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EFFICIENT CNN-BASED CLASSIFICATION OF WHITE BLOOD CELLS: A COMPARATIVE STUDY OF MODEL PERFORMANCE

Achraf Benba[1], **Sara Sandabad**[2]

[1]Mohammed V University in Rabat, Electronic Systems, Sensors and Nanobiotechnologies, National Higher School of Arts and Crafts, Rabat, Morocco,
[2]Higher Institute of Maritime Studies, Casablanca, Morocco

Abstract. *White blood cells (WBCs) are integral components of the immune system, playing a pivotal role in defending the body against various diseases and infections. Accurate quantitative and qualitative analysis of different WBC types is essential for the effective diagnosis and treatment of numerous medical conditions. Counting and classifying these cells are fundamental steps in blood sample examination and testing. This study focuses on evaluating three convolutional neural network (CNN)-based architectures – ResNet-50, VGG-16, and a classic CNN – for classifying blood cell image categories using a curated dataset from Kaggle. We trained and evaluated each model's performance using accuracy curves, confusion matrices, and classification reports. Among the tested architectures, the ResNet-50 model achieved the highest validation accuracy of approximately 80%, followed by VGG-16 at 79.6% and the classic CNN at 76.2%. Both VGG-16 and the classic CNN exhibited significant overfitting, with large gaps between training and validation accuracy. These findings highlight the challenges of image classification on imbalanced datasets and suggest directions for future improvements through data augmentation and architectural refinements.*

Keywords: white blood cells (WBCs), Convolutional Neural Network (CNN), medical image classification, hematological analysis, deep learning in healthcare

WYDAJNA KLASYFIKACJA BIAŁYCH KRWINEK W OPARCIU O CNN: BADANIE PORÓWNAWCZE WYDAJNOŚCI MODELI

Streszczenie. *Białe krwinki (WBC) są integralną częścią układu odpornościowego i odgrywają kluczową rolę w obronie organizmu przed różnymi chorobami i infekcjami. Dokładna analiza ilościowa i jakościowa różnych typów białych krwinek jest niezbędna do skutecznej diagnostyki i leczenia wielu schorzeń. Liczenie i klasyfikacja tych komórek to podstawowe etapy badania i analizy próbek krwi. Niniejsze badanie koncentruje się na ocenie trzech architektur opartych na konwolucyjnych sieciach neuronowych (CNN) – ResNet-50, VGG-16 i klasycznej CNN – pod kątem klasyfikacji kategorii obrazów komórek krwi przy użyciu wyselekcjonowanego zbioru danych z serwisu Kaggle. Przeszkoliliśmy i oceniliśmy wydajność każdego modelu przy użyciu krzywych dokładności, macierzy pomyłek i raportów klasyfikacyjnych. Spośród testowanych architektur model ResNet-50 osiągnął najwyższą dokładność walidacji wynoszącą około 80%, a następnie VGG-16 79,6% i klasyczna CNN 76,2%. Zarówno VGG-16, jak i klasyczna sieć CNN wykazały znaczne nadmierne dopasowanie, z dużymi różnicami między dokładnością szkolenia a dokładnością walidacji. Wyniki te podkreślają wyzwania związane z klasyfikacją obrazów w niezrównoważonych zbiorach danych i sugerują kierunki przyszłych ulepszeń poprzez rozszerzenie danych i udoskonalenie architektury.*

Słowa kluczowe: białe krwinki (WBC), konwolucyjna sieć neuronowa (CNN), klasyfikacja obrazów medycznych, analiza hematologiczna, głębokie uczenie się w opiece zdrowotnej

Introduction

In human blood, approximately 45% of the volume is occupied by blood cells, while the remaining 55% consists of plasma, the liquid component of blood. Blood comprises three primary types of cells: red blood cells, white blood cells, and platelets. Red blood cells are called erythrocytes, white blood cells are known as leukocytes, and platelets are referred to as thrombocytes. White blood cells are generated in lymphoid tissue and bone marrow and can be categorized into two groups: granulocytes and agranulocytes. Granulocytes include neutrophils, basophils, and eosinophils, while agranulocytes are classified as monocytes and lymphocytes. Each type of cell plays a unique role in defending the body against infections and diseases [1].

White blood cells (WBCs) are vital components of the immune system, playing a crucial role in resisting a wide range of diseases. Consequently, it is essential to perform quantitative and qualitative assessments of different types of WBCs. Counting these cells is particularly valuable for physicians as it aids in detecting and treating conditions such as leukemia [6]. As a result, accurately enumerating the various types of WBCs is a pivotal step in blood sample analysis and evaluation.

