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An Intelligent Approach for Blood Cell Detection Employing Faster RCNN

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Abstract- **A CBC (complete blood count) is essential to a thorough medical evaluation. The practice of medicine has had a significant impact on popular methodologies, such as manual counting and automated analyzers. The shape of blood cells and other cellular characteristics are highly sensitive to contamination levels in the human body. Tiny blood cell images are studied to spot disease and deviations from the norm that may indicate internal contamination. Correct cell segmentation enables more precise and powerful disease detection. Examining blood cells under a microscope is an important part of any pathological investigation. It emphasizes the examination of the correct malady after pinpointing its precise location and then ranking its anomalies, which plays a crucial role in determining the nature of a patient's condition, planning treatment, and evaluating the outcome of that treatment. Initially, the complete blood count (CBC) test of the patient is carried out if the report suggests that the blood is abnormal than the blood is poured on the strip and blood is stained out through the addition of coagulant. Expert hematologists are in short supply, particularly in underdeveloped nations, and are frequently overwhelmed. To help them with their burden, we provide a unique method for the automated assessment of family disease using artificial intelligence on blood smear images in this paper. Object detection needs to be quick and good at finding different things in an image to be useful in real life. Object detection improvements have been made, such as the Convolutional Neural Network and R-CNN family. Our research employs Faster R-CNN to look for RBCs, WBCs, and Platelets in the Blood Cell Count (CBC) and Detection dataset. The number, shape, and other meta-information, or any abnormalities in the different parts of blood, could help find problems and diseases like leukemia, anemia, lymphoma, sickle cell disease, thrombocytopenia, and leukopenia early on. Our model is accurate enough to find a bounding box on the blood parts. A box is drawn along with their name around the various components of the blood smear slide. Improving the efficiency and precision of cell detection is possible with the aid of the revolutionary algorithm. When it comes to determining the identities of moving cells, the approach offers significant benefits.**

***Index Terms*--** **Blood smear Images, Complete blood count, microscopic images, disease detection, RBC, WBC.**

I. INTRODUCTION

Typically, a person's health is determined by analyzing the various characteristics and numbers of blood cells. Previously, pathologists employed manual blood cell analysis techniques. It could lead to errors in disease prediction, as manual methods rely on the experience and expertise of pathologists. A drop of blood is deposited on a microscope slide. A spreader slide is dragged rearward over the drop to distribute the blood throughout the slide evenly. It is recommended that the spreader slide be slanted at an angle of 30°–45° concerning the blood base slide to achieve the highest level of precision and accuracy in the smear. Staining is performed after the blood smear has been dried using an air dryer. Absolute methanol or ethyl alcohol is employed to restore dried smears. After that, it's stained with one of several different liquids, such as the Leishman stain, rewmanosky stain, the may-grawald giema, or the Wright- Giemsa stain. This preparation of stained slides is then examined under a microscope. The microscopic image is then imported into the Artificial intelligence algorithm, where red and white blood cells are detected. A bounding box is drawn against each RBC employing the Faster RCNN algorithm. After that, patches are retrieved from RBC images and then classified using a deep learning algorithm. Consequently, it is proposed that a system of automated image processing be developed using various algorithms. It means that diseases could potentially be predicted and detected by analyzing microscopic images of blood. Disease detection needs to be simplified, automated, and cost-effective. Thus, the components above are analyzed to determine the health status of humans and thus to detect health-related anomalies. Blood is made up (Composed) of red blood cells (RBCs), white blood cells (WBCs), platelets, and plasma., the body's most vital fluid. Human blood may be broken down into two distinct components: cells and platelets, which account for roughly 45%, and plasma, the yellow fluid

