

Anemia Detection using a Deep Learning Algorithm by Palm Images

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Abstract— Our aim is to detect anemia through a comparative analysis of three convolutional neural network (CNN) models, namely EfficientNet B3, DenseNet121, and CNN AllNet. A collection of 3,000 microscopic palm pictures, including 1,500 anaemic and 1,500 non-anemic samples, was used to train and test the algorithms. The dataset was preprocessed to balance the classes, augment the images, and normalize the pixel values. The models were trained using transfer learning on the ImageNet dataset and fine-tuned on the anemia dataset. The performance of the models was evaluated based on accuracy, precision, recall, and F1-score. The results showed that CNN ALLNET achieved the highest accuracy of 96.8%, followed by DenseNet121 with 94.4%, and EfficientNet B3 with 91.2%. The precision, recall, and F1-score also followed a similar trend. The study concludes that CNN ALLNET is the optimal model for anemia detection due to its high accuracy and overall better performance when compared with the different models. The findings of this research could provide a basis for further studies on anemia detection using CNN models, ultimately improving the accuracy and efficiency of anemia diagnosis and treatment.

Keywords- Convolutional Neural Network (CNN); EfficientNet B3; DenseNet121; CNN AllNet

I. INTRODUCTION

Anemia is a medical condition that occurs when there is a deficiency of red blood cells or hemoglobin in the blood. It is a widespread health issue that affects millions of people worldwide and can cause fatigue, weakness, and other symptoms that can significantly impact a person's quality of life. Anemia can be caused by various factors, including nutrient deficiencies, chronic diseases, and genetic disorders.

Detecting anemia is crucial for timely diagnosis and treatment. There are various methods to detect anemia, such as blood tests, physical examinations, and imaging tests. However, these methods can be invasive, time-consuming, and expensive, making them less accessible, especially in resource-limited settings. Finding and treating drugs are two of the most important aspects of the drug industry. Thus, the computer-aided decision systems are becoming more essential to helping the doctors. There are numerous techniques in the literature that can be used in decision systems in the medical field.

The study proposes a mobile app for anemia detection using YOLO v5, aiding healthcare professionals in areas with limited mobile signals. The app utilizes a dataset of children

under five years old and their blood test results. While YOLO v5's performance decreases in a mobile app, the study achieves a 0.71 sensitivity and 0.89 specificity for anemia prediction [1].

Detecting and analyzing white blood cells, crucial for identifying diseases, is time-consuming and influenced by external factors. The study proposes a real-time detection process using YOLOv5s, YOLOv5x, and Detectron2 R50-FPN pretrained models with optimized activation function and a hybrid structure. The developed approach improves recognition rates by 0.006 and provides a 3.44-14.7% improvement in success rate. The hybrid structure achieves a maximum accuracy rate of 98% for detecting and classifying white blood cells [2].

Accurate detection and localization of angiodysplasia lesions is vital for early diagnosis of gastrointestinal bleeding and anemia. The study presents a solution for detecting and localizing angiodysplasia using deep neural networks and binary segmentation. The approach provides state-of-the-art performance and ranks among the top results for all subcategories in the task [3].

Histology is a widely-used technique to study microscopic structures of cells and tissues in pathology. In this study, a neural network is proposed for blood cell image classification, achieving an accuracy of 95.24%. The model outperforms existing architectures, reducing human error and laboratory workload for more efficient pathology [4].

Machine learning has potential in healthcare industry, including the classification of white for medical diagnosis. Haematologists currently examine blood smears to identify white blood cell subtypes, which is time-consuming and error-prone. This study proposes to use YOLOv3 object detection to localize and classify white blood cells accurately with 99.2% detection and 90% classification accuracy [5].

Automated, fast, and easy-to-use complete blood cell count (CBC) methods are in high demand to minimize healthcare costs and patients' burden. A deep neural network-based method using the YOLOv3 algorithm is proposed for CBC detection, with potential application in micro fluidic stage medical devices. The method was applied to blood samples from COVID-19 patients, where blood cell clots are a typical symptom. Experimental results show promise for machine learning methods in CBC tests [6].

Automating complete blood cell count is important for diagnosing disorders and reducing treatment costs. A convolution neural network was used to perform this task and detect malarial pathogens in blood smear images. The system has a precision of over 0.95 and detects malarial parasites with 100% accuracy. The software also is adapted for rapid prototyping on a low-cost microcomputer [7].

Techniques for non-invasive prognosis and the implementation of mobile health (mHealth) are gaining popularity in healthcare. Image analysis using smartphones and machine learning algorithms can assist in the analysis of anemia, liver disease, and COVID-19. These methods have high sensitivity and specificity, making them a promising tool for early diagnosis and increasing people's access to healthcare [8].

This paper discusses the classification of normal and poikilocyte cells, which are erythrocytes with varying sizes and shapes, using an artificial neural network. The presence of poikilocytes, including degmacytes, dchistocytes, dacrocytes, and elliptocytes, is a defining feature of iron deficiency anemia. In their study, the authors utilized data pre-processing, categorization, texture analysis, edge detection, and classification methods on microscopic images of blood smears to identify these cells. Overlapping cells were automatically and accurately separated using Matlab. [9].

Ensemble learning methods can improve the accuracy of computer-aided diagnosis. This study evaluates five methods for detecting anemia on four classifiers (voting, stacking, adaboost, bagging, and Bayesian Boosting). The stacking ensemble method achieves the highest accuracy, and combining decision tree and K-nearest neighbor outperforms artificial neural network. Using an ensemble of classifiers can lead to more accurate medical decision making [10].

