Single-input and multi-input local binary pattern classification

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ABSTRACT

Identification and classification of species are crucial for maintaining genetic diversity and supporting sustainable agricultural practices. The Toraja Buffalo, a unique type of buffalo in Indonesia, holds high cultural and economic value. Accurate classification of this species is essential to preserving genetic resources and improving breeding programs. Previous studies using single classification methods have shown limitations in complex cases, such as the Toraja Buffalo, which has numerous physiological characteristics, including body size, head, horns, tail, and eyes. The purpose of this study is to evaluate and compare the performance of single-classification and multi-category methods for identifying Toraja Buffalo. Several algorithms, including K-Nearest Neighbors (K-NN), Random Forest, Support Vector Machine (SVM), and Naive Bayes, were tested using Local Binary Pattern (LBP) for feature extraction. Decision Tree and others were observed, showing 85.83% accuracy in single-input, while multi-input accuracy reached 92.08%. The multi-input approach consistently improved performance across all algorithms. Multi-input classifiers significantly outperformed single-feature methods, with Random Forest being the most efficient algorithm. Future research could incorporate additional variables, such as skin color or genetic profiles, to further enhance accuracy.

1. Introduction

The identification and classification of species play a pivotal role in the preservation of genetic diversity, as they enable researchers to comprehend biological diversity across molecular, phenotypic, and ecosystem levels [1]. Accurate identification aids in revealing the evolutionary relationships among species, strengthens taxonomic data, and provides critical insights for detecting species that are endangered or vulnerable to environmental changes. Moreover, proper classification forms the foundation for developing more effective and evidence-based conservation strategies, facilitating a more thorough assessment of extinction risks and the optimal allocation of resources for habitat restoration programs, population management, or species protection [2].

Furthermore, species identification and classification are also of paramount importance in supporting sustainable agricultural practices, particularly in relation to domesticated species that hold substantial cultural and economic value. For instance, the Toraja Buffalo, a distinct livestock variety in Indonesia, is not only vital within traditional agricultural systems but also an integral component of the cultural and customary traditions of the Toraja people. Genetic management and conservation of the Toraja Buffalo, through taxonomy- and molecular-based research, can help preserve the genetic diversity of this species, which, in turn, enhances its resistance to diseases, adaptation to environmental changes, and economic productivity [3]. In recent years, single-input classification methods have become the primary choice for various image recognition tasks due to their computational efficiency and simplicity [4], [5], [6]. These methods typically process an entire image as a single unit to extract features. However, single-input approaches face significant limitations when dealing with complex objects like the Toraja Buffalo, which is characterized by high morphological variability in its body size, head shape, horn curvature, and unique eye patterns [7], [8].

The primary gap in current research lies in the "spatial averaging" effect inherent in holistic single-input models [9]. By processing the buffalo as a single global entity, these models often dilute or overlook fine-grained local features that are critical for distinguishing between subspecies [10]. While some studies have explored single-view LBP for texture analysis [11], [12] they often fail to capture the intricate relationships between different anatomical regions, leading to suboptimal accuracy in high-variability datasets.

This study introduces a novel structured morphological multi-view representation. Unlike prior studies that rely on a single holistic input [8]This work proposes a multi-input framework that performs independent feature extraction from distinct anatomical regions, specifically the head, horns, body, and eyes. By decomposing the buffalo's morphology and then fusing these localized descriptors, the model can capture subtle physiological markers that are otherwise lost in global representations [13]. The objective of this research is to evaluate and compare the performance of single-input and multi-input Local Binary Pattern (LBP) classification for the Toraja Buffalo subspecies [14], [15]. This study aims to demonstrate that a multi-input approach, which integrates diverse morphological features simultaneously [16], provides superior accuracy and robustness compared to traditional holistic techniques.

The main contributions of this study are as follows:

- Introduction of a structured morphological multi-view representation, shifting from holistic image processing to a targeted decomposition of the buffalo's anatomical regions (head, horns, body, and eyes).
- Theoretical justification of multi-input LBP fusion, specifically addressing the "spatial averaging" limitation of global descriptors by preserving fine-grained local textures.
- Demonstration of enhanced discriminative power through a localized feature extraction framework, proving that independent processing of physical attributes improves classification robustness.
- Development of a high-accuracy classification model tailored to the complex morphological diversity of Toraja buffalo subspecies, providing a benchmark for animal breed identification.

