Annual Methodological Archive Research Review
http://amresearchreview.com/index.php/Journal/about

Online ISSN 3007-3197
Print ISSN 3007-3189

http://amresearchreview.com/index.php/Journal/a

Deep Learning Based Automated Classification And Enumeration Of Blood Cells

Abusafyan[1]
Department of Computer Science, Minhaj University Lahore, Lahore, Pakistan.
Shahan Yamin Siddiqui*[2]
Department of Computer Science, NASTP Institute of Information Technology, Lahore, Pakistan.
Nida Ashraf[3]
Examination Department, Virtual University of Pakistan.
Aftab Ahmad[4]
Department of Computer Science, University of South Asia, Lahore, Pakistan.
Abdullah Dar[5]
Department of Computer Science, Minhaj University Lahore, Lahore, Pakistan.
Nusratullah Tauheed[6]
Department of Computer Science, University of South Asia, Lahore, Pakistan.

[1]abusafyan.bagga18@gmail.com, [*2]drshahan@niit.edu.pk, [3]nidaashraf.edu@gmail.com
[4]aftabahmadqadri99@gmail.com, [5]abdullah.dar014@gmail.com,
[6]nusratullah.tauheed@usa.edu.pk

ABSTRACT

For blood analysis, precise cell identification is key to successful disease diagnosis and subsequent treatment. In this project, we are developing deep learning models to count and classify blood cells in microscopic images. Our dataset will be sourced from publicly available datasets, collaboration with hematology clinics, and our own image acquisitions. Each image was preprocessed to normalize the staining process, quality check the image, and maintain metadata. Our most recent advances in cell detection have been achieved using the YOLOv10 object detection model. These system modules collectively help in creating a workflow that helps in image processing of blood cells through the GAN and then providing features as inputs to the convolution layers of YOLOv10. Features obtained in this way are used by the detection head in order to produce the bounding boxes and the class probability values for the detected blood cells. The loss function that is used for training the model is the combined loss of binary cross-entropy and bounding box regression loss and is calculated during backpropagation. There are four metrics that would be used for evaluation of the proposed method, namely, precision, recall, F1-score, and mAP. In terms of investigation, the advantage of deep learning is obvious since there is a measurable benefit in all criteria including accuracy and reliability as compared to the older traditional machine learning. More testing experiments are being carried out in order to have models which will be generalizable in larger databases whereby each model will be trained in all classes of the database (majority classification of any one particular cell type using all data).

KEYWORDS: *Blood cell classification, deep learning, YOLOv10, microscopic image*

Annual Methodological Archive Research Review
http://amresearchreview.com/index.php/Journal/about
Online ISSN 3007-3197
Print ISSN 3007-3189
http://amresearchreview.com/index.php/Journal/a

analysis, object detection, automated hematology, medical image processing.

Introduction

Blood is a very important fluid in the body, since it carries oxygen, nutrients, hormones, elements of the immune system, and wastes. Blood is made up of mainly of red blood cells (RBCs), white blood cells (WBCs), and platelets. The RBCs are responsible for carrying oxygen in the body by using hemoglobin [1]. On the other hand, WBCs help in fighting against infection, and the platelets play the role of preventing the body from any kind of bleeding. Any change in the shape, quantity, and location of blood cells occurs as a result of various diseases that affect the body's blood or other organs [2].

The Complete Blood Count (CBC) is an internationally used laboratory procedure which offers crucial diagnostic data in the assessment of various diseases. Although the automated method is used for hematology analyzers, the examination of blood smears is still a necessary procedure in order to analyze blood cell morphology and detect abnormal features that cannot be recognized by automation [3]. The process of reviewing blood smears contributes to correct classification of cells, distinguishing between normal and pathological states, disease monitoring and therapeutic reactions, and making individual clinical decisions [4].

For years now, laboratory professionals with training have used manual microscopy analysis of stained blood films for cell classification purposes. They analyze features such as morphology, color, size, and nuclear-cytoplasmic ratio on dry films. Even though considered the golden standard in the clinical setting, the method is tedious, lengthy, and subjective [5]. Factors like fatigue, variability among individuals doing the analysis, varying stains, and increased workload can affect the accuracy of the test [6].

Technological developments in digital pathology, computer vision, and artificial intelligence can automate image analysis of microscopic slides. Deep learning, particularly the Convolutional Neural Networks (CNN), is well-suited for disease diagnosis through image processing by learning hierarchical features without requiring any manual input [7]. The CNN has proven itself to be very efficient in all domains of medicine, including X-ray, CT, pathology, and dermatology by efficiently modeling spatial pixel interactions of blood cells [8].

Availability of digital microscopy data has triggered fast-paced research on the use of deep learning methodologies for automated analysis of blood cells [9]. The CNN models have shown much better accuracy than other methods when it comes to recognizing RBCs, WBCs, and platelets, and also the differentiation of different types of WBCs. However, automated blood cell classification is still difficult due to reasons such as intraclass variability, interclass similarity, overlap of cells, staining issues, noise in images, artifacts, and class imbalance [10].

The dependence of current automatic approaches on handcrafted features and traditional machine learning techniques is an additional constraint that limits their ability [11]. However, deep learning provides better robustness in terms of processing large numbers of blood smears due to the automatic representation of features at multiple levels [12].

An automatic classification of the blood cells is indispensable for providing healthcare services. The correct identification of the blood cells helps to diagnose the blood diseases at the early stages of their development; increases the efficiency of

Online ISSN 3007-3197
Print ISSN 3007-3189

monitoring the health of patients with diseases; contributes to the creation of personalized treatment programs; and makes the work of laboratories more efficient [13 -14].

Various works have been done by many researchers regarding the application of artificial neural networks for the classification of blood cells using deep learning approaches; nevertheless, various gaps exist in the research. The current works utilize either small numbers of datasets or a limited number of classes of cells, thus making it hard for the methods to be applied in real-life scenarios [15]. Thus, the development of an effective and computationally efficient deep learning model for the classification of blood cells is very essential [16].

