Categorizing Haemoprotozoan Diseases in Cattle using Mobile Device

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Abstract: The goal of this study is to streamline the identification and diagnosis of Haemoprotozoan diseases in cattle using machine learning algorithms to develop a model from a dataset of images and diagnoses gathered from local laboratories. The research is centered around three major Haemoprotozoan diseases, which are widespread and dangerous to cattle throughout India: Anaplasmosis, Babesiosis, and Theileriosis. The resulting model has been designed to operate on a hosted client-server web application, with a picture of the bloodstream sample transmitted to the server, which returns two parameters indicating whether the diagnosis is positive or negative and the type of disease. This has the potential to lower mortality rates by making the process quicker and more cost-effective. The model has been thoroughly tested and evaluated during the training and testing phases, with an emphasis on accuracy, speed, and cost-effectiveness. The ultimate model will be hosted on the client-server web application online, so that it can be used anywhere.

Index Terms – Neural Networks, Image preprocessing, Keras, Softmax, Streamlit, Convolution.

I. INTRODUCTION

Haemoprotozoan diseases have a significant impact on livestock populations, leading to loss of cattle, decreased milk production, and reduced animal health. Diagnosis of these illnesses can be challenging, and India has yet to determine the underlying economic losses caused by them. This study examines the health implications of Haemoprotozoan diseases and discusses the difficulties of diagnosing them. It also explores the potential of using image processing & deep learning techniques to detect and classify these diseases. The authors propose that neural network-based microscopic image diagnosis can improve accuracy, reduce misdiagnosis and missed diagnoses, and save time for doctors.

The use of deep learning and machine learning technologies has made it possible to diagnose Haemoprotozoan diseases quickly, accurately, and efficiently. The implementation of artificial intelligence in disease diagnosis is expected to have a far-reaching impact on the livestock industry, enhancing economic efficiency. Moreover, these technologies have the potential to provide a better understanding of disease epidemiology, improving prevention and control measures. The ability of deep learning and machine learning technologies to process large amounts of data enables researchers to gain insights into the epidemiology of these diseases. By automating diagnosis, resources can be allocated to research and development, further reducing the economic burden of Haemoprotozoan diseases.

II. LITERATURE SURVEY

Zhang, Hao, Hanlin, Xi, Chen, Yubing, Mario, Li, and Yang [1] provided segmentation for parasite images. Their work focuses on the use of deep learning techniques to identify protozoan parasites from microscopic images of cattle blood smears. The paper highlights the challenges associated with this technology and future trends in this field. The use of two-stage methods has been successful in detecting and counting red blood cells in microscopy images, and convolutional neural networks (CNNs) have demonstrated high accuracy in classifying infected cells. However, the complexity and data annotation requirements limit their application in developing countries. In clinical diagnosis, the identification of the parasite species and the detection of mixed infections are essential. The use of deep learning algorithms has resulted in improved accuracy and reduced workload for pathologists. However, some drawbacks include the dependence of the network's performance on input data and the need for shape information of macro-objects.

In a study by Rahmani, Idris, Ramli, and Arof [2], Circular Hough Transform algorithm was utilized to detect circular shapes in digital images. The algorithm is capable of determining the center and radius of a circle, making it an efficient tool for identifying various components in an image. By using the Hough transform, the algorithm can also detect non-circular objects such as sickle cells by finding intersections between circles. In cases where circles overlap, the contour of the circle of interest is monitored to

produce a new circle, and the intersections between the new and original circles are noted. The RBC proposed using the circular Hough transform to identify crescent shapes, achieving an overall accuracy of 92 when tested using a microscope. While the deformable detection feature can be enhanced to identify more shapes in the future, this technique currently stands as the best approach for segmenting and classifying anomalies in Haemoprotozoan cells.