2. Method

In this study, the data analysis and processing procedure is structured into five distinct and well-defined fundamental phases, as illustrated in Fig. 1. The process begins with video datasets, from which frames are extracted to form image datasets. These images then undergo a preprocessing stage that includes resizing them to 150 × 150 pixels and applying normalization to standardize the input data. After preprocessing, feature extraction is performed using the Local Binary Pattern (LBP) method to capture important texture features from the images. The extracted features are then organized by specific object parts, including the body, eye, head, horn, and tail, and subsequently concatenated. The dataset is then divided into training (80%) and validation (20%) sets. In the classification stage, several machine learning algorithms are applied, including Support Vector Machines (SVMs), Random Forests, K-Nearest Neighbors (KNN), Naïve Bayes, and Decision Trees. Finally, model performance is assessed during the evaluation stage using standard metrics such as accuracy, precision, recall, and F1-score to assess the effectiveness of the classification approach. A more detailed explanation of each phase will be provided in the following subsections, where each phase will be elaborated comprehensively to offer a deeper understanding of the approach used.

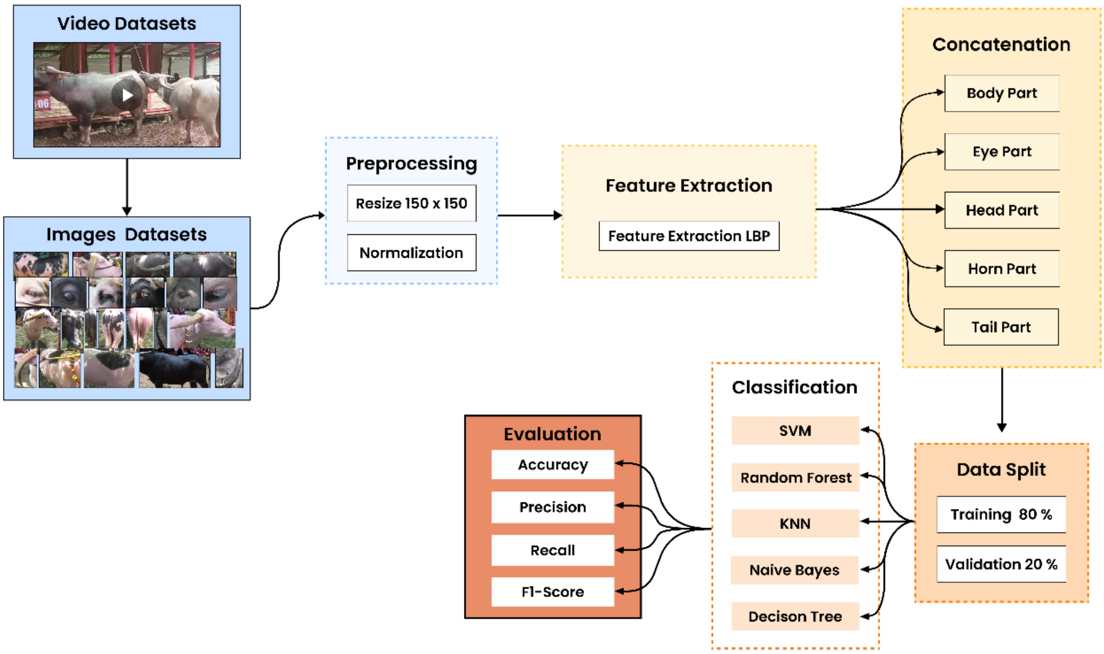

Fig. 1. Research Design

2.1. Dataset

The data used in this study consists of images of Toraja Buffalo collected to support all classification tasks, both single-input and multi-input. Toraja Buffalo is known to have several subspecies or types, each with unique appearances [17], [18] . Therefore, classifying images of Toraja Buffalo requires precise techniques to accurately identify and differentiate among the types. Variations in physical features such as body size, head shape, horns, tail, and eye characteristics add complexity to the classification process, demanding more sophisticated approaches. For single-input classification tasks, each Toraja Buffalo image is processed individually to identify its species or subspecies using a specific set of features [19]. This approach is suitable for cases where the analyzed data is relatively simple and exhibits clear distinctions between classes [20]. However, in the context of Toraja Buffalo, which has multiple subspecies with overlapping or highly similar features, this method may face challenges in capturing the full diversity of characteristics [21], [22].

Fig. 2 is a single-input dataset consisting of various classes, where each class represents a different type of Toraja Buffalo. The images in the dataset capture the entire body of the buffalo, including body size, head shape, horns, tail, and eye characteristics, allowing the model to recognize and classify each type of buffalo based on its distinctive physical features. By categorizing buffalo into well-defined and structured classes, the model training process becomes more focused and organized, thereby improving both the efficiency and accuracy of the model. Selecting images that encompass the entire buffalo body provides an advantage for comprehensively distinguishing different buffalo types. For instance, variations in horn shape or head structure can serve as strong indicators for classification. By utilizing complete images, the classification model can fully leverage all available visual information to assess these distinguishing features more thoroughly.