The authors offer a new approach to identify three different types of irregular red blood cells (RBCs) known as poikilocytes in iron-deficient serum samples. Preprocessing, categorization, edge detection, and classifying steps are included in the stated cell recognition method, which employs three distinct classifiers. The proposed method detects Schistocyte cells, Dacrocyte cells, and Elliptocyte cells with 100%, 99%, and 97% accuracy, respectively. The maximum voting concept is utilized to select the appropriate class [11].

Red blood cells (RBCs), plasma, white blood cells, and platelets are components of human blood, with RBCs occupying larger volume. Abnormal RBCs indicate blood disorders such as anemia, which are evaluated by variations in dimensions, structure, and color using conventional microscopy. To support medical technicians, hematologists, and pathologists, a proposed system using Raspberry Pi measures different parameters of RBCs and identifies 7 different types with 93.33% accuracy using a Support Vector Machine (SVM) classifier. This aids in early diagnosis of anemia types, but additional laboratory exams are needed for a conclusive disease diagnosis [12].

The goal is to create standalone application to divide red blood cells into four unusual types and offers a total RBC count using 13 geometric features. An artificial neural network and a decision tree are used and compared as classifiers. In classifying RBCs, the results show an accuracy of 85.82-96.06%. [13].

A non-invasive method for detecting anemia by measuring hemoglobin concentration is presented. The traditional blood sampling method is replaced with a neural network-based algorithm that uses images of patients' fingertip. For patient information, a mobile app is used, and the final output is generated by a machine learning algorithm. Early stage detection is possible [14].

The accurate classification and counting of white blood cells (WBC) is crucial for detecting illnesses such as infections, anemia, and cancer. Hematology analyzers and manual counting are traditional methods, but image processing with segmentation and classification techniques is emerging. This paper proposes a new method using HSV and CNN to segment and count WBCs accurately [15].

Microscopic blood analysis can help prevent and protect against various diseases. Object detection technology, like Faster R-CNN, can efficiently detect erythrocytes, lymphocytes, and platelets in blood samples. Early detection of anomalies in blood constituents can help detect diseases such as leukemia, anemia, and sickle cell disease. Our model accurately identifies and labels blood constituents [16].

Detecting sickle cell anemia (SCA) early is vital for patient care. This genetic condition causes RBCs to become sickle-shaped and obstruct blood vessels leading to severe anemia. Manual classification is challenging, and image processing is inefficient. Thus, a deep neural network is proposed to detect sickle-shaped cells in blood samples. Data augmentation and histogram equalization techniques are used to address the shortage of dataset. A CNN with five convolution layers achieved 94.57% testing accuracy in classifying RBCs as normal, sickle-shaped, and other components [17].

Chronic Kidney Disease (CKD) affects a large population worldwide with high mortality rates and an increased risk of adverse effects. Early diagnosis is crucial, and this work proposes using CNN to detect CKD from clinical data, outperforming other classifiers with an accuracy of 99.12%. Missing values are imputed using k-nearest neighbor and categorical data with most frequent category [18].

The YOLOv3 algorithm can be used in medicine to automate the recognition of red blood cells in the shape of a sickle in blood smear samples. The system processes grayscale images and achieved 100% accuracy in detecting sickle cells in 12 samples. A 50% level of certainty provided the highest accuracy, and unstained samples produced higher confidence detections [19].

The variation in White Blood Cell (WBC) count can lead to hematological disorders, including leukemia and anemia. A proposed Convolutional Neural Network (CNN) framework extracts features from images to classify monocytes, neutrophils, eosinophils, lymphocytes, and basophils. Experiments with benchmarking datasets showed GoogLeNet architecture had highest accuracy of 93.43% utilising Relu activation function [20].

Blood cells, comprising white blood cells, red blood cells, and platelets, account for 45% of the volume of blood. These cells are crucial in immune system's function to defense against infections and diseases like leukemia, cancer, and anemia. Deep learning using Convolutional Neural Networks can classify images of different blood cell subtypes. This paper discusses the use of this technique on a dataset from the Hospital Clinic of Barcelona's Core Laboratory [21].

II. INFERENCE FROM THE LITERATURE SURVEY

The literature survey suggests that anemia detection using deep learning techniques such as support vector machines (SVM) and convolutional neural networks (CNN) has shown promising results. These approaches have been implemented to various forms of input data, including retinal image and blood samples, and have the potential to improve anemia diagnosis accuracy and reduce the need for invasive procedures. However, further research is needed to validate their effectiveness in clinical settings.

Convolutional Neural Networks (CNNs) shown excellent potential in different medical applications, including the detection of anemia. CNNs are capable of learning complex features from images, which can aid in the diagnosis of anemia. In this study, we evaluate the results of three CNN models for detecting anemia: EfficientNet B3, DenseNet 121 and CNN AllNet.

III. METHODOLOGY

The following section outlines the methodology used for detecting anemia through the development of network architecture, image processing techniques, and a workflow. As depicted in Figure 1, the workflow comprised several stages, starting with the acquisition of the dataset, followed by data augmentation to improve size and robustness. The preprocessed image data was then fed to the CNN, where the network utilized automated feature extraction techniques to classify the images as Anemia (patient) or Non-Anemia (healthy).