Two primary approaches are employed to analyze and quantify different types of WBCs in blood samples: manual (non-automatic) and automated methods. In non-automatic methods, blood samples are manually examined by specialists. However, this process is slow, labor-intensive, time-consuming, and susceptible to human error. By contrast, automated systems are available for the quantitative evaluation and classification of WBCs. These systems utilize flowmeters and the chemical properties of the cells. Although automated systems can provide reliable quantitative data, they are often costly and relatively slow in operation.

To address these limitations, computer-aided techniques have been developed to streamline blood cell classification and reduce human errors. These techniques automate the process of identifying and classifying WBCs in blood cell images. Image classification models, such as Convolutional Neural Networks (CNNs), VGG, and RESNET, are particularly effective and widely used for this purpose [5, 9].

The primary objective of this study is to employ a CNN-based model to process white blood cells (WBCs) and accurately classify their types. This research focuses on detecting and identifying the different types of WBCs present in blood cell images, providing a reliable and efficient approach to WBC classification.

1. Related works

In recent years, various deep learning techniques have been proposed for the classification of white blood cells (WBCs). Cheuque et al. [2] introduced a hybrid, multi-level model in 2021 that significantly advanced WBC classification. Their approach utilized a Faster R-CNN network in the initial phase to identify regions of interest corresponding to white blood cells and differentiate between mononuclear and polymorphonuclear cells. In the subsequent phase, two parallel convolutional neural networks with MobileNet architecture were employed to classify the subtypes of WBCs. This innovative model achieved remarkable performance, with an accuracy of 98.4%, along with high precision, recall, and F1 score, using the Kaggle blood cell dataset.

Similarly, Çınar and Tuncer [3] in 2021 developed a hybrid CNN model that combined AlexNet, GoogLeNet, and Support Vector Machines (SVM). In their approach, feature vectors extracted from the final pooling layers of AlexNet and GoogLeNet were integrated and classified using SVM. Their model achieved exceptional accuracy rates of 99.73% and 98.23% on the Kaggle and LISC datasets, respectively. However, the total and trainable parameters of their model were not specified in their study.

In another significant study, Ekiz et al. [4] proposed a model for WBC classification in 2021 that utilized convolutional features combined with SVM. Although their model achieved an accuracy of 85.95%, it highlights the potential of leveraging traditional SVM methods with deep learning features.

Toğaçar et al. [11] in 2020 implemented three pre-trained models – GoogLeNet, AlexNet, and ResNet-50 – for feature extraction, followed by quadratic discriminant analysis (QDA) for classification. Their approach effectively classified WBC types with an accuracy of 97.95%. The authors further enhanced the model's performance through feature selection techniques during the classification stage.

In 2019, Özyurt [8] proposed a hybrid CNN-MRMR-ELM model. This model utilized pre-trained CNN architectures, including AlexNet, GoogLeNet, VGG-16, and ResNet, for feature extraction. The most relevant 400 features were selected using the Minimum Redundancy Maximum Relevance (MRMR) technique. These features were then classified using the Extreme Learning Machine (ELM) algorithm, achieving an impressive accuracy of 96.03%.

Earlier, in 2018, Vatathanavaro et al. [12] explored the use of two CNN architectures, VGG-16 and ResNet-50, for the classification of five WBC types. Among these, ResNet-50 demonstrated superior performance, achieving an accuracy of 88.3%.

Similarly, Nahzat et al. [7] in 2022 developed a CNN-based model for WBC classification using the Kaggle blood cell dataset, the same dataset employed in the present study. Their model was assessed with several optimizers, and the RMSprop optimizer yielded the best classification results.

2. Materials and methods

2.1. Dataset

This research utilized white blood cell images sourced from the Kaggle platform. The Kaggle dataset, titled "Blood Cell Images", comprises a well-curated collection of human blood cell images extracted from blood smears. The dataset contains a total of 2,502 images, classified into three distinct categories: TEST (497 images), TEST_SIMPLE (14 images), and TRAIN (1,991 images). Each image has dimensions of 320×240×3 and is meticulously labeled with its corresponding cell type, making it a highly annotated and reliable resource for machine learning applications. To prepare the images for model training, preprocessing techniques including resizing to 224×224 pixels and pixel value normalization (rescaling to [0, 1]) were applied. These steps ensured the images were standardized and suitable for downstream analysis. Published in 2017 by Paul Mooney, this Kaggle database serves as a valuable and widely accessible resource for medical imaging research. It has been extensively employed for training image classification and deep learning models, as well as for investigating innovative approaches to medical image segmentation and analysis.