that makes up the remaining 55% [1, 2]. When an object or microorganism from the outside makes its way into the bloodstream, it alters the physical qualities of the blood's components, including their size, shape, colour, and number. Diseases could be detected by a variety of pathological methods [3]. Microscopic imaging is often crucial in diagnosing diseases and predicting anomalies within the body. Antibodies of phagocyte foreign items, healing damage, defending against invading pathogens, and disease immunity are all tasks that rely heavily on the white blood cells. The first step in diagnosing an illness is determining how many white blood cells are present. Being able to identify white blood cells is crucial in the domain of clinical medicine. Extraction techniques for leukocytes have advanced to include the following in recent years. Thresholding [1], Region growth [2], Fuzzy clustering [3], Watershed [4], Means [5], and Edge detection [6] are just a few examples of the more conventional algorithms that have been used to segment white blood cells over the past five years. Kumar, Vagoda utilized the K-means clustering algorithm and Amin to separate white blood cell nuclei based on colour space [7-9]. White blood cell classification employing a learning-based deep convolutional neural network (CNN). Utilizing Caffe as a foundation and manual feature extraction to characterize white blood cells, Chen chang developed a leukocyte classification system [10].

In [11], Jia Hongfei retrieved white blood cells using a conventional algorithm, which was only 95% accurate when classifying white blood cells. White blood cell extraction accuracy impacts total classification accuracy. Traditional algorithms struggle with blood smear images because of their high resolution, high number of red blood cells, and the low number of white blood cells relative to the size of the image. Extracting cells manually takes a long time, a problem for large-scale studies. Segmenting adherent cells is challenging with conventional algorithms due to their lacklustre anti-noise abilities and extensive processing. High-throughput imaging and other clinical applications rely heavily on the ability to detect cells and classify cell types from biomedical images. Single-cell sample classification could be accomplished by employing conventional machine learning and computer vision techniques.

In contrast, analysis of multilabel samples (regions containing congregating cells) is more difficult since individual cell separation might be difficult, if not impossible (e.g., touching cells or overlapping cells).

To overcome the difficulty of evaluating multi-instance images when studying Red Blood Cells (RBCs), We develop a multi-instance cell identification and classification method for utilization in diagnosing the family of blood diseases. The method starts with staining the blood sample, then blood strips are prepared, and smear images are visualized under an optical microscope. This microscopic image is then fed into the model, which draws a bounding box against each RBC and WBC. Then each RBC is drawn individually for morphological study to predict the family of disease. Six networks are trained to employ these visual attributes as inputs for multilabel prediction of whether or not a particular patch includes cells of a certain cell type. The six networks could accurately identify cell types presented in multi-instance picture samples because they are trained on patches consisting of isolated cells and cells that touch or overlap. Finally, we employ the results from these six networks to create a machine-learning classifier that could determine whether or not a given picture patch contains an aberrant cell type for utilization in SCD testing. The experimental outcomes prove the viability of the proposed architecture for autonomous cell detection and classification.

II. LITERATURE REVIEW

Due to the time and effort required for manual evaluation of RBC images, automatic categorization and diseased cell detection based on cell texture and morphological traits have emerged as a viable and useful strategy for Sickle cell disease (SCD) diagnosis. More generally, high-throughput imaging and many other clinical applications rely heavily on automatic cell detection and type classification. Several tools, such as Cell Profiler [1], Cell Track [2], and Study in [3], have been created for the goal of cell detection and classification. Deep learning-based approaches [4]-[6] have recently demonstrated better performance in biomedical image analysis tasks such as cell categorization, detection, semantic segmentation, and counting. These techniques can extract more discriminative picture features with higher generalizability.

The occurrence of several cells congregating together in one sample image patch is a recurrent difficulty, even though deep learning-based techniques have shown good performance in categorizing single-cell patches [12]-[13]. To address this issue, we refer to it as the "multilabel classification" problem, where it is difficult (due to, for example, touching cells) or impossible (due to, for example, overlapping cells) to entirely separate specific instances of those samples. Because typical classifiers are taught to handle a single occurrence simultaneously, multilabel samples are deleted [5] during training. They might lead to inaccurate classification results if they are included in testing data. However, this multilabel classification issue is crucial because overlapping and contacting cells are ubiquitous in microscopic images. CapsNet [6] is one of the multi-instance techniques developed in the past; it has inspired various applications due to its ability to analyze objects that overlap significantly. Recent CapsNet-based models have primarily addressed the classification problem with a single label [6]-[8], given that many instances of the same class cannot be depicted in the original CapsNet illustration.