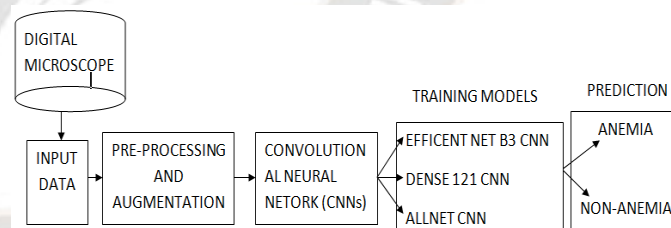


Figure 1. Anemia detection system

A. Input Data

The data is collected from various sources such as hospitals, and medical institutions databases. The data should include a large number of images of individuals with and without anemia. A USB Digital Microscope is an electronic device that magnifies and captures images of the palm through the use of a camera and LED lighting. This particular model provides a magnification range of 50X to 1600X and comes with eight built-in LED lights for improved image clarity. It also includes a metal stand for stable placement and can be connected to both Android and iOS smartphones via USB,

enabling the capture and storage of high-quality images for later analysis or examination.

To detect anemia using CNN, the palm regions must first be segmented, where preprocessing and color classification are required. The next step is to improve the feature extraction of the target area. The palm images of patient in Figure 2 (b) are based on the HSI color space and show the blood cells having better contrast than other components of the image.

In pre-processing, K-means clustering algorithm is often used in palm image analysis to group similar data points together based on their features or characteristics. In the case of palm image analysis, the algorithm is used to cluster the pixels of the image based on their color, intensity, and texture features. By clustering the pixels in this way, the algorithm can help to identify patterns and groupings within the image that might not be immediately apparent to the naked eye. This can be useful for a range of applications, such as identifying regions of interest within the image or for segmenting the image into different regions based on their characteristics. Overall, K-means clustering algorithm is a popular choice for palm image analysis because it is efficient, relatively easy to implement, and can provide valuable insights into the structure and composition of the image data.

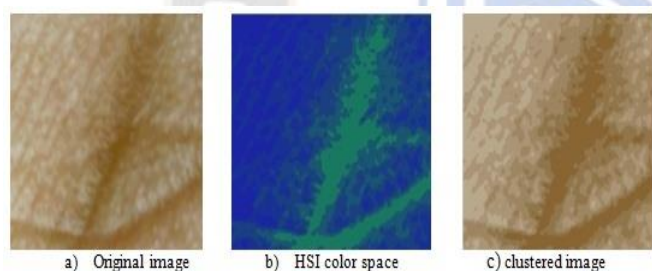


Figure 2. Pre-processing image.

There were an amount of 3000 samples from 850 people used to create the dataset, 1500 samples had shown as anaemia and 1500 samples as non-anemia. Each image in the dataset possessed identical dimensions (224x224x3) and contain blood cell entity of interest, with the background filled in with black.



Figure 3. Images from the dataset: (a) anemia; (b) non-anemia

B. Data Augmentation

In the feature extraction process, the amount of images fed into a neural network is a crucial factor. However, dataset used for this study had a disparity of images between two classes, potentially leading to classification bias. To mitigate this, the images underwent auto-orientation and resizing, followed by augmentation procedures such as randomized rotation transformation, reflection transformation, saturation jitter and random brightness jitter. After augmentation, final dataset contains 12,000 images, and 6,000 images in each class. Figure 4 provides a visual representation of the augmented images.

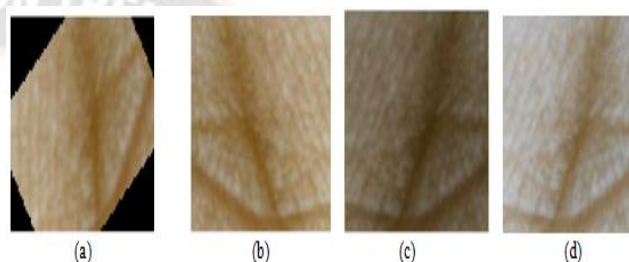


Figure 4. Augmented versions of the palm image dataset

C. Convolution Neural Network (CNN)

Convolution neural network (CNN) is composed of a sequence of layers that utilize a differential operation to convert an input image volume into an output volume. CNN architecture was inspired by the brain's visual cortex, which makes it a more efficient fit for image data. This is because CNNs have fewer parameters and weights that can be reused. The CNN consists of various layers, such as convolution (CONV), pooling (Pool), and fully connected (FC) layers.

Palm image datasets was collected from patients with and without anemia. In a ratio of 80:20, the dataset was partitioned into training and testing sets. The training set was employed to train CNN models, while the testing set was utilised to assess the model's effectiveness. Three CNN models were trained: EfficientNet B3, DenseNet 121 and CNN AllNet. The models were implemented using the Matlab. The input images were resized to 224x224 pixels and normalized. The trained models were created with a learning rate of 0.001 using Adam optimizer. The models were developed for 65 epochs using 32 batches.

D. CNN Efficient Net-B3

EfficientNet B3 is part of the EfficientNet family of models, which are designed to be highly efficient in terms of computational resources while maintaining high accuracy. The B3 variant has 12.2 million parameters and is larger than the B0 and B1 variants. EfficientNet B3 uses a combination of different techniques to achieve its high performance, including

the use of compound scaling to balance model depth, width, and resolution. It also uses a new type of building block called a "MBConv" block, which consists of a mobile inverted bottleneck convolution. The MBConv block aids in minimising the model's computational expense by limiting the number of input channels before to the convolution operation. EfficientNet B3 also uses a novel training approach called "RandAugment," which applies random data augmentations to the training images to improve generalization performance.