Sanaa Jadwa introduced the Canny edge detection method for retrieving medical images in a research paper [3]. The paper presents a method for effectively extracting shape features from digital photos using the Canny edge detection operator, which is a mathematical approach for detecting points in an image where the brightness changes abruptly. This approach helps in reducing the amount of data while preserving the image's structural integrity for further processing. The Canny edge detection algorithm is based on finding the most prominent edges in an image by minimizing error rates, optimizing position, and marking edges only once when there is a single edge present. This algorithm uses the first derivative of a Gaussian function to estimate the best filter for these requirements. The Canny edge detection method is a multi-step procedure that involves noise suppression to identify edges in an image. Experimental results show that this approach outperforms other methods.

Saban Ozturk and Bayram Akdemir presented the use of filters for pre-processing blood smear images [5]. The pre-processing step plays a crucial role in classifying histopathological images using Convolutional Neural Network (CNN) [6] architecture. In this study, three pre-processing techniques were examined, and the results showed that the normal pre-processing algorithm produced the best outcomes. Over-pre-processing was found to remove critical features from the image. Pre-processing algorithms are used to accentuate important features of an image and remove noise. Normal pre-processing involves subtracting the median value of the image from the original image, while over-pre-processing deletes all the information about the image's background texture. According to the results, normally preprocessed images produced more precise results than other preprocessed images, demonstrating that pre-processing techniques, such as cell enhancement, background noise reduction, thresholding, morphological operations, and adaptive Histogram equalization, are effective.

Emad, Mostafa, Behrouz Naugler, and Christopher proposed the FSA algorithm for feature extraction from processed images [7]. The automated analysis of images of peripheral blood smears involves image segmentation, feature extraction, and pattern classification. Various supervised and unsupervised learning classifiers such as ANN, SVM, decision trees, and K-nearest neighbour are used. This article discusses different techniques used for blood smear image segmentation, including multispectral imaging, watershed algorithm, support vector machine, and artificial neural network. Cell segmentation is achieved through watershed clustering and feature scale-space filtering. The use of Support Vector Machine (SVM) for acute lymphocytic and normal WBCs leukaemia detection in hematopathology is also discussed. Algorithms have been developed to reduce SVM training dataset and computational time. Feature Selection Algorithms (FSA) are used to reduce the data dimensions for the classifier. Filter-type FSA ranks features according to their predictive power, while wrapper-type FSA evaluates feature subsets in light of how well they work with a particular classifier. The article also discusses Sequential Forward Selection (SFS) and Sequential Backward Selection (SBS) algorithms.

In order to classify the three Haemoprotozoan diseases, a model needs to be trained, as discussed by Ümit, Zafer, and Zryan [8]. The authors proposed an end-to-end design for breast cancer detection based on a Fully Convolutional Network (FCN) and a Bidirectional Long Short-Term Memory (Bi-LSTM). The effectiveness of the proposed approach was evaluated using the BreaKHis database, and the results were found to be more efficient than those of earlier studies. To classify breast cancer histological image data, the study explored the use of pre-trained CNN architectures. The combination of CNN and logistic regression produced better results than other methods. Additionally, the authors proposed an end-to-end approach for breast cancer diagnosis that differs from traditional deep learning techniques, using FCN to process large-scale images and enable varying input sizes, while the Bi-LSTM was used to solve time series problems.

In order to decrease the number of features in a dataset, a hybrid feature selection method called Relief-PCA is used, as described by Divya Jain and Vijendra Singh [9]. The medical field is using feature selection as a pre-processing technique to identify disease-related signs and assist medical practitioners in making quicker and easier decisions with the help of high-throughput technologies and machine learning methods. Classification techniques and feature reduction techniques are being utilized for effective disease diagnosis. This study presents a hybrid approach for feature selection that combines ReliefF and Principal Component Analysis (PCA) methods to reduce the number of features in a dataset and improve the performance of a classifier. ReliefF is a weighting method that updates weights on nearest hits and misses, while PCA is a dimensionality reduction method that extracts the maximum variance from the variables. The ReliefF-PCA feature selection method was applied to a chronic disease dataset and evaluated by comparing the performance of a classification model with and without feature selection. The results were analyzed to determine the effectiveness of this method compared to other feature selection methods. The comparison showed that this method was the most effective for the given dataset and classification model, making it the best feature selection approach.