This research tries to tackle the difficulties associated with automated identification of blood cells by developing a system that uses a convolutional neural network to classify images of blood cells captured using a microscope from blood samples. AI algorithms have been incorporated in the second and third stages of development of the technology, making the technology essentially automated (or one that needs minimal user input). This level of automation is intended to make the technology more accurate compared to other existing technologies [17].

In this research, we present a full deep learning approach to automatic classification of blood cells, which includes:

- Effective image preprocessing algorithm that improves image quality prior to classification.
- Deep convolutional network that automatically extracts discriminative features without the need for designing them manually.
- Automatic classification and counting of several types of blood cells in one image.
- Tolerance to variations in images, such as overlapped cells, differences in staining, and different morphology of cells.
- Less burden on laboratory technicians along with more accurate diagnosis and faster medical assistance.
- Detailed experimental analysis proving its applicability.

Related Work

The recent progress in the development of AI and deep learning technologies for the automatic analysis of blood cells has led to the prevalence of CNN-based techniques for identifying and categorizing cells based on their images [18]. The techniques for object detection such as RCNN and Faster R-CNN successfully identify and categorize red and white blood cells in difficult microscopic images that contain several overlapped blood cells. However, despite their advantage over image processing in the feature discrimination process, there are certain problems related to their applicability in the clinic [19].

Various scholars are investigating lightweight architectures as well as transfer learning for improved classification accuracy at reduced computational cost. Architectures such as ShuffleNet, DenseNet, ResNet, EfficientNet, and even customized CNNs have exceeded 94% accuracy on blood cells' benchmark dataset. Dense connectivity, transfer learning, and efficient feature propagation improve feature extraction, and customized CNNs perform better than the general pre-trained architectures. But most of the works use only normal blood samples, very

Online ISSN 3007-3197
Print ISSN 3007-3189

few classes of blood cells, or a pre-defined dataset [20].

The second important aspect of research is related to the quality of datasets and generalization of models. Datasets such as Raabin-WBC have increased the number of annotated blood smear images and facilitated the replicability of deep learning experiments. Transfer learning, data augmentation/Generative Adversarial Networks (GANs), and semi-supervised learning techniques are being utilized by researchers to overcome annotation limitations and improve classification accuracy. However, despite this progress, large domain shifts owing to various factors reduce performance [21].

Automated analysis of white blood cells for disease treatment is extensively studied by various researchers in the context of diseases such as acute lymphoblastic leukemia, acute myeloid leukemia, malaria, sickle cell anemia, inflammation, and Alzheimer's disease [22]. Image processing techniques that integrate deep learning have revolutionized computer-aided diagnosis through early detection. However, most of the disease-oriented systems have little generalizability for other types of hematological disorders. This is because it is difficult to recognize rare cells [23].

It has been seen that recent studies prove the efficiency of deep learning as compared to ML in terms of blood smear analysis by end-to-end learning and feature extraction. Microfluidics, lab-on-chip technology, digital holography, and AI have been used to develop point-of-care devices [24]. This enhances the speed and automation of smart hematology applications. However, the application has not been extended yet owing to smaller benchmark data sets, lack of external validation, staining differences, overlapping cells, and computation [25].

There are significant deficiencies in the field of automated blood cell classification. These deficiencies include the use of small and homogenous datasets, the testing of only one cell type at once, extensive preprocessing time, manual processes, and the inability to deal with overlapping cells, differences in cell stains, noise in images, rare cells, and transferability of the algorithms between clinical centers [26]. Therefore, there is a need to create an effective deep learning architecture which is capable of automatically identifying important features, classify various cells in an image accurately and be transferred to other clinical settings. This study proposes to design and train a CNN classification algorithm that will integrate image preprocessing and automated feature identification [27].

Proposed Methodology

A deep learning supported system has been designed to automate grading and counting blood cells from images of blood smears taken under a microscope. The system has three components or layers working together to achieve accurate and efficient evaluation of blood cell makeup: a data layer; a training layer; and an application layer that are representing in figure 1.

Annual Methodological Archive Research Review
http://amresearchreview.com/index.php/Journal/about
Online ISSN 3007-3197
Print ISSN 3007-3189
http://amresearchreview.com/index.php/Journal/a