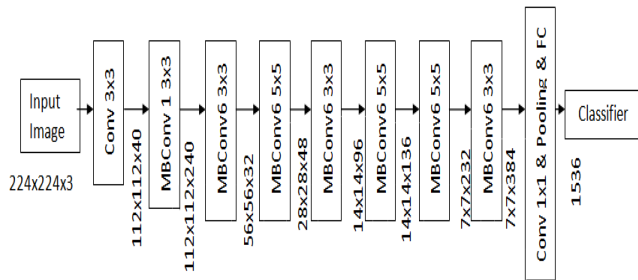


Figure 5. The architecture of Efficient Net-B3

E. CNN Dense Net 121

The DenseBlock comprises layers with feature maps of equal sizes that can be connected within the channel dimension. Nonlinear DenseBlock utilizes BN + ReLU + 3 × 3 convolution function. The output image features are determined by the Convolutions of the different layers' DenseBlocks, which is dependent on the type of ResNet being used. The total number of layers is increased by adding the input feature map layer to the channel layer. If every layer of the DenseNet-A structure, that which gives DenseBlock its size while having a lower input, reuses distinctive features. A larger input necessitates the introduction of an extra bottleneck layer inside of the DenseBlock, typically by adding a 1 × 1 convolution to the basic form, yielding a DenseNet-B structure. The addition of 1 × 1 convolution improves computational efficiency by reducing the number of features. This can be seen in Figure 6.

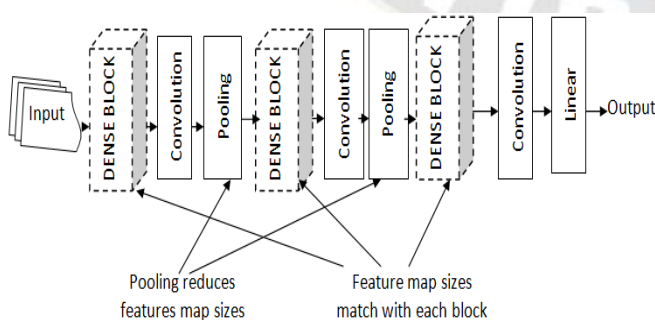


Figure 6. The architecture of DenseNet-121

F. CNN Allnet

A deep convolutional neural network architecture called CNN AllNet was created for image categorization tasks.

It consists of 6 blocks with 4 convolutional layers each and a max pooling layer, totaling 25 convolutional layers. Following the convolutional layers, batch normalisation and ReLU activation functions to capture local features of the input image and introduce non-linearity into the model, respectively.

1) Convolution (CONV) Layers: The primary components of a CNN are the convolution layers, which are responsible for the network's feature extraction. These layers are made up of a collection of filters that, when combined with the input volume, generate a neural activation map. By utilizing a multi-layered architecture, useful features can be extracted from the input images. Each filter can be of a distinct type, detecting various features like lines and edges in the horizontal and vertical planes. Through the process of convolution, the CNN layers extract these features, which are subsequently used in the decision support system. Ultimately, the acquired deep features play a significant role in defining the output of network.

The 2D convolution present the equations (1) and (2), respectively,

$$y[m, n] = x[m, n] \times h[m, n] \tag{1}$$

$$y[m, n] = \sum_{i=-\infty}^{\infty} \sum_{j=-\infty}^{\infty} x[i, j], h[m - i, n - j] \tag{2}$$

Where $x[m, n]$ = Input data

m, n = Number of rows and number of columns

i, j = Index of row and index of column

$$size = \left\lceil \left[\left(\frac{m+2p-n}{s} + 1, \frac{m+2p-n}{s} + 1 \right) \right] \right\rceil \tag{3}$$

Where m = number of input feature

N = convolution kernel size

P = padding

S = stride

2) Pooling (POOL) Layer: POOL layer is frequently used to compress information and speed up computation. This layer can be implemented using max pooling and average pooling, and it summarises local regions of networks in the convolutional layers. Whereas average pooling keeps track of the total value to every feature map patch, maximum pooling keeps track of its maximum value. Because the largest value has the most bearing on the image patch, other values can be discarded when employing max pooling.

3) Fully Connected (FC) Layer: The FC layer carries in the layer's output and normalises it into a vector that can be fed into the next stage's input layer. In this layer, a softmax layer is used to make an accurate label prediction (0 or 1). Each layer's cumulative probability is reported in the output

layer. The most accurate weights are determined by the completely connected portion of the CNN using backpropagation. Being a binary classification task, the weights of the individual nodes are utilized to determine which labels will paid the most weight.

4) *Batch normalization*: Covariance shift, or the variation in hidden unit values, can be reduced by a method called batch normalising. Retraining is required if the distribution of the input variable x changes after it has been mapped to the target variable y for training. With batch normalisation, each layer can learn independently. The latter advantage is that it permits faster rates of learning by preventing extremes of activation. In addition, it has regularisation effects that help decrease the chances of overfitting. Batch normalisation standardises the outputs of earlier activation layers to stabilise the neural network. In this method, the normalised output from each layer is multiplied by gamma (the standard deviation) and beta (the mean).

$$\mu_B = \frac{1}{m} \sum_{i=1}^m x_i \quad (4)$$

Mini-batch variance is given in equation (5)

$$\sigma_B^2 = \frac{1}{m} \sum_{i=1}^m (x_i - \mu_B)^2 \quad (5)$$

Normalization is given in equation (6)

$$\hat{x}_i = \frac{x_i - \mu_B}{\sqrt{\sigma_B^2 + \epsilon}} \quad (6)$$

5) *Dropout*: To combat early overfitting in deep neural networks, dropout is employed as a regularization method that approximates training multiple parallel neural networks along various architectures. Dropout layers are omitted at random over training to give the impression of a new layer, which the neural network is then trained to adjust it. As a result, the layer is updated with a new opportunity at each iteration, making the network more robust against the introduction of new noise.