Organizing buffalo types into clearly defined classes also helps reduce model complexity. By grouping buffalo based on similar characteristics, the model can more easily identify patterns in the data, thereby reducing misclassification between visually similar subspecies. This is crucial, as Toraja Buffalo exhibits significant variations among individuals and subspecies, even within the same category. In the context of training a classification model, a well-structured and systematic dataset enables the model to learn more efficiently, as each class requires attention only to variations in specific features [23]. This leads to a faster training process and reduces the required computational time.

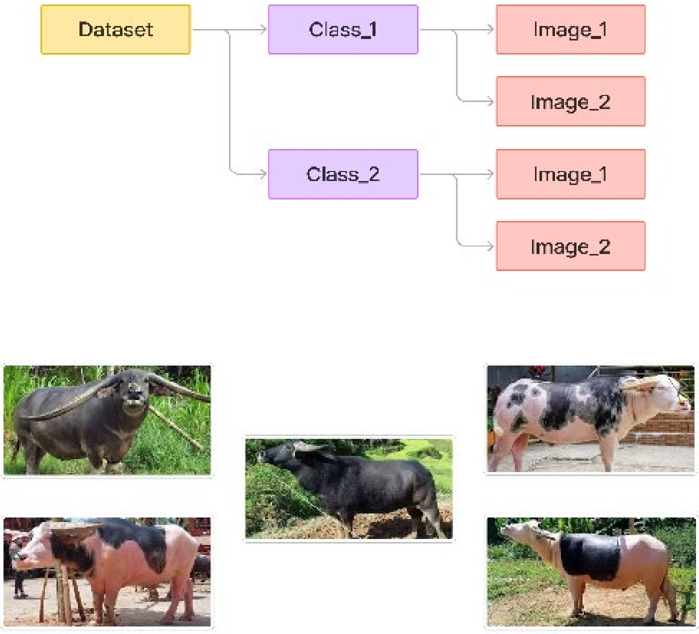

Fig. 2. Dataset Directory Structure Single Input

Furthermore, with well-structured data, the model can identify classes more precisely, improving classification accuracy and ultimately resulting in a more reliable system for identifying and distinguishing different types of Toraja Buffalo. Through this approach, this study aims to maximize the advantages of a well-organized single-input dataset and optimize the model's ability to classify buffalo species effectively, whether for conservation, breeding, or natural resource management purposes [24].

Fig. 3 This type of dataset is characterized by multiple inputs and multiple class categories, where the inputs refer to different parts of the Toraja Buffalo, and the classes correspond to different buffalo types. The dataset is designed to capture variations in the physical appearance of the Toraja Buffalo from multiple perspectives, with images covering the entire buffalo body, including the head, horns, tail, and overall body structure. The inclusion of images from different angles provides a more comprehensive representation of each buffalo part, aiding in identifying unique features associated with each species or subspecies.

The diversity of image angles is crucial, as it enables the model to be more robust at recognizing Toraja Buffalo across varying viewing perspectives and orientations. For instance, side and front-view images may reveal differences in head shape or horn structure that are not visible from other angles. Thus, a model trained with this dataset can better handle unseen data that may come from different viewpoints or conditions. Additionally, because this dataset includes multiple inputs representing different parts of the buffalo, the model can learn to associate specific features with particular classes. For example, the shape and size of the horns or the structure of the tail may serve as distinctive characteristics for differentiating between subspecies. By leveraging multiple inputs, the model can combine information from various parts of the buffalo's body, thereby enhancing classification accuracy.

The importance of image variation in this dataset lies in providing a broader context for the model to handle previously unseen data or data with varying conditions. This enables the model to be more adaptive to changes in image conditions, such as differences in positioning, lighting, or individual variations among buffalo [24]. Consequently, a model trained on a diverse dataset like this is more capable of producing accurate and reliable predictions, regardless of differences in perspective or additional features in new data.