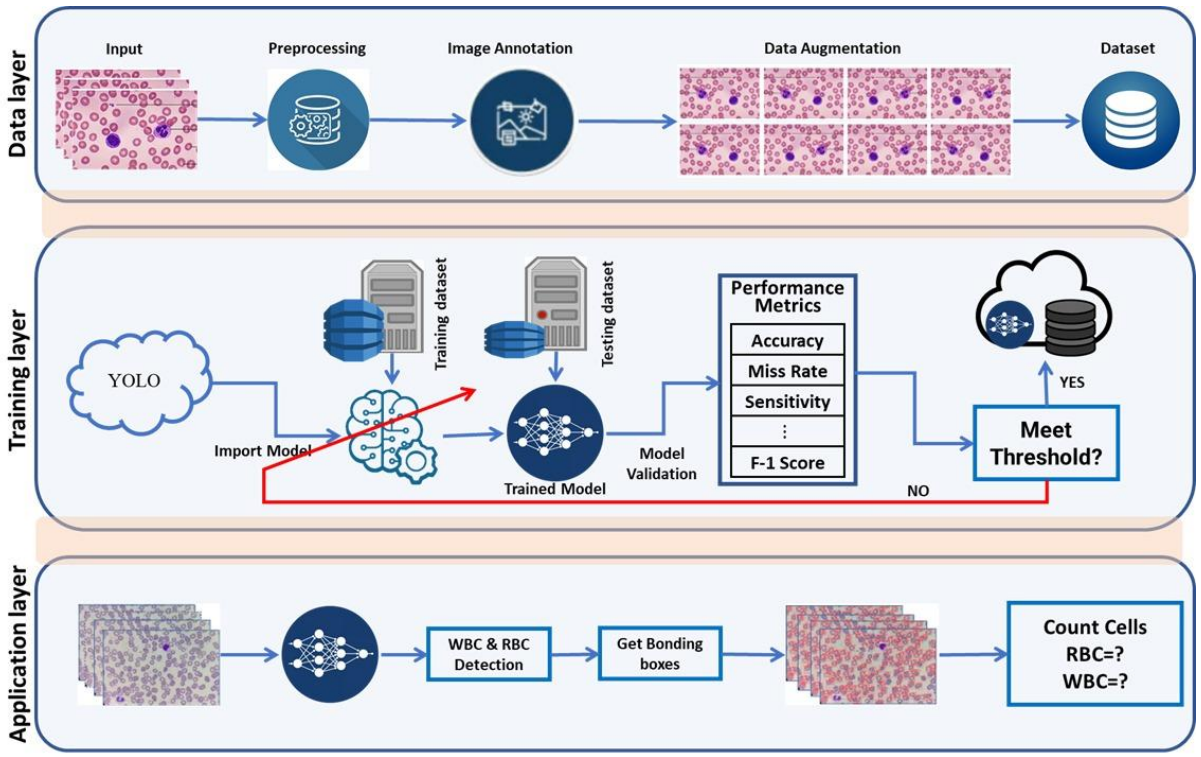

Figure 1: Proposed Model

The data layer takes high-resolution photos of blood samples, applies preliminary classification to the images using annotations provided by users during image acquisition/pre-processing, and ensures that the photos used to create the training dataset are of appropriate quality for model development purposes. Our training dataset was provided by Al Faisal Laboratory and consists of approximately 400 sets of images taken using a microscope (including both red and white blood cells) from set of images taken at one of their laboratories. For each of the images within each of the blood samples in this study's dataset, a series of pre-processing techniques were used to improve the quality of the image, thereby improving accuracy of feature extraction used to identify cells within the dataset based upon their respective features. That series of pre-processing techniques included Gaussian, median and adaptive filtering in order to reduce background noise while still keeping the individual cellular structure intact. After applying these types of filters, additional pre-processing steps should be taken to apply some sort of image enhancement technique (i.e., histogram equalization; CLAHE) in order to improve the contrast between adjacent pixels and emphasize the morphologic features necessary for proper evaluation/classification purposes. Image standardization was done by making all the images into the same size and having consistent colors using pixel normalization while maintaining their proportions. Ground truth is obtained manually by labeling all the images that have been processed and identifying the blood cell type for each image region. To train the Deep Learning Model to differentiate between blood cell types, ground truth data from previous sessions will be used for feature detection. The training process will use the prepared dataset for optimizing a Convolutional Neural Network (CNN) by feature learning. This allows different hierarchical layers to be learned from microscope images.

Annual Methodological Archive Research Review
http://amresearchreview.com/index.php/Journal/about
Online ISSN 3007-3197
Print ISSN 3007-3189
http://amresearchreview.com/index.php/Journal/a

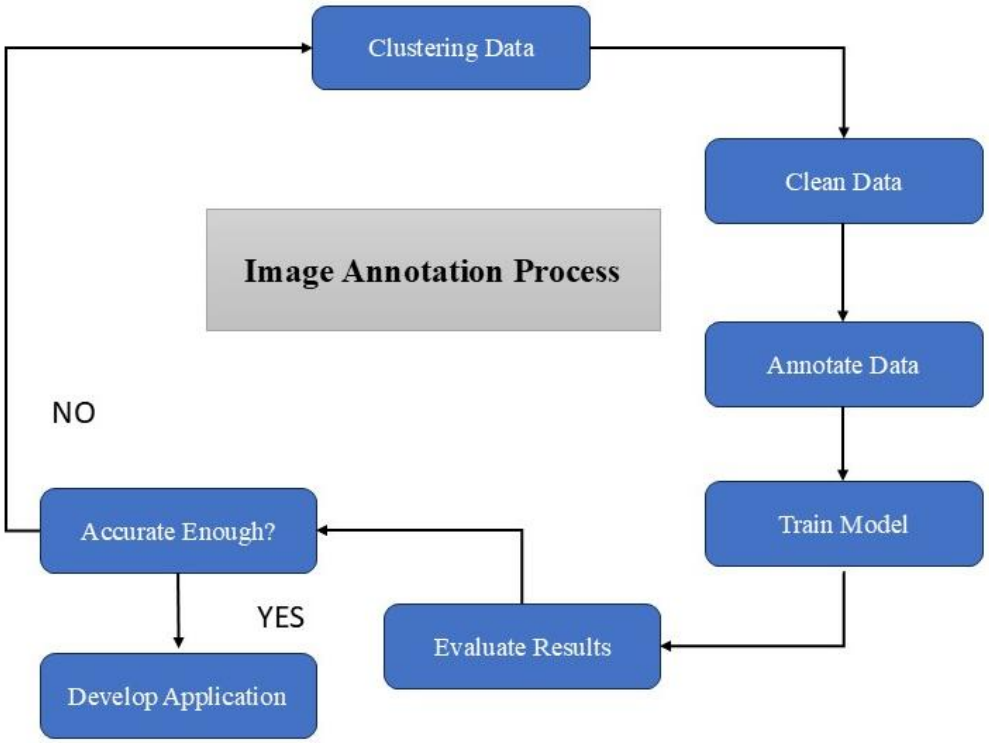

Figure 2: Annotation Process

Figure 2 illustrates the automated workflow for blood cell classification. Our approach begins with clustering all images into data clusters. Then, our datasets are cleansed of noises and duplicate/misclassified data. All blood smears are annotated with their categories and ROI (ground-truth data). After obtaining proper labeling and ROI information, we can train a deep learning network and validate its performance on the basis of predetermined accuracy metrics. In case our model fails to meet the requirements, we go back to the earlier stage of the workflow and perform clustering, cleansing, and annotation again to obtain better datasets. When the required performance is achieved, our network can be deployed to perform automated cell classification and counting tasks.