6) *Loss function*: The categorising cross-entropy loss function applied to this binary classification model, which has outputs ranging from 0 to 1. This loss function assesses the model's performance by comparing the prediction distribution to the true distribution, with class probability set to 1 and other classes' probability set to 0.

$$L(y, \hat{y}) = - \sum_{j=0}^M \sum_{i=0}^N [y_{ij} \times \log(\hat{y}_{ij})] \quad (7)$$

Where \hat{y} predicted denotes the expected value and y denotes measured value.

7) *Optimizer*: Optimizers algorithms utilized to modify neural network attributes, such as weights and learning rates, to minimize loss. The adaptive movement estimation (Adam) algorithm is used in the model. Root mean square propagation

(RMSProp) and the adaptive gradient algorithm (AGA) are the two components of Adam (AdaGrad). In an effort to automatically extract features of the image, the convolutional neural network architecture seen in Figure 2 includes convolutional, pooling, fully connected, dropout, and batch normalisation layers. The use of convolutional and pooling layers facilitates feature extraction. There are a total of eight layers in the model, including four convolutional layers, four max-pooling layers, and three fully linked layers. In order to prevent overfitting, disappearing, and exploding gradients, techniques like dropout and batch normalising are used. The full count of the model's parameters is 95,098,266. Figure 7 depicts the architecture of the created model, while Table 1 provides a more in-depth description of the model.

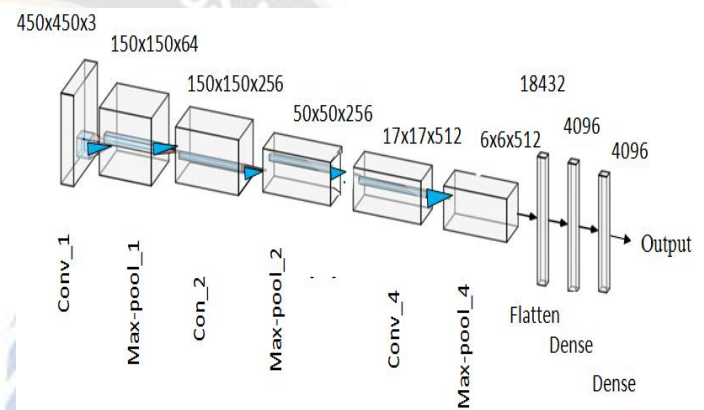


Figure 7. The architecture for CNN allnet

TABLE 1: ALLNET ARCHITECTURE

Layer (Type)	Layer Shape	Number of parameters
Conv2D	(450,450,3)	1792
Max_Pooling_2D	(150,150,64)	-
Conv2D	(150,150,256)	147712
Max_Pooling_2D	(50,50,256)	-
Conv2D	(50,50,384)	885120
Batch_Normalization	(50,50,384)	1536
Max_Pooling	(17,17,384)	-
Droupout	(17,17,384)	-
Conv2D	(17,17,512)	1769984
Batch_Normalization	(17,17,512)	2048
Max_Pooling	(6,6,512)	-
Droupout	(6,6,512)	-
Flatten	18232	-
Dense	4096	75501568
Droupout	4096	-
Dense	4096	16781312
Droupout	4096	-
output	2	8194

Total Parameters:-95,098,266, Trainable Parameters:-95,096,474, Non-Trainable Parameters:-1792.

IV. RESULT AND DISCUSSION

F1 score, accuracy, precision, and recall are some of the estimated performance metrics.

Accuracy: Accuracy refers to overall proportion of correct predictions made by model and is presented in Equation (8).

$$\text{Accuracy} = \frac{\text{True positive} + \text{True negative}}{\text{Total samples}} \times 100 \quad (8)$$

Precision: Precision refers to proportion of positive predictions that were actually correct and is given in Equation (9).

$$\text{Precision} = \frac{\text{True Positive (TP)}}{\text{True Positive (TP)} + \text{False Positive (FP)}} \times 100 \quad (9)$$

Recall: Recall refers to proportion of actual positive cases that were correctly identified by the model and is given in Equation (10).

$$\text{Recall} = \frac{\text{True Positive (TP)}}{\text{True Positive (TP)} + \text{False Negative (FN)}} \times 100 \quad (10)$$

Specificity: Specificity refers to proportion of actual positive cases that were correctly identified by the model and is presented in Equation (11).

$$\text{Specificity} = \frac{\text{True Negative (TN)}}{\text{True Negative (TN)} + \text{False Positive (FP)}} \times 100 \quad (11)$$

F1 Score: The F1 score is a weighted sum of recall and precision and is given in Equation (12).

$$\text{F1 Score} = 2 \times \frac{\text{True Negative (TN)}}{\text{True Negative (TN)} + \text{False Positive (FP)}} \times 100 \quad (12)$$

A. Training and validation Accuracy

The training accuracy and validation accuracy of a model are essential factor that are utilised to calculate the efficiency of the model. In research of anemia detection using CNN training models such as EfficientNet B3, DenseNet 121, and CNN AllNet, training and validation accuracy are key metrics that researchers would be interested in analyzing.