Jane, Allen, and Deepali [10] suggest that R-CNN is one of the methods that can be used to classify images. For fast processing of large image sets in cell identification, Keras R-CNN can be employed. This method is more effective than traditional segmentation techniques as it can handle noisy images, variations in lighting, and clumped cells more efficiently and requires less preparation, algorithm selection, and parameter tuning. By utilizing deep learning algorithms for object detection, R-CNN can quickly and accurately detect individual cells and their phenotypes in a single step, which is much faster than pixel-level segmentation. As a result, R-CNN is ideal for various tasks such as digital pathology, high-throughput drug screening, and basic biology research. The R-CNN approach involves creating bounding boxes and classifications for an image. The model is trained on a batch of images with known bounding box coordinates and labels for prediction of the image. The accuracy of the model is evaluated by comparing the predicted outcomes with the recognized ground truth annotations.

A study conducted by Aiche chian, Bin Dong, and Zuowei Shen [11] proposes a frame-based model for the segmentation of medical images. Medical image segmentation is a challenging task that is addressed in this paper. The proposed model is designed to quickly and effectively segment generic medical images. Numerical studies indicate that the frame-based model outperforms the total variation-based model in capturing important characteristics of biological structures. The study also includes the segmentation of blood arteries and aneurysms in 3D CT angiography images. Deep learning for parasite identification is currently limited due to the lack of publicly accessible datasets. The use of tight frame redundancy can result in a sparse approximation of images, which is desirable for image restoration challenges such as denoising, inpainting, and deblurring. The segmentation of medical images can simplify the image and enhance it for further analysis.

Salwa-Abdul Latif and Mohanad Salman [12] provide an explanation of image segmentation as a crucial step in image pre-processing. The effectiveness of this step determines the accuracy of object identification and image recognition tasks. Image segmentation involves dividing an image into distinct, homogeneous segments, leading to simpler and easier-to-understand representations of the image. The article discusses various image segmentation techniques, including their advantages, disadvantages, and specific use cases. Additionally, it presents real-life applications for these techniques. However, the article lacks detailed analysis of data and performance comparisons between multiple models for a particular use case. It suggests that edge and region-based segmentation analysis is the best approach for differentiating and identifying various Haemoprotozoan cells.

III. METHODOLOGY

The system that has been proposed includes six phases: data scraping, image pre-processing, image segmentation, feature selection, softmax classification, and real-time hosted webapp implementation. The initial five stages are part of an image processing and neural network solution, while the last stage involves implementing a hosted application. A block diagram depicting the proposed system is provided below:
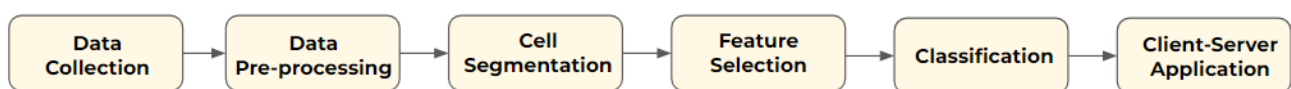

Figure. 1 Block diagram of proposed image Collection

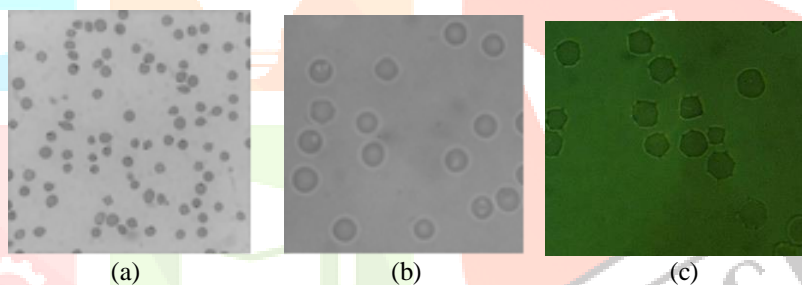### 3.1 Image Collection & Scraping

(a) (b) (c)