The process of building deep learning datasets for such voids as identifying blood cells entails the need to label manually correctly. This is done through LabelImg which a graphic interface is used for labeling the Red and White Blood Cells using the bounding box technique thus coming up with the correct format that YOLOv10 needs for training that are represented in figure 3.

Annual Methodological Archive Research Review
http://amresearchreview.com/index.php/Journal/about
Online ISSN 3007-3197
Print ISSN 3007-3189
http://amresearchreview.com/index.php/Journal/a

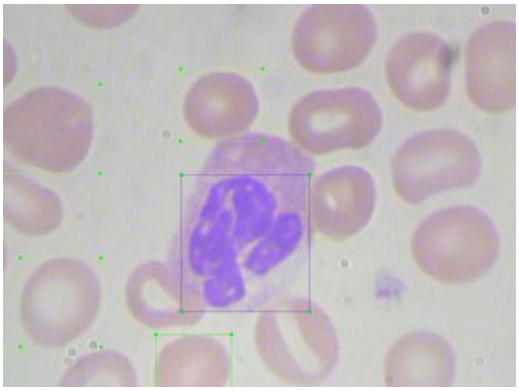

Figure 3: Image Annotation using Labeling

The proposed YOLOv10-based blood cell classifier is used to detect, classify, and quantify blood cells in real-time from microscopy images. To enhance the robustness of the model, data augmentation was performed in terms of rotation, flips horizontally and vertically, random scaling, color jitter, adding of Gaussian noise, and elastic transformations during data preprocessing. The augmented data helped in training a YOLOv10 model that incorporated the following elements: a deep learning feature extractor, feature fusion at multiple scales, and optimized detection layer. Compared to previous YOLO models, YOLOv10 possesses enhanced feature extraction ability, fast inference speed, higher localization accuracy, and better generalization. The ratio of splitting the dataset into training (70%), validation (15%), and testing sets (15%) was done. In the training process, hierarchical feature learning is performed by the convolutional layers, and the output consists of bounding boxes with associated class probabilities. For training and deploying YOLOv10, the predictions made by the model are compared to the actual values of the labels through classification and localization losses via backpropagation until convergence. After training, the YOLOv10 model is deployed in the application layer for performing detection, classification, and automated counting of RBCs and WBCs (along with their subtypes). It can cope with overlapping cells, different morphologies, and artifacts in the images. Multiple microscopic methods (bright-field, phase-contrast, DIC, fluorescence) are supported by the framework, which uses publicly available datasets (BIB, Kaggle Blood Cell Images) and clinical laboratories to provide more diverse data set. Developed using Python with PyTorch, OpenCV, and Labeling, it will be trained in Google Colab with GPU support.

Experimental Tools and Results

The use of cloud-based deep learning configuration has been applied to facilitate the process of training, testing and deploying the object-detection blood cell classification model. Google Colab is used in the model owing to its GPU capabilities which significantly reduce training time for models of huge size. The architecture used in YOLOv10 has been used to detect objects accurately and in real time within the proposed model of microscopic analysis of blood cells. Images for training, validation and testing have been manually labeled using LabelImg tool for RBC and WBC with bounding boxes and classes to generate accurate ground truth datasets for supervised learning. These datasets have been arranged separately into training, validation and testing using Python to allow objective testing of performance. For this project, the model will be trained and optimized using the

Annual Methodological Archive Research Review
http://amresearchreview.com/index.php/Journal/about
Online ISSN 3007-3197
Print ISSN 3007-3189
http://amresearchreview.com/index.php/Journal/a

PyTorch framework. The handling and processing of data are done using NumPy and Pandas libraries whereas the visualization of training and evaluation of the model will be done using the Matplotlib library.

Data collection, processing, labeling, and splitting of data into train, validation, and test set will be performed. After that, training, validation, testing, and real-time inference on unseen microscopic images of blood cells will be performed. The evaluation of model performance will be done using metrics such as box loss, classification loss, DFL, precision, recall, and mAP. Losses of both training and validation are decreasing, which means that the model has better feature extraction and classification capability. The recall was at 98%, indicating the sensitivity of the method to detect blood cells regardless of the imaging modality. In addition, the YOLOv10 model performed well in terms of localization, where mAP 0.5 went from 92.0% at the start of the learning process to over 98.0% at convergence, and mAP 0.5:0.95 went up to 85.0%. Such figures show good generalization capabilities in relation to the dimensions, morphological structures, and IoU threshold values of the blood cells. Reductions in loss and increases in precision, recall, and mAP values indicate that the model successfully learned how to differentiate red blood cell features and localize/classify them at a microscopic level that are represented in the figure 4 and 5.

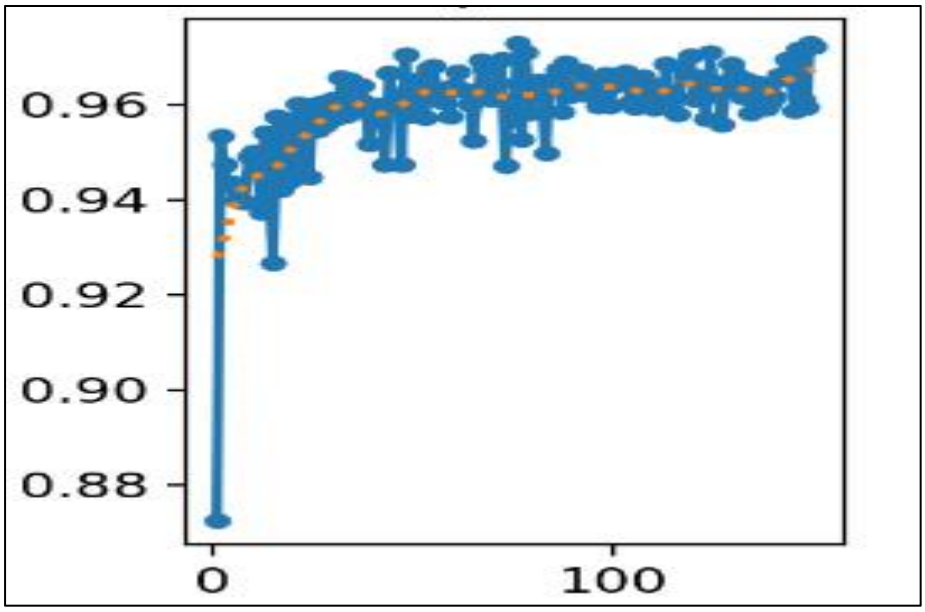

Figure 4: Training Graph

Annual Methodological Archive Research Review
http://amresearchreview.com/index.php/Journal/about
Online ISSN 3007-3197
Print ISSN 3007-3189
http://amresearchreview.com/index.php/Journal/a