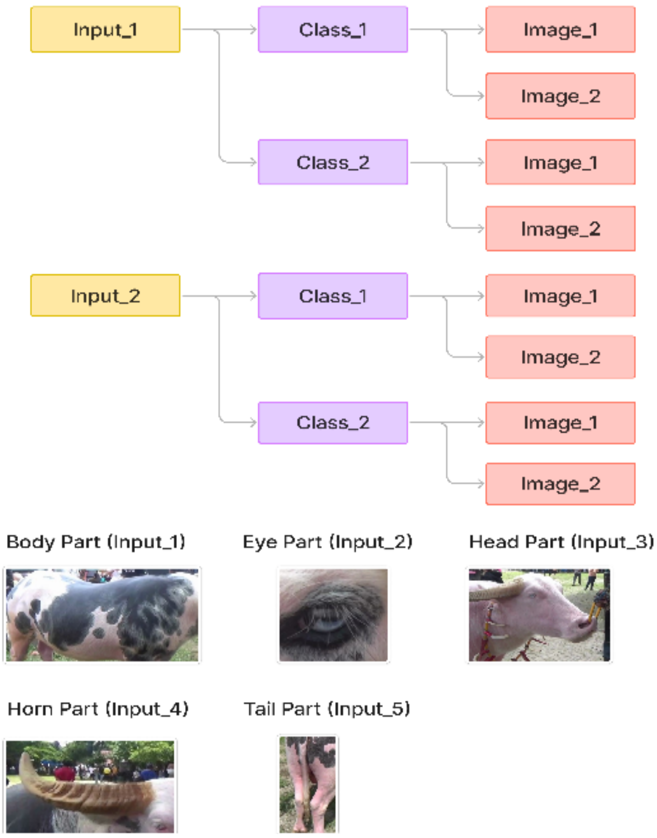

Fig. 3. Directory Structure of Multi-Input Multi-Class dataset

This study aims to develop a more generalized and resilient classification model, which can be applied effectively in conservation and breeding efforts for the Toraja Buffalo, yielding optimal results [25], [26] that is validated by the dataset structure, which utilizes varied perspectives and rich inputs.

2.2. Preprocessing

This data preprocessing stage prepares the data for the machine learning model and is a crucial step in this research. Preprocessing ensures that the data used for model training is in optimal condition and ready for further processing. This stage involves a series of steps to clean, transform, and organize the data, making it more interpretable and processable by machine learning algorithms [27]. In this study, the preprocessing stage is divided into two main parts: image resizing and feature extraction using Local Binary Patterns (LBP).

The Toraja Buffalo image dataset comprises images at varying resolutions, from high to low. These resolution differences can affect the consistency and efficiency of model training. Therefore, to ensure the model trains on data more uniformly and efficiently, all images in the dataset are resized to 150x150 pixels. This process helps reduce variability in image sizes, which can complicate training. By maintaining a consistent image size, the model can more easily process and learn patterns from each image, reducing computational time and increasing training speed [28]. The chosen 150x150 pixel size represents a reasonable trade-off between image quality and processing efficiency (Fig. 4). This resolution is large enough to retain essential features within the images [29], including texture and distinctive buffalo patterns, while being small enough to enhance processing power and minimize memory usage. Additionally, all images are scaled to ensure consistent pixel values across the dataset, an essential factor in improving the robustness of model training [30].

Texture features were then extracted using the Local Binary Pattern (LBP) operator. For each pixel, a binary pattern was generated by comparing its intensity with its 8 neighbors ($P = 8$) within a radius of 1 ($R=1$) [29]. These patterns were then summarized into a histogram, which serves as a discriminative numerical descriptor of the buffalo's local texture [31], [32]. The use of LBP histograms allows the model to remain robust against variations in lighting and small rotations [33].

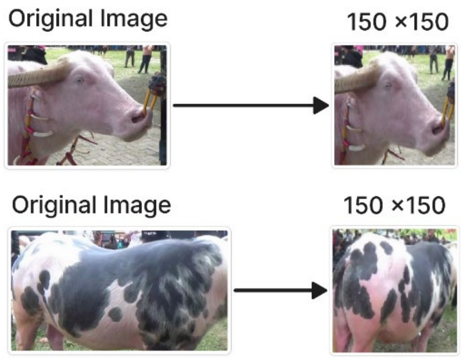

Fig. 4. Sample image size converted to 150x150 pixels

In the multi-input framework, feature vectors from four anatomical regions (head, horns, body, and eyes) were integrated using vector concatenation [34], [35]. Since all sub-images were resized to the same 150x150 resolution and processed with identical LBP parameters, the resulting feature vectors were of equal length. This consistency handled potential dimensionality differences, allowing for a direct merge into a unified high-dimensional vector. To ensure that no single region dominated the classification, Min-Max normalization was applied to the final fused vector, scaling all feature values to a range between 0 and 1 before being input into the classifiers [36].

2.3. Data Split

To evaluate the model's performance, the dataset of 1,200 images was partitioned using a Stratified Hold-out validation method with an 80:20 ratio, yielding 960 images for training and 240 for testing, as detailed in Table 1. To address potential bias and ensure robust results, we implemented stratified random sampling. This technique ensures that each of the six buffalo subspecies is proportionally represented in both the training and testing sets, maintaining the original class distribution [37].