Training accuracy is a measure of how well the model has learned to classify training data. During training, model is presented over labeled training data, and it adjusts its internal parameters to reduce the variance between its true and prediction labels. Divide the number of successfully identified data by the total amount of training data to calculate training accuracy. The model's ability to generalize to new data that it was not exposed to during training is measured by the validity accuracy. It is derived by dividing the entire amount of validation data by the amount of validation data that were correctly categorised.

To compare performance of EfficientNet B3, DenseNet 121, and CNN AllNet models for anemia detection.

A training set made up of 80% of the dataset and a test set, 20% of it. The training set was further separated into 2-fold cross-validation to prevent overfitting. The holdout validation set was then tested using the fold that performed the best. For each fold of the cross-validation, the proposed model was evaluated on 600 photos across 65 epochs after being trained on 3,000 images. In order to give a greater variety of training examples, enhanced data was combined with the original data, which improved the model's ability to generalize. Figures 8, 9, and 10 demonstrate the model's accuracy curves, accordingly. As depicted in Figure 10, the categorical cross-entropy loss function began to significantly decrease within the first 10 to 30 epochs. Although the model was operating effectively at this stage, terminating the training at this time may have led to underfitting. The loss function showed minimal fluctuation after 35 epochs and decreased steadily. Throughout each of the five distinct training procedures, this tendency persisted. Beyond 65 would have resulted in a further reduction in loss, an improvement in accuracy, but also a greater risk of overfitting, as was seen when the model was assessed against the holdout test set. We may conclude that the CNN Allnet model with high validation accuracy and little overfitting would be the recommended one for anemia detection by comparing the training and validation accuracy of each model. Beyond 65 would have resulted in a further reduction loss, an improvement in accuracy, but also a greater risk of overfitting, as was seen when the model was assessed compared with the holdout test set. By comparing training and validation accuracy of each model, we can determine that the CNN Allnet model with high validation accuracy and minimal overfitting would be the preferred best for anemia detection.

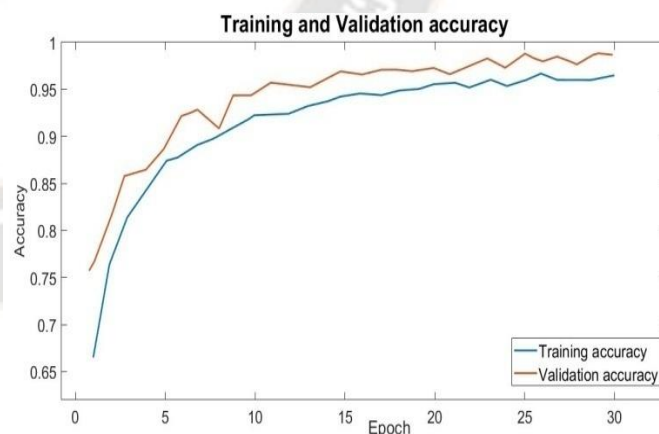


Figure 8. The training and validation accuracy of a model, EfficientNet B3

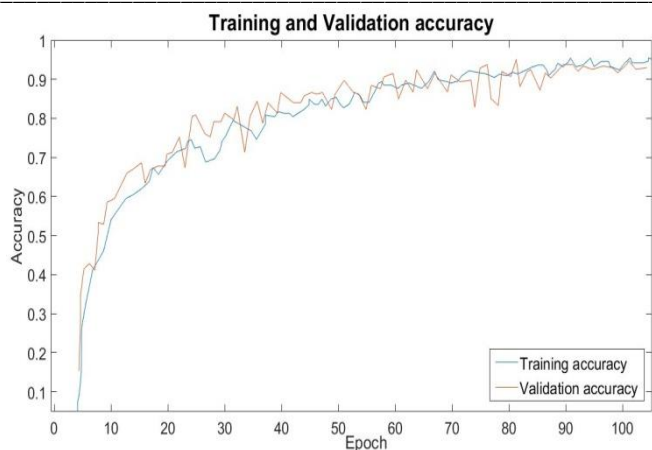


Figure 9. The training and validation accuracy of a model, DenseNet 121

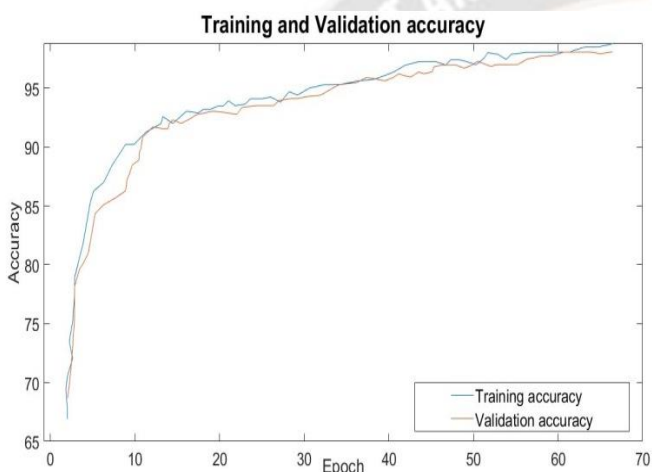


Figure 10. The training and validation accuracy of a model, CNN AllNet

B. The training and validation loss

The training and validation loss are important metrics that are utilised to calculate the performance of a model. Performance metrics provide an indication of how well model is fitting the training samples and how well it is generalizing to new, unseen data. The model is modified while training to reduce the variation among its predictions and the actual labels. A loss function is used to calculate the variation among the predicted and true labels. Training and validation losses are calculated as the average of the losses over all training and validation samples, respectively.