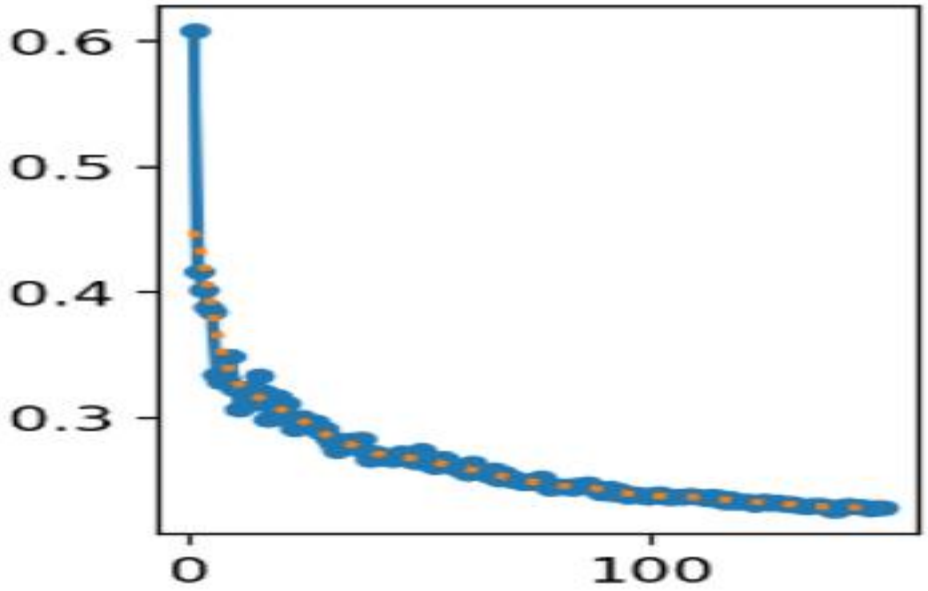

Figure 5: Loss Graph

The following confusion matrix is an evaluation of the accuracy of classification of RBC, WBC, and Background objects according to their predicted labels compared to their actual labels. The rows are the predicted labels while the columns are the actual labels.

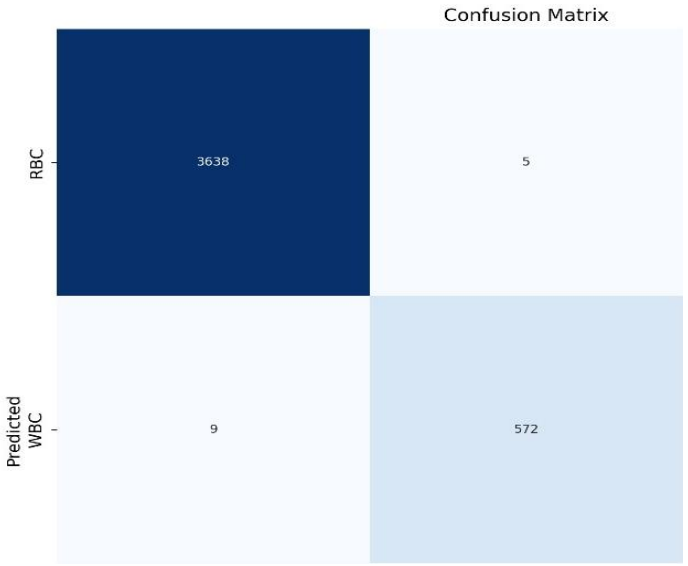

Figure 6: Performance Matrix

Based on the confusion matrix that are shown in figure 6, the performance of the suggested deep learning approach to detecting blood cells is outstanding. The number of RBCs detected was 3,638 and WBCs detected was 572, and there was a near perfect true positive ratio. There was only a small number of errors, as there were 9 RBCs that were detected as WBCs and 5 WBCs that were classified as RBCs. Therefore, the overall accuracy is 99.67%. This means that the model is highly accurate and robust when classifying RBCs from WBCs. The RBC detection algorithm is precise with fewer false positives, while the WBC detection algorithm is

Annual Methodological Archive Research Review
http://amresearchreview.com/index.php/Journal/about
Online ISSN 3007-3197
Print ISSN 3007-3189
http://amresearchreview.com/index.php/Journal/a

highly precise regardless of morphological variance. The red blood cells classification are shown in figure 7.