Figure. 2 Blood smear scans: (a) Anaplasmosis
(b) Babesiosis (c) Theileriosis

Collecting data in the form of images is an essential step in machine learning, and the quality and quantity of the data used to train the model greatly impact its performance. In this research, cell images were obtained from blood sample analysis laboratories to detect three Haemoprotozoan diseases. Data collection is a time-consuming process that involves acquiring relevant data and organizing it to create datasets suitable for machine learning. For this study, cell image samples were collected from laboratories that analyze and process bovine blood samples. These samples represent three Haemoprotozoan diseases: Anaplasmosis, Babesiosis, and Theileriosis.

3.2 Image Pre-Processing

Preprocessing is a crucial step in preparing image data for machine learning algorithms to effectively detect features and solve problems. Its purpose is to simplify the data and improve the accuracy of the resulting model. Preprocessing techniques can help reduce complexity and remove unwanted distortions while enhancing relevant characteristics for specific applications.

3.2.1 Normalization

Images captured in real-world settings often vary greatly in terms of lighting, which can significantly affect colour distribution. As a result, it is necessary to account for these variations when performing object recognition based on pixel information. A number of algorithms have been developed to address this issue, including techniques for colour constancy or colour normalization. Some examples of these algorithms include whitening, normalization of colours across all colour spaces, and colour rotation.

3.2.2 Gaussian Filters

To smooth the relevant image, a Gaussian filter is applied. This step helps to reduce the visibility of noise, which may affect the edge detection process. The Gaussian filter equation depends on the size of the filter, which is given by (2k+1) (2k+1). In order to apply a size-dependent Gaussian filter, the two-dimensional Gaussian function provided in equation (3.1) is utilized.

$$g(x,y) = \frac{1}{2\pi\sigma^2} \, e^{-(x^2+y^2)/(2\sigma^2)} \qquad (3.1)$$

3.2.3 Sobel Edge Detectors

The Sobel edge detector employs two 3x3 convolution masks, Gx and Gy, to estimate the gradient in the x and y directions, respectively. This operator calculates a 2-D spatial gradient measurement on an image and highlights regions with high spatial frequency that correspond to edges [13]. By combining these two masks, the absolute gradient magnitude and orientation can be determined at each point. The magnitude of the gradient can be calculated using equation (3.2), as shown below:

$$|G| = \sqrt{G^{x^2} + G^{y^2}} \qquad (3.2)$$

3.2.4 Intensity Equalization

A histogram is a graphical representation of the distribution of pixel intensity values in an image. It shows the number of pixels at each intensity value. Histogram equalization is a technique used to enhance the contrast in images. The transformation equation for histogram equalization is given as (3.3):

$$S_k = T(r_k) = (L-1)\sum_{j=0}^{k} p_r(r_j) \qquad (3.3)$$

The output pixel intensity Sk and input pixel intensity rk are related by the transformation equation (3.3), where L is the maximum intensity value and p_(r) (r_j) represents the probability of intensity level r_j in the image.

3.3 Segmentation

The Circular Hough Transform method is commonly used to identify shapes of distinct components in an image, particularly circles. It is an extended form that can distinguish between multiple circle forms in an image. The Canny Edge Detector is often used to detect edges, which are then used as input for the Circular Hough Transform to extract nucleus cells. By using a simple feature extraction method, circles can be located in imperfect images. The Hough parameter space is "polled" to generate circle candidates, and the local maximum is selected from an accumulator matrix.