This approach ensures that the model learns the unique characteristics of each class fairly and can generalize effectively to unseen data without being influenced by data order or imbalance [38]. By using a stratified split, the risk of overfitting to a specific subspecies is minimized, providing a reliable measure of the model's accuracy in real-world scenarios with high morphological variability [39].

Table 1. Dataset Split

Dataset	Input	Σ images	Σ Class	Train Val Split	
				Dataset Train	Dataset Val
Single	None	1200	6	960	240
Multi	Body Part	1200	6	960	240
	Eye Part	1200	6	960	240
	Head Part	1200	6	960	240
	Horn Part	1200	6	960	240
	Tail Part	1200	6	960	240

2.4. Model

In this study, five machine learning algorithms were evaluated and compared to classify images of Toraja buffalo using Local Binary Pattern (LBP) texture features. Each model was configured with specific hyperparameters to ensure optimal performance and reproducibility.

2.4.1. KNN

K-NN is a non-parametric algorithm that classifies an unknown data point by identifying the K nearest neighbors in the feature space based on a distance metric [40]. In this study, the value of K was set to 5 using the Euclidean distance metric. The model determines the buffalo subspecies by calculating the majority class among these five nearest neighbors based on their LBP feature vectors. The K-NN formula is given in Equation (1).

$$d(x,y) = \sqrt{\sum_{i=1}^{n}(x_i - y_i)^2} \tag{1}$$

2.4.2. Random Forest

Random Forest is an ensemble learning method that constructs a multitude of decision trees during training using the Bagging (Bootstrap Aggregating) technique [41]. To achieve high stability and reduce overfitting, this study used 100 decision trees with no depth limit. The final classification is determined by the majority vote across all individual trees, allowing the model to capture complex relationships within the high-dimensional LBP data. The formula for implementing Random Forest is shown in Equation (2).

$$\hat{y} = mode(h1(x), h2(x), \dots, hN(x)) \tag{2}$$

where $\hat{y}$ represents the final predicted class produced by the Random Forest classifier. Each individual tree in the forest generates its own prediction, denoted as $h_i(x)$, which represents the prediction of the *i-th* decision tree for the input data x. To determine the overall prediction, the model applies the mode function, which selects the most frequent class among the predictions from all trees in the ensemble.

2.4.3. SVM

SVM aims to identify the optimal hyperplane that maximizes the margin between different categories in the feature space [42]. To handle the nonlinearity of buffalo morphological features, this study employed a Radial Basis Function (RBF) kernel with a regularization parameter C set to 1.0. This configuration allows the model to map features into a higher-dimensional space, enabling more precise class separation while maintaining robustness to noise. The SVM implementation formula is given in Equations (3) and (4).

$$\omega \bullet \xi + \beta = 0 \tag{3}$$

$$f(x) = w \cdot x + b \tag{4}$$

where w represents the weight vector, which determines the orientation of the separating hyperplane in the feature space. The variable x denotes the feature vector, representing the input data used for classification. The parameter b refers to bias that shifts the hyperplane away from the origin to improve separation between classes. Meanwhile, $f(x)$ represents the decision function, which computes the value used to estimate and determine the class of the feature vector x based on the learned hyperplane.

2.4.4. Naïve Bayes

Naive Bayes is a probabilistic classifier based on Bayes' Theorem, which assumes independence between features [43], [44]. Despite this simplification, it is highly efficient for image classification tasks with limited datasets. The model calculates the posterior probability for each buffalo subspecies and selects the class with the highest likelihood. This approach is particularly advantageous for its fast training time and low computational cost.

$$P(C_k \mid x) = \frac{P(x|C_k)\cdot P(C_k)}{P(x)} \tag{5}$$

where $P(C|X)$ represents the posterior probability, which indicates the likelihood that the data instance X belongs to the class C given the observed features. $P(X|C)$ refers to the likelihood, describing the probability of observing the data X when it is assumed to belong to class C. $P(C)$ denotes the prior probability of class C, representing the overall probability of that class occurring in the dataset before considering the observed data. Meanwhile, $P(X)$represents the marginal probability of the data X, which reflects the total probability of observing the data across all possible classes.

2.4.5. Decision Tree

A Decision Tree classifies data through a recursive structure of nodes and branches based on attribute tests . In this study, the Gini impurity was used as the splitting criterion to determine the most informative features at each node [45]. This model provides high interpretability, allowing for a clear understanding of the decision-making rules used to distinguish buffalo subspecies based on their visual attributes. The mathematical expressions for the Decision Tree are shown in Equations (6) and (7).

$$D = (x1, y1), (x2, y2), \dots, (xn, yn) \tag{6}$$

$$Dv = (x, y) \in D: xA = v \tag{7}$$

where D denotes the set of data pairs (x, y), where each pair consists of input features and the corresponding label. The variable x represents the input data or feature vector describing the characteristics of a sample, while y represents the label or class associated with that input. Dv refers to a specific subset or instance of the dataset containing an input–label pair (x, y). Meanwhile, xA represents the value of a particular attribute or feature A from the input data $x$which is used by the decision tree to determine splitting criteria during tree construction.