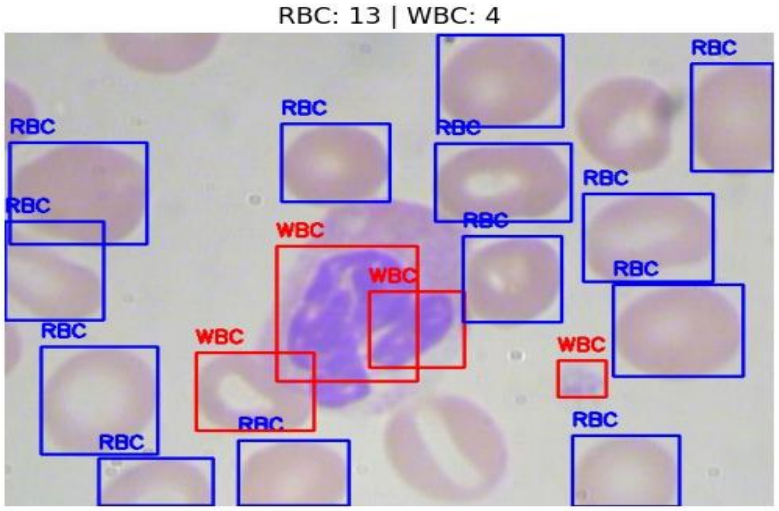

Figure 7: Blood Cell Classification

The suggested model has an overall accuracy of 99.67% while categorizing red and white blood cells (RBCs and WBCs). Both high F1-scores for the two classes suggest reliable and consistent results by providing a good trade-off between precision and recall. In addition, sensitivity is 99.86% for RBCs and 98.44% for WBCs, meaning that the system is capable of clearly distinguishing one cell from the other even in different imaging situations. Moreover, the results obtained from the confusion matrix show that only nine RBCs have been misclassified as WBCs and vice versa, which proves the successful distinction between the two even with a small number of mistakes. There are no significant errors caused by the background and other aspects usually occurring during the process of classification using conventional approaches that are shown in figure 8. However, the biggest problem to be solved still lies in the confusion of similar-looking RBCs and WBCs.

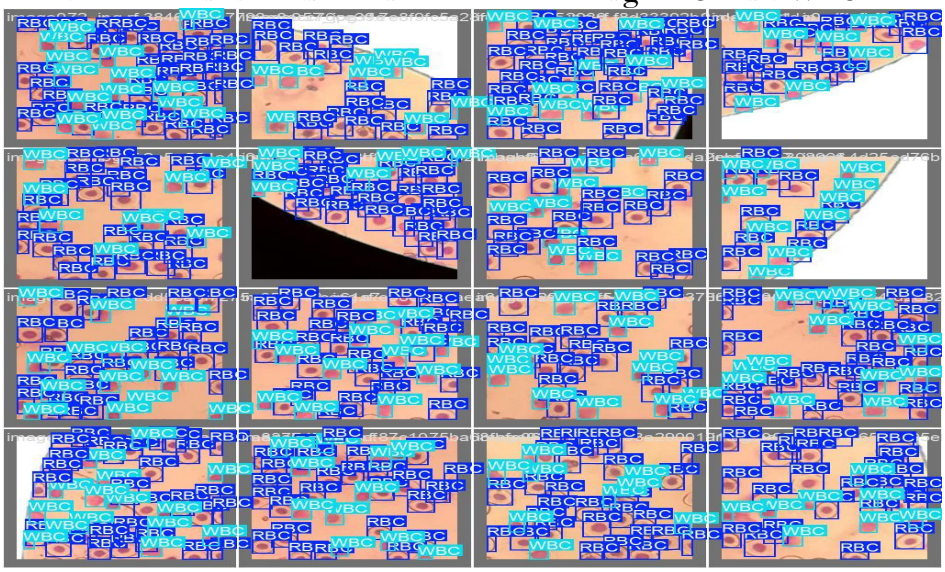

Figure 8: Blood Cells Classification and Enumeration

There are four main criteria to be taken into account when assessing a classification

Annual Methodological Archive Research Review
http://amresearchreview.com/index.php/Journal/about
Online ISSN 3007-3197
Print ISSN 3007-3189
http://amresearchreview.com/index.php/Journal/a

algorithm. These include accuracy, recall (sensitivity), precision, and the F1-score. With their help, we can analyze how efficient our model performs in classifying RBC and WBC with little mistake.

Accuracy is calculated as follows: (True Positives + True Negatives) / (TP + TN + FP + FN). For example, 99.67%.

Recall: TP / (TP + FN). For instance, 98.45%.

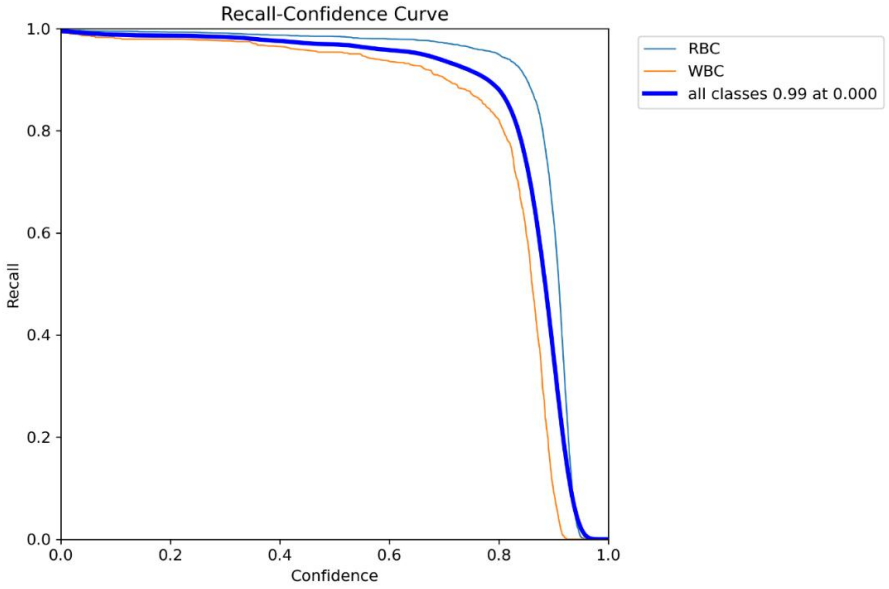

Figure 9: Recall Confidence Curve

Figure 9 illustrated the recall confidence Graph, the relationship between the recall of RBC and WBC classifications and confidence thresholds. In this graph, the X-axis denotes confidence while the Y-axis denotes recall. RBC is denoted by Light Blue and WBC by Orange; Overall is Thick Blue. Recall begins very high at first (<0.85) and then declines drastically; this implies that there were some missed targets. The model detects RBCs more effectively than WBCs because the curve of the former lies above that of the latter. The graph depicts the relationship between confidence and recall; the increase in confidence results in better recall and decrease in target misses. Miss rate shows how many actual positives were not predicted by the algorithm and is the inverse of recall, showing the frequency with which positives are missed. One should have a lower miss rate.