2.2. Data preparation and pre-processing

We performed a data split of 80% for training and 20% for validation using Keras's ImageDataGenerator with a validation_split parameter of 0.2. Image pixel values were normalized by rescaling to the range [0, 1] (dividing by 255). All images were loaded in batches of 32 using the flow_from_directory method, with categorical class mode for multi-class classification. All three models were trained for 100 epochs using the Adam optimizer and categorical cross-entropy loss function.

For preprocessing, the images were resized to dimensions of 224×224×3, as this specific input size is required by all three architectures (VGG16, ResNet50, and the custom CNN). This resizing step ensures uniform input dimensions across models while maintaining image quality for effective feature extraction and classification.

2.3. VGG16 architecture

The VGG16 (short for VGG-16) is a highly regarded convolutional neural network (CNN) architecture developed by the Visual Geometry Group (VGG) at the University of Oxford. As its name suggests, the model contains 16 layers and has been extensively used in the field of computer vision.

CNN architectures typically consist of two main components:

1. Feature extractor: Also referred to as the "backbone" or "body," this component extracts meaningful features from the input image. In VGG16, this role is fulfilled by five convolutional blocks, each containing a sequence of convolutional layers that progressively learn complex features. In our implementation, the pre-trained VGG16 base is loaded with ImageNet weights and all its layers are frozen (non-trainable), preserving the learned feature representations during training.
2. Classifier: Often called the "head," this component converts the extracted features into class predictions. In our implementation, the original VGG16 classifier is removed (include_top=False), and the feature maps are passed through a Flatten layer followed by a fully connected Dense layer with 256 neurons and ReLU activation, culminating in a softmax output layer.

VGG16 was initially trained on the ImageNet dataset, which contains 1,000 classes. In this study, we employ a transfer learning approach by loading the pre-trained VGG16 weights and freezing all base layers to preserve the learned feature representations [10]. The original 1,000-class output layer is replaced with a custom classifier consisting of a Flatten layer, a Dense layer with 256 neurons and ReLU activation, and a final Dense layer with softmax activation matching the number of target classes. This configuration allows the model to leverage VGG16's powerful feature extraction while adapting the classification head to the specific blood cell classification task.

2.4. ResNet50 architecture

ResNet50 is another widely used deep convolutional neural network architecture in computer vision, designed to process images with dimensions of 224×224×3. In this study, we employ a transfer learning approach using a ResNet50 model pre-trained on the ImageNet dataset, with all base layers frozen to retain the learned feature representations. ResNet50 stands out for its innovative use of residual blocks, which allow the training of deep networks without suffering from performance degradation.

1. Residual blocks: Each block contains convolutional layers, batch normalization, and residual connections. These connections address the vanishing gradient problem by enabling information to skip layers, improving training efficiency and performance.
2. Layer composition: The architecture includes a sequence of residual blocks interspersed with pooling and normalization operations, ensuring robust feature extraction.

In our implementation, the original classification head of ResNet50 is removed (include_top = False), and the extracted features are passed through a Global Average Pooling layer, which reduces each feature map to a single value by computing its spatial average. This is followed by a fully connected Dense layer with 256 neurons and ReLU activation, and a final Dense layer with a softmax activation function that outputs class probabilities. This architecture allows the model to leverage the powerful feature extraction capabilities of ResNet50 while adapting the classifier to the specific task at hand.

2.5. Classic CNN architecture

In addition to the pre-trained models, a custom CNN was designed from scratch to serve as a baseline comparison. The architecture is a sequential model that accepts input images of 224×224×3 dimensions. It consists of three convolutional blocks, each comprising a Conv2D layer followed by a MaxPooling2D layer. The first block uses 32 filters with a 3×3 kernel and ReLU activation, the second block uses 64 filters, and the third block uses 128 filters, all with 2×2 max-pooling. After feature extraction, a Flatten layer converts the 2D feature maps into a 1D vector, which is then passed through a fully connected Dense layer with 256 neurons and ReLU activation. A Dropout layer with a rate of 0.5 is applied for regularization to reduce overfitting. The final output layer is a Dense layer with a softmax activation function corresponding to the number of target classes. The model is compiled using the Adam optimizer and categorical cross-entropy loss function.

2.6. Model evaluation

The evaluation of a classification model relies on key metrics such as accuracy, recall, and precision, which collectively assess its performance in correctly classifying images. These metrics are crucial for ensuring the reliability of the model, particularly in minimizing diagnostic errors and providing accurate analytical results.