In anemia detection using CNN training models such as EfficientNet B3, DenseNet 121, and CNN AllNet, training and validation loss are important metrics that researchers would be interested in analyzing. The training loss measures how well model is fitting training data. During training, the objective is to reduce training loss as far as is feasible so the neural network is able to appropriately categorize the data. If training loss decreases over time, it indicates that the model is learning to fit the data better. The validation loss measures

how well the model is generalizing to new data that it has not seen during training. If the validation loss remains low while the training loss decreases, it indicates that the model is generalizing well to new data.

To compare the performance of the EfficientNet B3, DenseNet 121, and CNN AllNet models for anemia detection, researchers would typically plot the training and validation loss over time. Ideally, we would like to see the training loss decreasing and the validation loss remaining low, indicating that the model is learning to fit the data well and is generalizing to new data.

However, if the training loss decreases while the validation loss remains high, it may indicate that the neural network is overfitting to training data and is not generalizing well to new data. On the other hand, if both the training and validation loss remain high, it may indicate that the model is underfitting and is not capturing the complexity of the data.

By comparing training and validation loss of each model, researchers can determine model CNN allnet with low validation loss and minimal overfitting would be the preferred best choice for anemia detection.

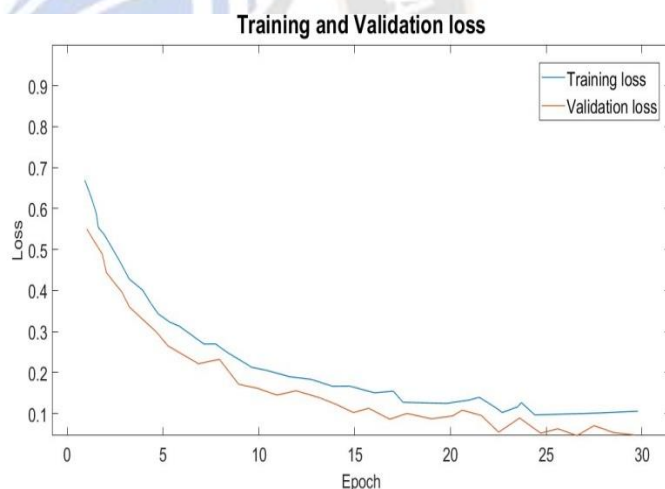


Figure 11. The training and validation loss of a model EfficientNet B3

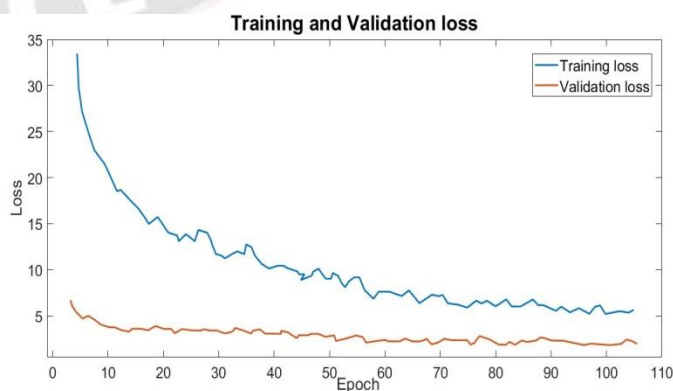


Figure 12. The training and validation loss of a model Dense net 121

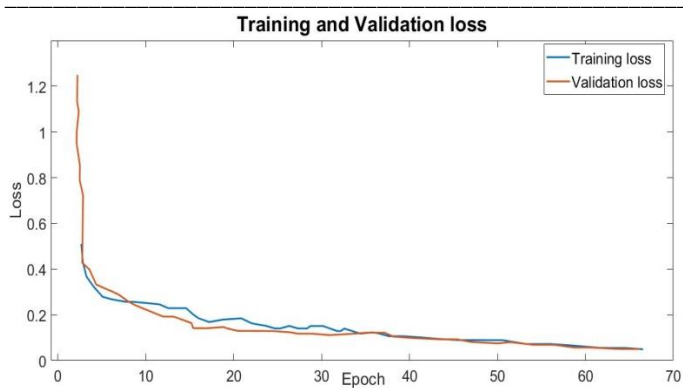


Figure 13. The training and validation loss of a model CNN AllNet

C. Confusion matrix

A confusion matrix is a representation of data that enables an analysis of a classification algorithm's performance. It is often used to evaluate the accuracy of an algorithm in identifying a specific condition or class. In the case of anemia detection using CNN training models such as EfficientNet B3, DenseNet 121, and CNN AllNet, a confusion matrix could function as an excellent tool for evaluating the accuracy of each model's anemia detection.

The confusion matrix for these models would consist of four cells: true positive (TP), false positive (FP), true negative (TN), and false negative (FN).

True Positive (TP): The amount of cases the approach properly predicted anemia.

False Positive (FP): The amount of cases the approach incorrectly predicted anemia (i.e., a false alarm).

True Negative (TN): The amount of cases the approach properly predicted non-anemia.