Miss Rate = 1 – Recall; hence, the miss rate is 1.55%.

Precision shows how good the prediction of the positives was. Precision is higher when there are fewer false positives.

Precision = TP/(TP+FP) = 99.13%

Online ISSN 3007-3197
Print ISSN 3007-3189

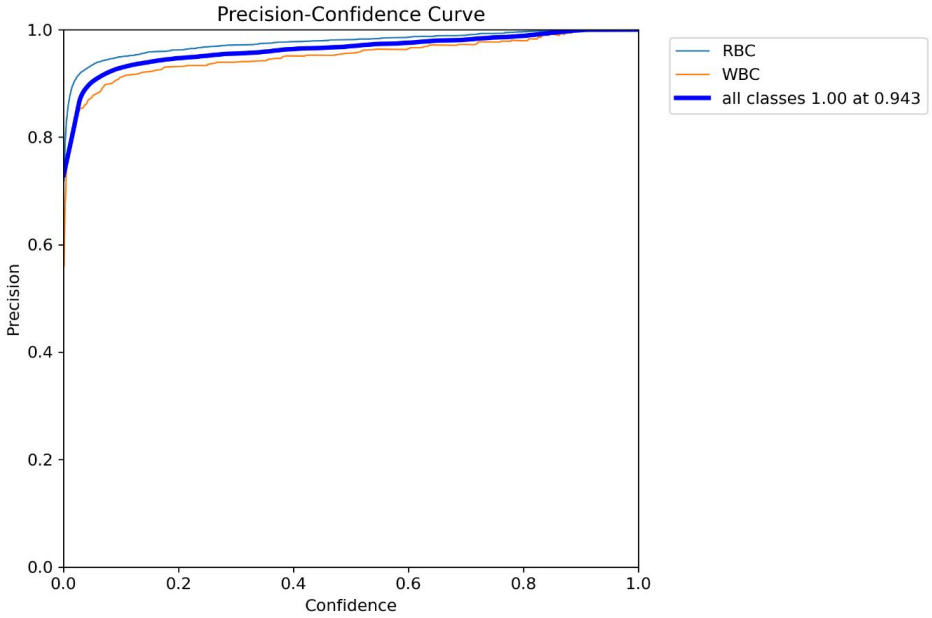

Figure 10: Precision Confidence Curve

Figure 10 represents the precision versus confidence Graph that demonstrates the relation between precision and confidence while classifying blood cells into RBCs or WBCs. X-axis represents Confidence, and Y-axis represents Precision. Blue for overall, light blue for RBC, and orange for WBC demonstrate that the graph shows the increase in precision with increase in confidence. Low confidence results in high false positives, most data points reach approximately 100 percent precision when the confidence is above 0.94. F1 Score measures the combined performance of precision and recall that are shown in table 1.

Table 1: Performance Evaluation

Class	Precision	Recall	F1-Score
RBC	0.9975 (99.75%)	0.9986 (99.86%)	0.9981 (99.81%)
WBC	0.9845 (98.45%)	0.9845 (98.45%)	0.9845 (98.45%)
Overall Accuracy	99.67%		

Conclusion

Deep learning-based automated classification and counting of blood cells is highly efficient in terms of employing distinctive features from microscope images. ML is capable of doing multi-class counting at minimal computational expense. The three datasets used dynamic staining and had no computational challenges. The algorithm managed to achieve an accuracy of 96% on classifying blood cells by taking advantage of the distinctive features provided by deep learning. Deep learning makes it possible for there to be real-time, high precision, high recall, and high F1 scores on the identification of blood cells. Automated identification helps in detecting anemia, leukemia, and infections. Model enhancements can include having more data, good segmentation, domain adaptation in the future, and its implementation in real-life scenarios for improving its interpretability, acceptability, and reliability among physicians.