1. Accuracy: Measures the overall capability of the model to correctly classify both positive and negative cases.
2. Recall (Sensitivity): Evaluates the model's effectiveness in detecting true positive cases, reflecting its ability to identify positive instances.
3. Precision: Assesses the model's ability to correctly classify positive cases among all instances classified as positive.

By leveraging these metrics, we can gain insights into the model’s strengths and weaknesses, ensuring robust and dependable performance in practical applications. The metrics are calculated based on the following terms:

- TP (True Positives): Observations correctly classified as positives.
- FP (False Positives): Observations incorrectly classified as positives when they are actually negatives.
- FN (False Negatives): Observations incorrectly classified as negatives when they are actually positives.
- TN (True Negatives): Observations correctly classified as negatives.

Each metric plays a critical role in evaluating the model's diagnostic accuracy and guiding its optimization for real-world use cases.

3. Results and discussions

This section presents the results and evaluates the performance of three models used for blood cell image classification: ResNet-50, VGG-16, and a classic CNN. The dataset from Kaggle contains three categories – TEST, TEST_SIMPLE, and TRAIN – with a highly imbalanced distribution (497, 14, and 1,991 samples, respectively). Each model was assessed using accuracy and loss curves, confusion matrices, and classification reports. The goal is to determine which architecture provides the best generalization and classification capability on this imbalanced dataset.

3.1. Performance analysis of ResNet-50

The ResNet-50 model achieves the best performance among the three tested architectures, as indicated by its accuracy and error curves (Fig. 2). The training accuracy curve rapidly achieves near-perfect levels, while the validation accuracy stabilizes at approximately 80%. The relatively small gap between the two curves suggests reasonable generalization compared to the other models. The training loss curve decreases sharply and stabilizes at a low value, while the validation loss curve stabilizes at a slightly higher but consistent level. These patterns highlight effective learning and convergence, with minimal fluctuations reflecting the model’s relative robustness in handling this classification task.

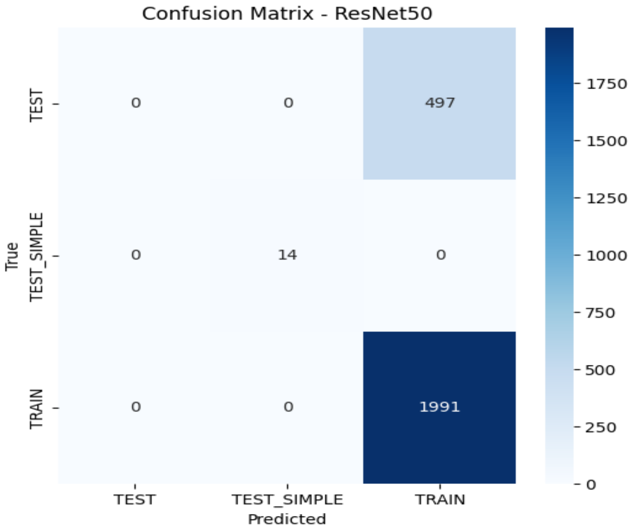

Fig. 1. Confusion matrix of the ResNet-50 model

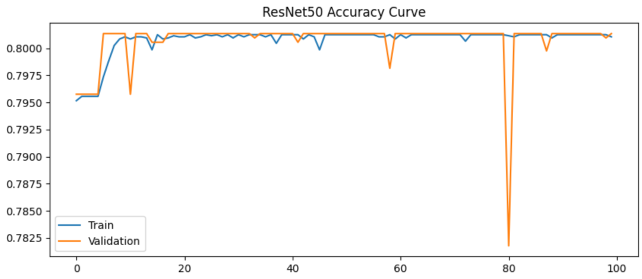

Fig. 2. Accuracy and error curves of the ResNet-50 model

The confusion matrix for ResNet-50 (Fig. 1) reveals that the model correctly classified all 1,991 TRAIN samples and all 14 TEST_SIMPLE samples. However, it misclassified all 497 TEST samples as TRAIN, indicating that the model struggles to distinguish the TEST class from the dominant TRAIN class. Despite this limitation, ResNet-50 achieves an overall accuracy of approximately 80%, the highest among the three models evaluated.

The classification report (Fig. 3) reveals an overall accuracy of approximately 80%. The TEST_SIMPLE class achieved perfect metrics, with a precision of 1.00, recall of 1.00, and F1-score of 1.00. The TRAIN class showed a precision of 0.80, recall of 1.00, and F1-score of 0.89. However, the TEST class scored 0.00 across all metrics, indicating a complete failure to identify this class. Despite this limitation, ResNet-50 achieves the best overall performance among the three models due to its stable validation accuracy and minimal overfitting.

