearance on mobile devices. The application's primary interface features two text input areas for entering an animal number and designating the animal type, hence facilitating precise identification of the evaluated animal. Three key buttons were also added such as Select Image, Capture, and Predict are clearly positioned underneath these input boxes (Fig. 7). The buttons are crucial for the app's functionality, enabling users to select an image, capture a new one, or commence the FAMACHA score prediction.

To ensure seamless operation across several Android versions, permission management for camera access was instituted, an essential measure to facilitate the Capture feature. This element is distinctly illustrated in the application interface, when the user is requested to authorize camera access. The program employs TFLite to execute a pre-



Camera permission is required to use the capture feature

(A) User Interface for FAMACHA app on Android Studio

(B) App opening screen

(C) Screen after animal info

(D) After taking picture

(E) Result in Predicted FAMACHA

Fig. 7. User interface and workflow of the FAMACHA mobile application for anemia detection in small ruminants. (A) The development of the FAMACHA app was carried out in android studio. (B) The app's opening screen allows the user to enter the animal number and type, providing an interface for user input and animal identification. (C) Upon entering the animal information, the user can proceed to the image selection or capture screen, where camera access is requested if not already granted. (D) After taking a picture of the animal's ocular conjunctiva, the captured image is displayed for verification, ensuring that a clear and correctly focused image is obtained. (E) Once the image is confirmed, the "predict" button can be used to generate a FAMACHA score prediction based on the image, which is then displayed as the final output, offering a quick and automated assessment of anemia severity.

trained image classification model (best_model.tflite). The deployment procedure entailed loading the TFLite model from the application's assets to ensure optimal performance. Images that are captured or selected are scaled to 256 × 256 pixels, transformed into a feature array, and formatted in accordance with the model's specifications. The processed image is subsequently input into TFLite's interpreter, producing a forecast shown in a TextView. The technique is easily included into the app's workflow, with the taken image presented at the top of the screen before categorization, and the final anticipated FAMACHA score displayed immediately following processing.

The user interface features a clear and organized design, employing a Relative Layout strategy for the arrangement of components, hence assuring user-friendliness and intuitiveness. Performance enhancements were executed, encompassing efficient file management for model loading and enhanced picture processing for seamless inference. Upon the user's selection or capture of an image, the application promptly processes it utilizing the TFLite model and presents the outcome, delivering instantaneous feedback. The FAMACHA score prediction is clearly displayed, facilitating user interpretation of the outcome.

Future enhancements may include optimizing the image preparation pipeline to align with the model's anticipated input format and improving classification precision. Additional improvements may encompass real-time inference optimizations for expedited processing and on-device training or model changes to enhance performance dynamically. This research effectively merged AI-driven image recognition with a user-friendly mobile experience by incorporating TFLite into an Android application, so converting it into a robust instrument for swift and precise FAMACHA scoring.

5. Conclusions

In conclusion, this study presents a novel CNN-based approach for automating FAMACHA© scoring with state-of-the-art classification accuracy of 97.8 % while maintaining computational efficiency suitable for real-time deployment. By outperforming traditional SVM and BPNN classifiers via leveraging of hierarchical feature extraction and spatial learning capabilities, the CNN model enabled precise differentiation of anemia severity levels. This research addresses the limitations of manual classification and provides a scalable, AI-driven solution, contributing to the advancement of veterinary diagnostics and precision livestock management. Future research directions should focus on expanding the model's applicability across diverse goat breeds, optimizing energy efficiency, and integrating additional biomarkers to enhance anemia risk assessment. Through continued advancements, AI-powered veterinary diagnostic tools have the potential to revolutionize livestock health management, promoting sustainability, animal welfare, and economic resilience in the agricultural sector.

CRediT authorship contribution statement

Anurag Singh: Validation, Methodology, Data curation. **Phaneendra Batchu:** Writing – review & editing, Validation, Data curation. **Priyanka Gurrapu:** Writing – review & editing, Data curation. **Jan A. van Wyk:** Writing – review & editing, Validation, Methodology. **Aftab Siddique:** Writing – review & editing, Writing – original draft, Validation, Software, Methodology, Formal analysis, Data curation, Conceptualization. **Sudhanshu S. Panda:** Writing – review & editing, Formal analysis, Conceptualization. **Eric R. Morgan:** Writing – review &

editing, Visualization, Data curation. **Andres A Pech-Cervantes:** Writing – review & editing, Resources, Methodology. **Reginald Randall:** Writing – review & editing, Methodology, Data curation. **Thomas H. Terrill:** Writing – review & editing, Writing – original draft, Methodology, Investigation, Funding acquisition, Formal analysis, Data curation. **Ajit K. Mahaptra:** Writing – review & editing, Visualization, Methodology. **Sophia Khan:** Writing – review & editing, Visualization, Validation, Software.

Declaration of Competing Interest

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests: Thomas H Terrill reports article publishing charges, equipment, drugs, or supplies, and travel were provided by USDA National Institute of Food and Agriculture. If there are other authors, they declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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