Reference

Online ISSN 3007-3197
Print ISSN 3007-3189

[1] H. Abbad Ur Rehman, C. Y. Lin, Z. Mushtaq, and S. F. Su, "Performance analysis of machine learning algorithms for thyroid disease," *Arabian Journal for Science and Engineering*, vol. 46, no. 10, pp. 9437–9449, 2021, doi: 10.1007/s13369-020-05206-x.
[2] H. Abdallahi, *Automatic Analysis of Malaria Infected Red Blood Cell Digitized Microscope Images*, Ph.D. dissertation, University College London, London, U.K., 2016. [Online]. Available: https://discovery.ucl.ac.uk/id/eprint/1474475/
[3] P. Akbari *et al.*, "A genome-wide association study of blood cell morphology identifies cellular proteins implicated in disease aetiology," *Nature Communications*, vol. 14, no. 1, Art. no. 5023, 2023, doi: 10.1038/s41467-023-40679-y.
[4] J. G. Almeida *et al.*, "Computational analysis of peripheral blood smears detects disease-associated cytomorphologies," *Nature Communications*, vol. 14, Art. no. 39676, 2023, doi: 10.1038/s41467-023-39676-y.
[5] K. Almezhghwi and S. Serte, "Improved classification of white blood cells with the generative adversarial network and deep convolutional neural network," *Computational Intelligence and Neuroscience*, vol. 2020, Art. no. 6490479, 2020, doi: 10.1155/2020/6490479.
[6] R. Asghar, S. Kumar, and A. Mahfooz, "Classification of blood cells using deep learning models," *arXiv preprint* arXiv:2308.06300, 2023. [Online]. Available: https://arxiv.org/abs/2308.06300
[7] A. Bogdanova, L. Kaestner, G. Simionato, A. Wickrema, and A. Makhro, "Heterogeneity of red blood cells: Causes and consequences," *Frontiers in Physiology*, vol. 11, Art. no. 392, 2020, doi: 10.3389/fphys.2020.00392.
[8] F. Bozkurt, "Classification of blood cells from blood cell images using dense convolutional network," *Journal of Scientific, Technology and Engineering Research*, vol. 2, no. 2, pp. 81–88, 2021, doi: 10.53525/jster.1014186.
[9] P. K. Das, V. A. Diya, S. Meher, R. Panda, and A. Abraham, "A systematic review on recent advancements in deep and machine learning based detection and classification of acute lymphoblastic leukemia," *IEEE Access*, vol. 10, pp. 81741–81765, 2022, doi: 10.1109/ACCESS.2022.3196037.
[10] T. A. M. Elhassan, M. S. M. Rahim, T. T. Swee, S. Z. M. Hashim, and M. Aljurf, "Feature extraction of white blood cells using CMYK-moment localization and deep learning in acute myeloid leukemia blood smear microscopic images," *IEEE Access*, vol. 10, pp. 16269–16280, 2022, doi: 10.1109/ACCESS.2022.3149637.
[11] A. Gangadhar, H. Sari-Sarraf, and S. A. Vanapalli, "Deep learning-assisted holography microscopy for in-flow enumeration of tumor cells in blood," *RSC Advances*, vol. 13, pp. 4222–4235, 2023, doi: 10.1039/D2RA07972K.
[12] G. V. Grigorev, A. V. Lebedev, X. Wang, X. Qian, G. V. Maksimov, and L. Lin, "Advances in microfluidics for single red blood cell analysis," *Biosensors*, vol. 13, no. 1, Art. no. 117, 2023, doi: 10.3390/bios13010117.
[13] R. U. Khan, S. Almakdi, M. Alshehri, A. U. Haq, A. Ullah, and R. Kumar, "An intelligent neural network model to detect red blood cells for various blood structure classification in microscopic medical images," *Heliyon*, 2024, doi: 10.1016/j.heliyon.2024.e26149.
[14] H. Kim, A. Zhbanov, and S. Yang, "Microfluidic systems for blood and blood cell characterization," *Biosensors*, vol. 13, no. 1, Art. no. 13, 2023, doi: 10.3390/bios13010013.

Online ISSN 3007-3197
Print ISSN 3007-3189

[15] W. Kudisthalert, K. Pasupa, and S. Tongsima, "Counting and classification of malarial parasite from Giemsa-stained thin film images," *IEEE Access*, vol. 8, pp. 76334–76345, 2020, doi: 10.1109/ACCESS.2020.2990497.
[16] T. M. Makki and K. Al-Dulaimi, "Blood cell microscopic image classification in computer-aided diagnosis using machine learning: A review," *Iraqi Journal for Computer Science and Mathematics*, vol. 4, no. 2, pp. 43–55, 2023, doi: 10.52866/ijcsm.2023.02.02.002.
[17] A. Malkawi, B. Sheyab, R. Al-Assi, H. Alquran, T. Salameh, and A. M. Alqudah, "White blood cells classification using convolutional neural network hybrid system," in *Proc. IEEE 5th Middle East and Africa Conf. Biomedical Engineering (MECBME)*, 2020, pp. 1–6, doi: 10.1109/MECBME52094.2020.9265154.
[18] Z. Mousavi Kouzehkanan *et al.*, "A large dataset of white blood cells containing cell locations and types, along with segmented nuclei and cytoplasm," *Scientific Reports*, vol. 12, no. 1, Art. no. 1123, 2022, doi: 10.1038/s41598-021-04426-x.
[19] E. Nader, Y. Garnier, P. Connes, and M. Romana, "Extracellular vesicles in sickle cell disease: Plasma concentration, blood cell types origin distribution, and biological properties," *Frontiers in Medicine*, vol. 8, Art. no. 728693, 2021, doi: 10.3389/fmed.2021.728693.
[20] A. Sadafi, M. Bordukova, A. Makhro, N. Navab, A. Bogdanova, and C. Marr, "RedTell: An AI tool for interpretable analysis of red blood cell morphology," *Frontiers in Physiology*, vol. 14, Art. no. 1058720, 2023, doi: 10.3389/fphys.2023.1058720.
[21] A. Shah, S. S. Naqvi, K. Naveed, N. Salem, M. A. U. Khan, and K. S. Alimgeer, "Automated diagnosis of leukemia: A comprehensive review," *IEEE Access*, 2021, doi: 10.1109/ACCESS.2021.3114059.
[22] M. Shahzad *et al.*, "Blood cell image segmentation and classification: A systematic review," *PeerJ Computer Science*, vol. 10, Art. no. e1813, 2024, doi: 10.7717/peerj-cs.1813.
[23] H. Song and Z. Wang, "Automatic classification of white blood cells using a semi-supervised convolutional neural network," *IEEE Access*, vol. 12, pp. 1–10, 2024, doi: 10.1109/ACCESS.2024.3380896.
[24] C. Trejo-Soto, G. R. Lázaro, I. Pagonabarraga, and A. Hernández-Machado, "Microfluidics approach to the mechanical properties of red blood cell membrane and their effect on blood rheology," *Membranes*, vol. 12, no. 2, Art. no. 217, 2022, doi: 10.3390/membranes12020217.
[25] F. Ucar, "Deep learning approach to cell classification in human peripheral blood," in *Proc. 5th Int. Conf. Computer Science and Engineering (UBMK)*, 2020, doi: 10.1109/UBMK50275.2020.9219480.
[26] F. Zhang *et al.*, "Causal association of blood cell traits with inflammatory bowel diseases: A Mendelian randomization study," *Frontiers in Nutrition*, vol. 11, Art. no. 1256832, 2024, doi: 10.3389/fnut.2024.1256832.
[27] H. Zhong *et al.*, "Using blood transcriptome analysis for Alzheimer's disease diagnosis and patient stratification," *Alzheimer's & Dementia*, 2023, doi: 10.1002/alz.13691.