The multilabel RBCs classification problem is too complex for CapsNet to handle because of the large number of patches containing clusters of cells belonging to the same class. This research aimed to enhance Blood disease diagnosis by resolving the problem of multilabel classification in biomedical image processing. This research presents an infrastructure for cell detection and classification that could automatically extract image patches containing single or multiple cells. We then apply multilabel classification and aberrant cell detection to these regions. There are three phases to the plan put forward. We first

employed a Faster-RCNN to segment a tiny picture into single-cell and multicell patches automatically. After using a bounding box against each red and white blood cell in the patches, we extract individual RBCs for morphological structure investigation to make disease family predictions from the resulting images. The following are some of the primary improvements that our method provides. At first, this study utilizes the Faster RCNN identification of cells in RBC microscopic images. Finally, we present a straightforward yet powerful multilabel classification strategy that could simultaneously categorize single-cell patches and groups of cell patches. Whole microscopic images are used for training and testing the suggested method. The proposed framework is effective for the automatic detection and multilabel classification of RBCs, as evidenced by the high accuracy achieved in both tasks. This is the first study to tackle the challenge of classifying RBCs using several labels. Various approaches employed for detecting blood disease are discussed below in Table I.

TABLE I
VARIOUS APPROACHES EMPLOYED FOR BLOOD DISEASE DETECTION

Ref	Method	No of Images	Accuracy	Remarks
[10]	CNN, GLCM	256	BPNN 93.2% CNN 92.6%	Fewer samples
[11]	ANN	473 Cases	96.5%	Employing RDW, MCV, RDW
[12]	KNN, Watershed segmentation	100	For Thalassemia & SCA 80.6%	Combined method was developed.
[13]	GLCM Features, ANN	100	For IDA 75-81%	Classified 4 types of poikilocytes
[14]	Deformable U-Net	266	For SCD RBC 99.12%	Method may separate RBCs despite their fuzziness, clustering, or irregular shapes.
[15]	Multiclass SVM Deep Learning	Among 100 to 250	For SCD 99.5%	Present three CNN models with varying numbers of layers and filter functions.
[16]	Naive Bayes, random forest	200	96.1 %	Utilized 18 features from CBC reporting
[17]	Deep learning Alex Net	750 Single RBC	For SCA 95.9%	Since there were fewer normal cells, specificity was low.
[18]	Semantic Segmentation U-Net	96 Sample	For SCD 98%	Designed mobile phone microscope
[19]	SVM, MLP and KNN	304	SVM 83% MLP 92%	Using the RBC, MCV, Hb, and HCT parameters

III. METHODOLOGY

The Feature Network, the Detection Network, and the Region Proposal Network are the three distinct neural networks that go into the construction of Faster R-CNN (RPN) (see Fig. 1). The input image is used to create feature maps by the Feature Network. The network's output preserves the original image's form and structure. Convolutional layers are found in RPN, which has three total. BOTH bounding box regression and classification share a single input layer. Bounding boxes representing regions of interest are created by RPN. These boxes have a high probability of containing the objects in question. In addition to the bounding boxes, a value (1) if the object is inside the box, (0) if it is outside, and (-1) if it could be ignored) is also generated. During the testing phase, the top N proposals out of roughly 2k are used. The Detection Network is in charge of generating the final class and bounding boxes, and it receives its data from both the Feature Network and the RPN.