False Negative (FN): The amount of cases the approach incorrectly predicted non-anemia (i.e., a missed diagnosis).

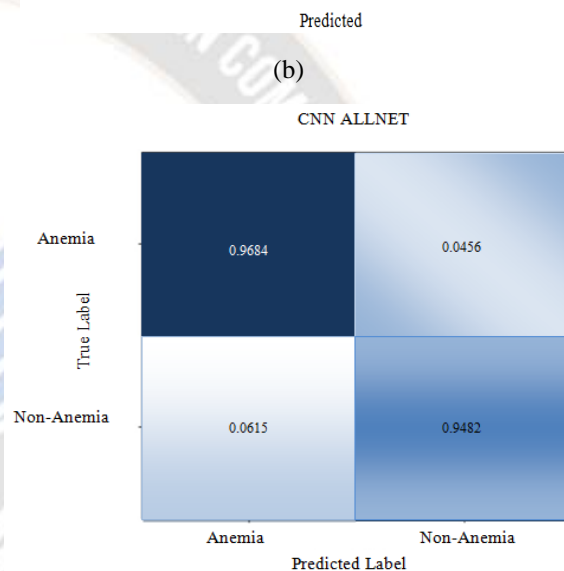
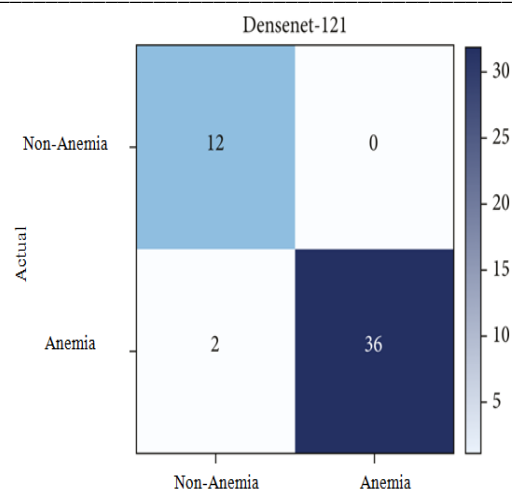
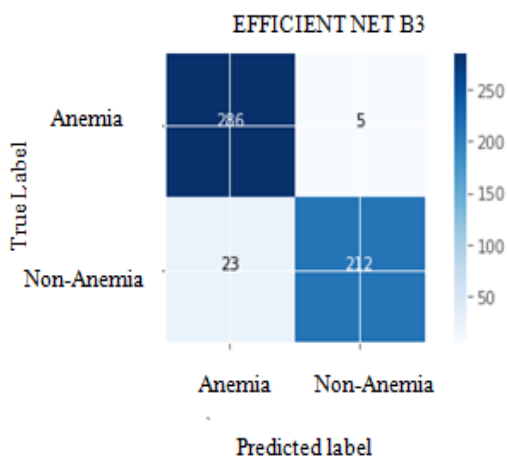


Figure 14. Confusion Matrix for the Models Efficient net b3, Dense net 121 and CNN allnet.



(a)

TABLE 2: MODEL EVALUATION RESULTS

	Accuracy	Precision	Recall	F1 Score
Efficient net B3	91.2	93.5	89.5	91.2
Dense net 121	94.4	96.4	92.5	94.4
CNN allnet	96.8	97.7	95.9	96.8

In examinations comparing the results of three CNN models for anemia detection, EfficientNet B3, DenseNet121, and CNN AllNet, the CNN AllNet model scored the greatest accuracy of 96.8%. DenseNet121 model achieved an accuracy of 94.4%, while EfficientNet B3 achieved an accuracy of 91.2%.

The results showed that CNN AllNet outperformed the other two models with respect of precision, recall, accuracy, and F1score. Precision score for CNN AllNet was 97.7%, recall was 95.9%, and F1score was 96.8%. The precision and recall scores for DenseNet121 were 96.4% and 92.5%, respectively, and F1score was 94.4%. For EfficientNet B3, the precision score was 93.5%, recall was 89.5%, and F1score was 91.2%.

Overall, experiment results suggest that CNN AllNet is the most effective model for anemia detection, achieving the highest accuracy and overall higher efficiency compared to other two models. The results of this research could have important implications for the healthcare industry, as an accurate and efficient diagnosis of anemia is critical for timely treatment and management of the disease.

V. CONCLUSION

In conclusion, this research explored the effectiveness of three CNN models, EfficientNet B3, DenseNet121, and CNN AllNet, for detecting anemia from microscopic palm images. The study evaluated the models based on precision, recall, accuracy, and F1score and concluded CNN AllNet is optimal model for anemia detection. The CNN AllNet model achieved an accuracy of 96.8%, which is significantly higher than the other two models. The research also highlighted the importance of preprocessing, data augmentation, and transfer learning in improving the performance of CNN models for anemia detection. The findings of this study could have significant implications for the healthcare industry, as anemia is a normal blood issue suffered by millions and millions of people global.. An accurate and efficient diagnosis of anemia is critical for timely treatment and management of the disease. The use of CNN models for anemia detection could help medical professionals to make quicker and more accurate diagnoses, ultimately improving patient outcomes.

Future research might discuss the application of alternative deep learning approaches, like recurrent neural networks, for detecting anemia. Further investigation into the effectiveness of transfer learning and data augmentation techniques for anemia detection could also be explored. Overall, this research provides a valuable contribution to field anemia detection and has potential to improve accuracy and efficiency of diagnosis and treatment for this common blood disorder.

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