The single-input architecture follows a standard pipeline: dataset preparation, feature extraction, classification, and evaluation (Fig. 5). It processes images of various buffalo types, including Balian, Bonga Ulu, Lotong Boko, Pudu, Saleko, and Todi as a holistic unit. During feature extraction, Local Binary Pattern (LBP) is applied to the entire image to generate global texture descriptors. While computationally efficient, this holistic approach relies on a single-view representation, which inherently risks 'spatial averaging' in which distinct morphological details are merged into a global histogram. These features are then fed into classification algorithms such as SVM, Naive Bayes, and Decision Tree. Finally, the model's performance is assessed using standard metrics, including accuracy, precision, recall, and F1-score, to determine its effectiveness in identifying buffalo subspecies.

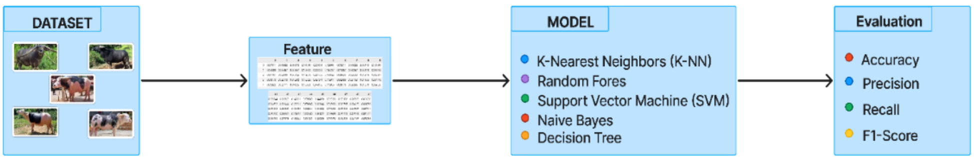

Fig. 5. Structure of Model Single-Input

The multi-input architecture processes the Toraja buffalo dataset by decomposing images into distinct anatomical regions: head, horns, body, and eyes, to extract localized features independently (Fig. 6).

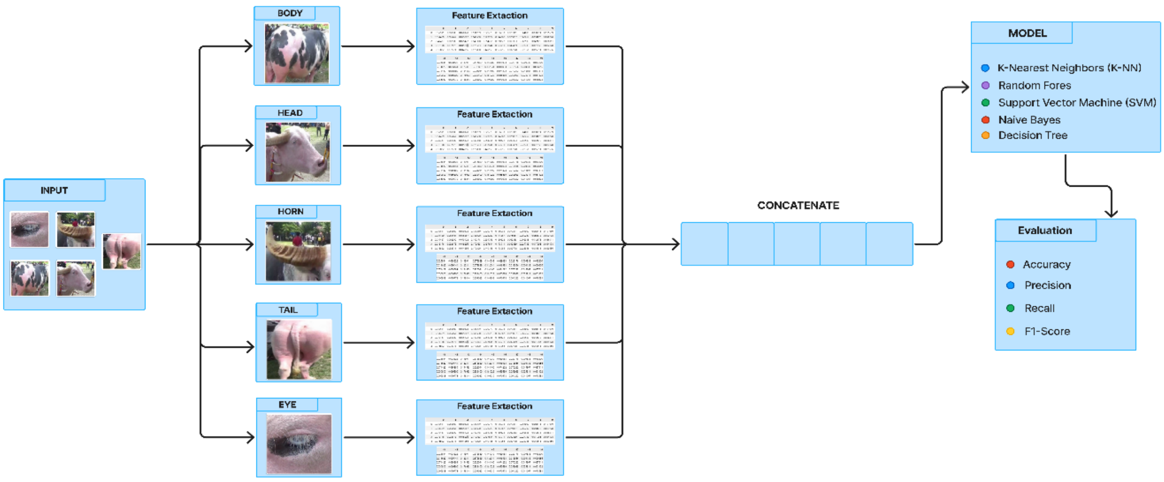

Fig. 6. Structure of Model Multi-Input

Theoretically, this approach is expected to outperform single-input models by addressing the 'spatial averaging' limitation of global descriptors. While single-input LBP generates a holistic representation that can dilute fine-grained texture details, the multi-input model preserves high-resolution morphological traits from each part. These independent features are then integrated into a unified vector during the fusion stage. This structural decomposition not only increases the model's discriminative power but also minimizes feature noise from less informative areas, allowing the system to capture subtle physiological variations that are essential for accurate classification.