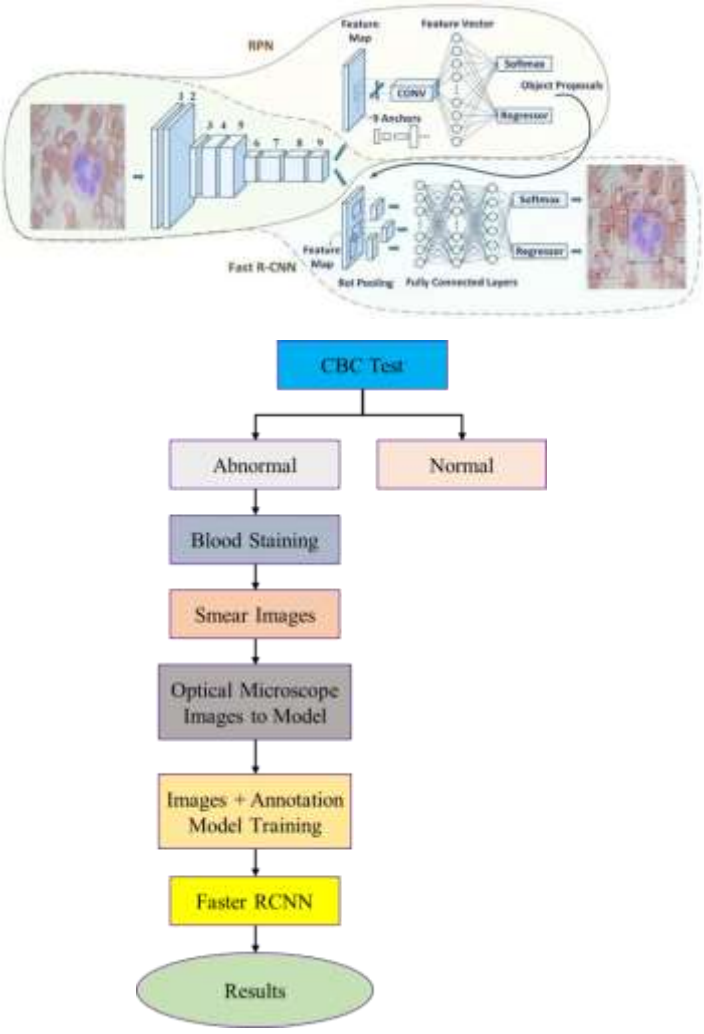

FIGURE 1: Working Flowchart of Faster RCNN

The Detection Network consists of four interconnected layers. In a layered design, the bounding box regression

layer and the classification layer share layers 2 and 3. To aid in the identification of the bounding box contained within an image, the Detection Network's features are clipped. To accomplish this, this study employs bounding boxes to do our cropping. This research utilized a public data set that included information about blood cells. There are 364 images of blood cells in the original data set, and their original resolution was 640 pixels by 480. The dataset includes three types of blood cells: red blood cells, platelets, and white blood cells. Figure 2 displays several database samples.

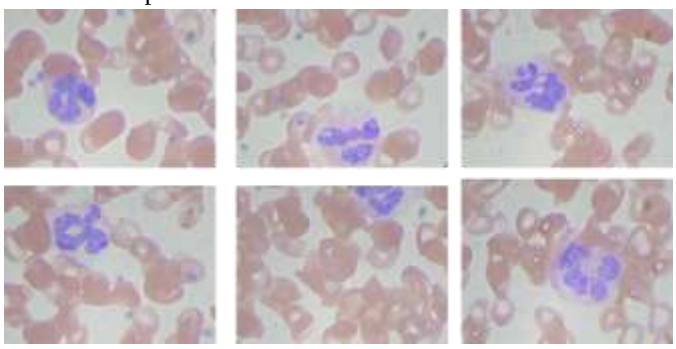

FIGURE 2: BCCD Image Dataset

After meticulously compiling the dataset, we discovered that it possesses the following traits. 1. (a) Red blood cells (RBCs) make up a larger percentage of human blood cells. Thus, RBSs are linked and often overlap in the resulting data image, while WBCs and platelets are typically found singly 2. The data images reveal that there are significant color differences only slight variances, which makes sense given that different cells often have distinct forms. Platelets are the tiniest blood cells, whereas white blood cells (WBCs) are the largest 3. The pictures included in this dataset were acquired in a controlled laboratory setting using high-quality medical imaging equipment. As a result, there is a lot of consistency between the images in terms of brightness and darkness.