3.3.1 Parametric equation of a circle

Formula for the Parametric Equation of a circle is given as (3.4):

$$(x-a)^2 + (y-b)^2 = r^2 \qquad (3.4)$$

The focus of this equation lies on three primary parameters, namely a, b, and r. The center of the circle in the x and y directions is represented by a and b. Equations (3.5) and (3.6) are used to represent the circle's parameters.

$$x = a + r \times cos(\theta) \qquad (3.5)$$

$$x = a + r \times \sin(\theta) \qquad (3.6)$$

3.3.2 Edge Detection methods

To decrease the amount of data to be processed and still obtain essential structural information from various visual objects, the Canny edge detection technology is employed. The Canny Edge detection technique is used to identify basic shapes in the image. The criteria for standard edge detection are:

- Low error rate, meaning every edge visible in the image should be detected accurately.
- The operator's edge point detection should precisely locate the center of the edge.
- The generation of fake edges should be prevented, and image noise should be minimized. The edges in a blurred image may point in different directions, so the Canny algorithm employs four filters to differentiate between horizontal, vertical, and diagonal edges. The edge detection operator, G_y, calculates the first derivative in both horizontal (G_x) and vertical (G_y) directions, which helps to identify the edge gradient and direction as shown in Equation (3.7):

$$\theta = atan\,2(G_y, G_x) \qquad (3.7)$$

3.4 Feature Selection

To prepare the dataset for machine learning, it is important to select relevant features and eliminate irrelevant ones. One method for feature selection is the Relief algorithm, which utilizes a filter-based approach to generate feature scores based on the segmentation output in order to rank and select the most significant features.

For building neural networks, we utilized the Keras library from TensorFlow, which provides pre-built layers such as "Conv2D," "MaxPooling2D," "Dense," "Flatten," and "Dropout" that were used in the feature selection process.

3.4.1 Conv2D Layer

It is used to extract important features from a given image and find out complex patterns. It can be finding edges, corners or blobs. The way the layer works is by applying a filter which is a 2D matrix which is used to find the dot product over each pixel of the input image. The resultant output is feature map which is represented in 2-dimension.

3.4.2 MaxPooling2D

This is a layer in the neural network that retains the most significant features by maximizing their values and minimizing the less significant features. This a useful layer in feature selection as it gives us a cost-efficient output for further computation. Thus, the down sampled output image is of great significance.

3.4.3 Dense

This function taken in the input as image parameters and finds similarity for classification. It applies linear transformation to the input image and each neuron present in the layer is connected to the previous layer to learn and minimize the error in the weights using backpropagation and optimization like stochastic gradient descent, which is basically how neural networks work. This layer finds out the complex relationships with the input and output images.

3.4.4 Flatten

It allows the model to do classification or regression tasks in the fully connected layers and learn intricate representations of the input data in the convolutional layers. The Flatten layer rearranges the input tensor into a 2-dimensional tensor by concatenating the values along the last axis and lacks any trainable parameters.

3.4.5 Dropout

This feature layer helps us avoid overfitting in the neural network. But it sets some of the values to zero to reduce sensitivity. This makes the model focus and learn only the important features present in the image. The input values that are set to zero is decided by dropout rate which is specified by us, the rest of the values are scaled up by a factor of 1/(1-drop_out_rate) to maintain the overall magnitude.

3.5 Classification

Image classification refers to the process of labeling groups of pixels within an image according to specific rules. There are two main techniques for classification: "supervised" and "unsupervised." Multinomial logistic regression, also called SoftMax regression, is a commonly used method for multiclass classification in machine learning. This type of neural network model uses a SoftMax activation function to convert the model's output into probabilities for each class.

SoftMax regression involves computing a linear combination of the input features and applying a SoftMax function to the result. The SoftMax function is a generalization of the logistic sigmoid function that can handle multiple classes. When training a SoftMax regression model, cross-entropy loss is typically used to measure the difference between the predicted probability distribution and the true label. The objective is to minimize the cross-entropy loss over the training data.