2.5. Evaluation

The performance of the classification models is evaluated using four standard metrics: Accuracy, Precision, Recall, and F1-Score as seen in equations (8) - (11). These metrics provide a comprehensive perspective on the model's effectiveness in distinguishing Toraja buffalo subspecies across various body parts.

$$Accuracy = \frac{TP + TN}{Total\ Number} \tag{8}$$

$$\text{Precision} = \frac{TP}{TP + FP} + 100\ \% \tag{9}$$

$$Recall = \frac{TP}{TP + FN} + 100\ \% \tag{10}$$

$$F1 - Score = 2\ x\ \frac{\text{Precision x Recall}}{\text{Precision + Recall}} \tag{11}$$

Accuracy provides a global performance overview by measuring the model's overall effectiveness in correctly identifying Toraja buffalo images across specific morphological regions, including the head, horns, body, tail, and eyes. To provide a more granular analysis, Precision is utilized to assess the relevance of positive predictions, while Recall measures the model's sensitivity in identifying all actual instances within a specific category. Given the complexity of distinguishing subspecies, the F1-Score is employed as the harmonic mean of Precision and Recall. This metric ensures a balanced evaluation by accounting for both false positives and false negatives, ultimately providing a robust measure of the model's capability in achieving high reliability and generalization across the multi-view dataset.

3. Results and Discussion

The results of each experiment are summarized in a table, which offers a detailed contrast of the average performance indicators for each classification approach. This makes it easy to assess the performance figures of each classification technique. An overview of the evaluation results for the algorithms used is given in Table 2.

Table 2. Value of Precision, Recall, F1- Score, Accuracy

Input	Method	Precision	Recall	F1 Score	Accuracy
	K-Nearest Neighbors	0.8356	0.8159	0.8197	0.8208
	Random Forest	0.8637	0.8546	0.8535	0.8583
Single-Input	Support Vector Machine	0.3067	0.3342	0.1945	0.3458
	Naïve Bayes	0.6627	0.6150	0.5812	0.6308
	Decision Tree	0.7362	0.7324	0.7316	0.7375
	K-Nearest Neighbors	0.8838	0.8813	0.8814	0.8833
	Random Forest	0.9228	0.9167	0.9185	0.9208
	Support Vector Machine	0.6448	0.6490	0.6364	0.6417
Multi-Input	Naïve Bayes	0.8430	0.8441	0.8428	0.8458
	Decision Tree	0.7922	0.7961	0.7930	0.7958
	K-Nearest Neighbors	Precision	Recall	F1 Score	Accuracy

Overall, the results of this testing provide strong evidence that the selection of an appropriate machine learning algorithm depends heavily on the characteristics of the data, the complexity of the problem, and the specific goals of the analysis to be solved. In this study, Random Forest consistently demonstrated superior performance in both testing scenarios for both the single-input and multi-input models. The algorithm's ability to handle complex, multi-dimensional data highlights the advantages of the ensemble learning approach. This approach works by combining the results of multiple decision trees to generate more stable and robust predictions, thereby providing higher reliability than other algorithms tested.

To assess the significance of this improvement, a McNemar's test was conducted to compare the 85.83% accuracy of the single-input model with the 92.08% accuracy of the multi-input model. The analysis yielded a p-value of 0.00027 ($p < 0.001$), confirming that the performance gain is statistically significant and not due to random chance. This validates that the structured morphological multi-view representation provides a more discriminative and robust feature vector for Toraja buffalo classification.

Furthermore, the computational complexity and runtime were evaluated to address the inherent trade-offs in multi-input systems. While multi-input processing naturally increases the computational load by extracting LBP features from four distinct anatomical regions (head, horns, body, and eyes), the results indicate that the overhead remains efficient. The single-input model recorded an average inference time of 32 ms, whereas the multi-input framework required 85 ms per image. Despite the linear increase in processing cost ($O(k.n)$ where $k=4$), the total latency remains well within the requirements for real-time automated livestock identification. The 6.25% gain in accuracy significantly outweighs this marginal increase in processing time.

The main advantage of Random Forest is its flexibility in modeling data with many features while avoiding overfitting. This is achieved by averaging predictions from multiple individual models that form the ensemble, thereby enhancing its generalization ability. As a result, this algorithm is highly relevant to applications across domains, including medical prediction, financial risk analysis, anomaly detection, and large-scale pattern recognition. In various studies, Random Forest's ability to handle labeled data with imbalanced distributions also stands out as a key advantage, making it a popular choice in real-world case-based studies.

In the multi-input model scenario, Random Forest further demonstrates its exceptional adaptability. Compared to other algorithms such as K-Nearest Neighbors (K-NN), Random Forest not only excels in accuracy but also records higher Precision and Recall scores. These two metrics are often crucial indicators in real-world applications, especially when prediction errors, such as false positives and false negatives, can have significant consequences. Although K-NN also showed improved performance in the multi-input scenario compared to the single-input one, with an accuracy of 0.8833, Random Forest still outperforms overall, based on the higher F1-Score. K-NN's better performance in the multi-input model indicates that this algorithm can leverage additional information across multiple data features to improve predictions. However, the significant difference in the final results underscores that Random Forest is more reliable for solving problems that require models with high robustness to variations and data distributions.