A uniform, uncomplicated background is used throughout the image. 4. Due to the field of view constraints or image clipping, some cell images would be cut off at the image's edges. 5. The dataset only contains a tiny number of photos and few total samples. There are 364 photos of blood cells in the original image data file, and each of those images has a corresponding mark file that labels its position and category information. We improved by slicing. We improved the dataset by tenfold, to ten thousand records, and matched the tagged files accordingly. We conducted our experiment using a dataset [12] of blood cell smear images. The Blood Cell Count and Detection (BCCD) Dataset was created to detect blood cells. This study employs the Keras implementation of Faster R-CNN to recognize the cellular component of blood in blood smear slide images. Keras is a Python library that operates on the TensorFlow or Theano backend [14]. Keras 2.2.4 was combined with TensorFlow 1.15.0 for this project. Faster R-CNN was copied from the GitHub repository [15], where the Keras implementation was found. A model was trained with train frcnn.py. After a successful training session, train frcnn.py wrote the training weights to an hdf5 file and the training run's configuration to a pickle file. Using the test pictures supplied to the model, the inference was carried out using the pre-trained weights, and the settings read in when running test frcnn.py. You can see how our model functions in the diagram below. It has created bounding boxes around several image features and labelled them with their respective classes.

IV. RESULT

In this section, we present the results of our analysis. There were 72 pictures in the test folder that was given to the model. Platelets, white blood cells (WBCs) and red blood cells (RBCs), all had their expected box boundaries included in the model. We compared the model's anticipated number of red blood cells, white blood cells, and platelets in test photos with our manual count. Accuracy for the RBCs was calculated at 91.83%. It's because it's hard to visually distinguish between individual erythrocytes when they're packed together in clusters like in the examples above. Predictions of the WBCs were accurate to within 2.10%. White blood cells, or WBCs, are larger than red blood cells, or Erythrocytes, and may be easily identified on blood smear slides as massive blots. This allowed for more precise forecasting of WBC. The accuracy for predicting platelets was 88.36%. The predictability of platelets is low since they appear as tiny bright dots on a microscope slide. For 1000 iterations, the model was trained. It has been shown that increasing the epoch size improves accuracy across the board for all cell types.

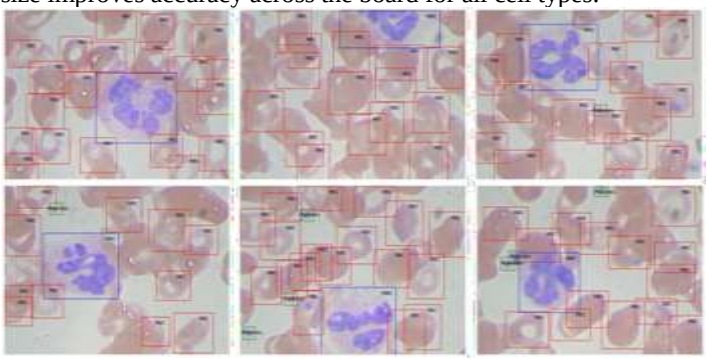

FIGURE 3: Preprocess Images

The results shown in Fig. 3 were obtained from experiments in which the anchor box was left unchanged, altered in size, or altered in proportion.

a) Experimentation revealed that altering the anchor box ratio to match the ratio of cell morphology improved the precision and decreased anchor boxes. Though, this method was not effective in detecting stacked cells. Future research should consider using morphology-based tools such as the watershed algorithm.

b) The good results for recognizing stacked cells and detecting small targets like platelets after modifying the anchor box scale. However, the process was slowed down due to the larger number of anchor boxes created. Additionally, manual labelling is often used to label cell data sets, which means that the accuracy of the labels is dependent on the quality of the labelling workers. Furthermore, labelling platelets in cell data sets are often imprecise due to their small size, and

adjusting the anchor box scale does not produce desirable results (see Table II).

TABLE II

Time Performance Analysis

Method	MTT	TTT
Faster RCNN (ResNet 50 & Anchor box)	2.61	176.473
Faster RCNN (ResNet 50 & Reduced Anchor box)	0.75	52.312
Faster RCNN (ResNet 50)	0.852	60.681

The curves of the loss functions for the various experimental approaches are depicted in Fig. 4. In the instance of epoch, the three-way drop rate was relatively constant both before and after modifying the anchor box. However, the loss was less severe when the anchor box ratio was modified than it would have been without the modification. The amount of time needed to progress one level once the scale slightly increased.