To implement SoftMax regression, a single-layer neural network with a SoftMax activation function (3.8) can be used. The input layer includes the input features, and the output layer consists of the scores for each class. During training, the model's weights and biases are learned using backpropagation.

$$\sigma(\bar{z}) = \frac{e^{z_i}}{\sum_{j=1}^{K} e^{z_j}} \qquad (3.8)$$

Figure. 3 SoftMax process

3.6 Hosted Webapp Implementation

A software program that is distributed across two or more computers connected through a network is known as a client-server application. The client computer sends a request to the server, which then performs some action and sends the results back to the client.

The client-server architecture is widely used in various software applications, such as web applications, file-sharing systems, and database applications. In this model, the client computer initiates a request for information or a service, and the server responds to the request.

Using a client-server architecture has many benefits. One of these advantages is better resource management, as the server can handle multiple clients simultaneously. Another advantage is that it allows for easier maintenance and updates, as the server can be updated independently of the client.

To process and classify images captured by a microscope, a suggested machine learning model can be integrated with a phone camera or a web application. The server then provides the response back to the application after the image is processed and classified. This integration can be achieved using the Streamlit framework and Tornado server.

Methodology

Protozoan parasites that invade the blood cells of animals, including cattle, can transmit haemoprotozoan diseases that can severely affect the health and productivity of infected animals. It is crucial to promptly diagnose and treat such infections with accuracy.

In this regard, the use of portable instruments for disease classification can significantly aid in the diagnosis and treatment of haemoprotozoan infections in cattle. By providing rapid and precise diagnosis in the field, such devices can prove valuable, especially in large herds or situations where access to laboratory facilities is limited. However, the effectiveness of a portable device for Haemoprotozoan disease classification in cattle depends on the specific features of the device and the precision of its diagnostic algorithms. More research may be required to evaluate the potential of portable technology for this application.

A system for detecting Haemoprotozoan diseases in cattle using image processing and machine learning is outlined in this study with the aid of a portable device. The system employs algorithms to detect circular edges and anomalies caused by the infection, allowing for accurate classification even with a limited dataset.

IV. RESULT

We see that out of 1000 images in the dataset we get 800 accurate correct results in Figure. 4. With an accuracy of 98.53%, which is the best result we could get for out model.
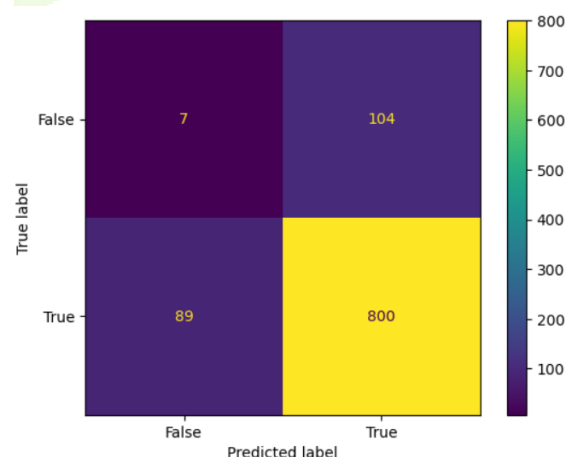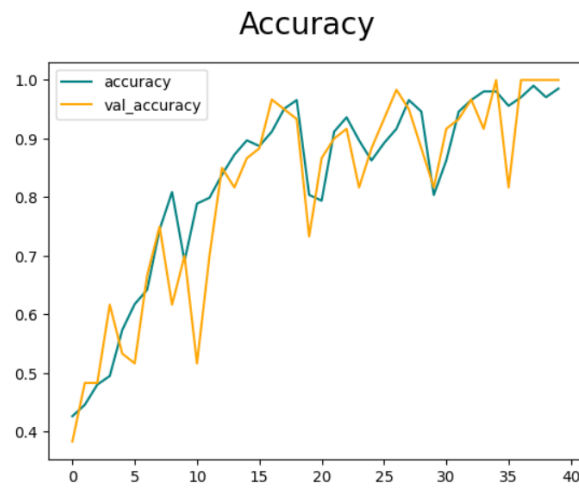

Figure. 4 Confusion matrix for the trained model

Figure. 5 Accuracy graph for the trained model

By creating a user-friendly interface that allows for the upload or real-time capture of sample blood images, the prediction and classification of Haemoprotozoan diseases such as Anaplasmosis, Babesiosis, and Theileriosis can be made more efficient and accurate. This can save time and provide more advanced predictions, ultimately assisting laboratory technicians in their work.