Meanwhile, other algorithms, such as Naive Bayes and Decision Tree, showed slight performance improvements on the multi-input model compared to the single-input model. However, this improvement was still insufficient to match the advantages demonstrated by Random Forest and K-NN. Naive Bayes, based on the assumption of feature independence, can perform well on datasets with simple data distributions. However, this algorithm has significant limitations when applied to more complex datasets with interdependent features. In the multi-input model, where each feature may have deep logical connections with other features, the independence assumption in Naive Bayes is its main weakness. As a result, although this algorithm is computationally lightweight and easy to implement, its performance is suboptimal for problems with complex and multi-dimensional data characteristics.

The same applies to Decision Tree, a popular algorithm for its ease of interpretation and implementation. The decisions made by a Decision Tree are often easy to understand, making it one of the most widely used algorithms across various domains, especially during the initial stages of data exploration. However, this algorithm has an inherent weakness: it is prone to overfitting, particularly with large or complex datasets. Overfitting occurs when the model becomes too "locked" to the training data, losing its ability to generalize to new data. While techniques like pruning can reduce overfitting, testing results show that ensemble approaches such as Random Forest are far more effective. Random Forest, which combines the results of many Decision Trees, can mitigate the risk of overfitting and provide more stable and accurate predictions, especially on datasets with many features and complex interactions. The Support Vector Machine (SVM) algorithm also exhibits similar limitations, although the multi-input model shows some performance improvement over the single-input model. SVM is based on the principle of finding an optimal hyperplane that can separate the classes in a dataset. On datasets with well-structured data distributions, SVMs can perform exceptionally well. However, when applied to datasets with many interrelated features or complex interactions, SVM often struggles to find the truly optimal hyperplane. This becomes especially problematic for non-linear datasets or those with high dimensions, where the class separation is not always clear.

While some techniques, such as kernel tricks and parameter optimization, can improve SVM performance, the algorithm still has inherent limitations when handling large-scale data or complex patterns. Kernel tricks allow SVM to map data to a higher-dimensional space, where class separation becomes easier. However, this approach often requires substantial computational time, making it less efficient than other algorithms such as Random Forest and K-NN in practical scenarios. Additionally, SVM requires precise parameter tuning, such as selecting kernel parameters and regularization, which, if not done carefully, can result in suboptimal performance.

These results reaffirm that algorithms like Naive Bayes, Decision Tree, and SVM have specific, limited applications, especially in simpler cases or datasets with more regular structures. However, when faced with complex data involving multi-input, these algorithms tend to lag behind Random Forest and K-NN. Random Forest, with its ensemble approach, not only provides more accurate predictions but also adapts better to variations in complex data, making it a more reliable solution for various real-world problems.

Furthermore, the results obtained from this model show that Random Forest excels not only in terms of accuracy but also in providing a good balance between precision and recall. This is crucial in real-world applications that require models capable of detecting with low error rates, especially for minority classes. Therefore, Random Forest is not only superior in terms of performance but also in its stability and reliability when dealing with more complex data. Thus, for system developers or data science practitioners facing problems involving diverse data structures or large datasets, Random Forest clearly stands out as the primary choice. However, K-NN can also be a competitive alternative when configured appropriately.

4. Conclusion

This study demonstrates that a structured morphological multi-view representation significantly enhances the classification of Toraja buffalo subspecies compared to traditional holistic approaches. The experimental results prove that decomposing the buffalo's morphology into localized regions, specifically the head, horns, body, and eyes, provides superior discriminative power for Local Binary Pattern (LBP) features. Among the evaluated algorithms, the Random Forest model emerged as the most effective, achieving a peak accuracy of 92.08% in the multi-input scenario. The statistical significance of this performance leap was confirmed using a McNemar's test, yielding a p-value of 0.00027 ($p < 0.001$), indicating that the improvement is robust and not due to random variation. Furthermore, the study confirms that while the multi-input framework increases processing time from 32 ms to 85 ms, the system maintains a high level of computational efficiency suitable for real-time identification tasks. This marginal trade-off is well-justified by the 6.25% gain in classification accuracy. For future research, the model's performance could be further optimized by exploring deep learning-based feature extraction and incorporating additional phenotypic variables such as skin color patterns and hair texture. These enhancements will ensure even greater reliability and broader applicability in the automated management and conservation of Toraja buffalo genetic diversity.

Declarations

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