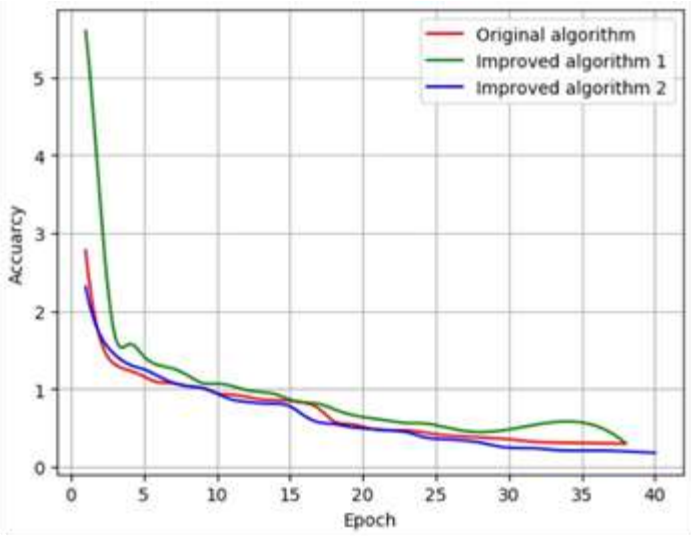

FIGURE 4: Experimental strategies for Loss function

The cell form stabilizes for the ratio of one-to-one, one-to-two, and two-to-one to one-to-one following the morphological properties of cells. As a result, once the anchor box ratio is optimized for the experimental data, which dramatically improves search speed. By focusing on the subset of the search that corresponds to the target graphics attributes, the strategy improves MAP while increasing the precision with which it can recognize cells. Experiments on-time performance reveal that an optimized anchor box ratio can somewhat boost MAP and performance. The anchor box ratio was shifted to [16,32,64,128,256] to detect the tiny, hard-to-see target platelets. Increases in the ratio result in a corresponding rise in the total number of anchor boxes. As a result, MAP and temporal performance suffer from diminished computational power.

Meanwhile, the inclusion of finer scales improves the clarity of small objects and cell stacks, making it much simpler to spot tiny targets like platelets and stacked red blood cells. The study recommends a strategy to enhance the effectiveness. The method improves the efficiency of model detection in less time by optimizing the network structure to collect cell properties.

V. CONCLUSION

Object Detection's many applications in computer vision and image processing help steer humanity toward a more promising future. Numerous methods have been devised since the invention of object detection to improve the speed and accuracy with which it may be applied to detect objects in moving or still images. To better understand how different blood cell types develop into erythrocytes, leukocytes, and platelets, we applied Faster R-CNN. Faster R-application CNN's to blood cell images reveals that it detects boundary boxes for WBCs with higher accuracy than RBCs. This is the case for various reasons, including the larger size of WBCs compared to RBCs and the fact that RBCs are often found in clusters in the blood, making it challenging to get precise tangible images in blood slides. Increasing the number of epochs used in training improves the model's overall accuracy. This study provides the Fatser R-CNN model, specifically designed to overcome obstacles in blood cell detection.

Experiments revealed improved MAP and time performance when the anchor box ratio was modified. Changing the anchor box's size has a negative effect on MAP and recognition speed, although even small targets and groups of RBCs are easily identified. Detection in a cell flow video could also be performed with respectable MAP efficiency. The setup can be further improved to enhance the precision and speed due to the small sample size and short period. For large data sets, adding labels to the training process could improve test accuracy and help produce a better-tailored model for future use. Using many data sets, the detection accuracy of multi-scale and stacked cells might be improved using techniques. When more advanced algorithms are created, and more extensive data sets are amassed. The system's usefulness extends beyond its original intent of detecting cells in images.

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The authors declare they have no conflicts of interest to report regarding the present study.

CONFLICT OF INTEREST

The Authors declare that they have no conflicts of interest to report regarding the present study.

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