As shown in Figure 6, the client-server application provides a clear and simple interface for users to upload or capture an image. Once the image is sent to the server, the machine learning model runs to classify the image as infected or not, as well as identifying which of the three Haemoprotozoan diseases is present.
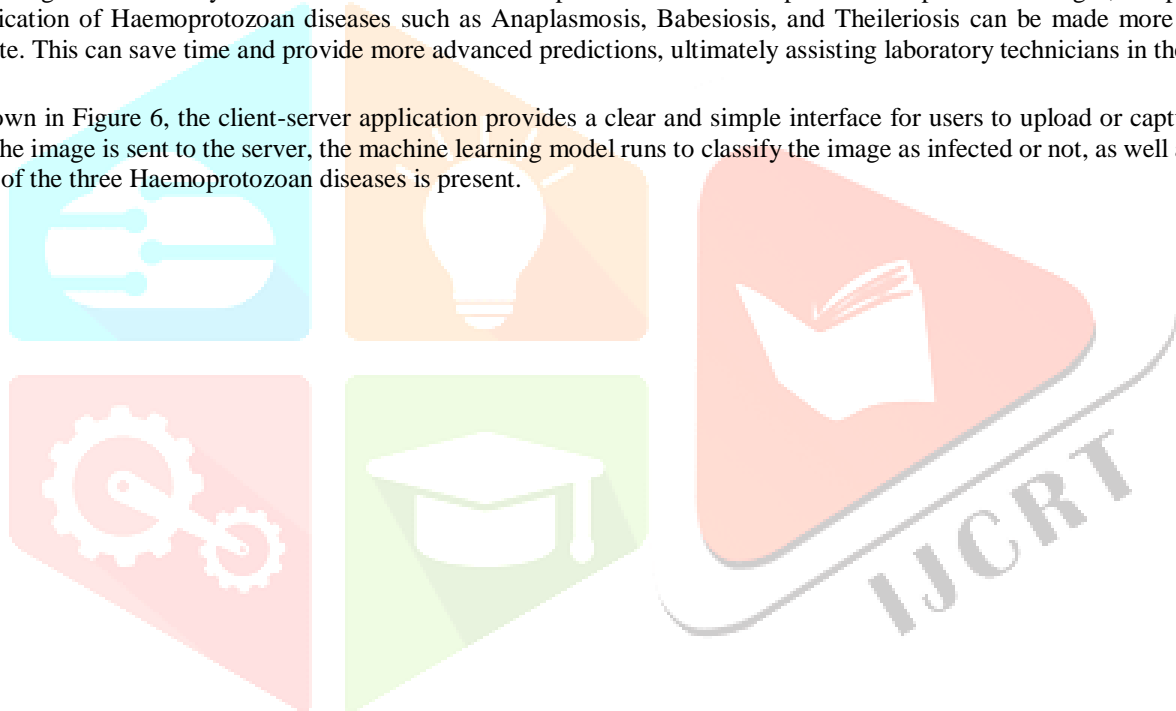
Figure. 6 Client-server interface for Haemoprotozoan disease classification

V. CONCLUSION

A novel processing method has been proposed in this study to effectively predict various Haemoprotozoan diseases. In this project, we have proposed a portable application method to predict if the given blood sample image is diseased or not and also classifies the images among the three Haemoprotozoan diseases, Anaplasmosis, Babesiosis, and Theileriosis using machine learning techniques. The system was implemented using all the Neural Network model and their performance was evaluated. For further work, we need to gather more images for the dataset to increase the accuracy and implement a bteer classifying model for better predicted values, calculate the computational complexity of all the algorithms and find out which is the most efficient.

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