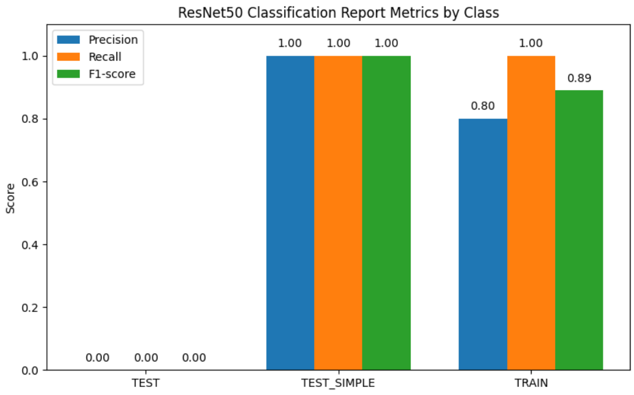

Fig. 3. Classification report of the ResNet-50 model

3.2. Performance analysis of VGG-16

The VGG-16 model demonstrates moderate classification performance, as reflected in its accuracy and error curves (Fig. 5). The training accuracy curve rapidly approaches near-perfect levels (close to 1.00), while the validation accuracy stabilizes at approximately 80%, revealing a significant gap indicative of overfitting. The training loss decreases sharply, but the validation loss remains notably higher, suggesting that the model memorizes training data rather than learning generalizable features. This overfitting behavior is more pronounced than in ResNet-50.

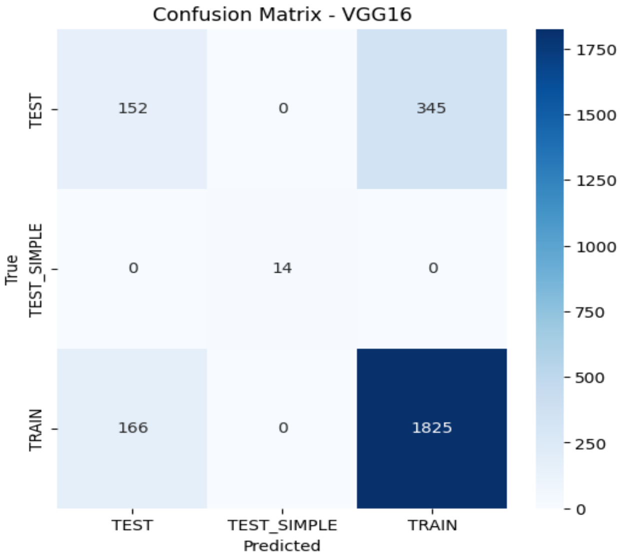

Fig. 4. Confusion matrix of the VGG-16 model

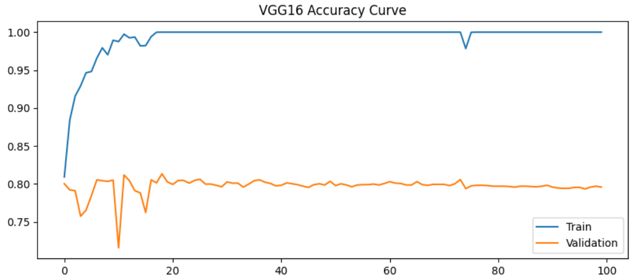

Fig. 5. Accuracy and error curves of the VGG-16 model

The confusion matrix for VGG-16 (Fig. 4) shows mixed classification results across the three classes. The TRAIN class is classified with reasonable accuracy, with 1,825 correct predictions out of 1,991, while 166 TRAIN samples were misclassified as TEST. The TEST_SIMPLE class was correctly classified with all 14 samples identified. However, the TEST class showed significant misclassifications, with only 152 out of 497 correctly classified and 345 misclassified as TRAIN. This indicates that VGG-16 struggles to distinguish the TEST and TRAIN classes, likely due to overlapping feature representations in the imbalanced dataset.

VGG-16 achieves an overall accuracy of approximately 79.6%, slightly lower than ResNet-50. The classification report (Fig. 6) shows that the TEST_SIMPLE class achieved perfect metrics (precision 1.00, recall 1.00, F1-score 1.00). The TRAIN class showed reasonable performance with precision of 0.84, recall of 0.92, and F1-score of 0.88. However, the TEST class performed poorly with precision of 0.48, recall of 0.31, and F1-score of 0.37, reflecting the model's difficulty in correctly identifying this class. The significant overfitting observed in the accuracy curves, combined with poor TEST class metrics, indicates that VGG-16 is less effective than ResNet-50 for this imbalanced classification task.

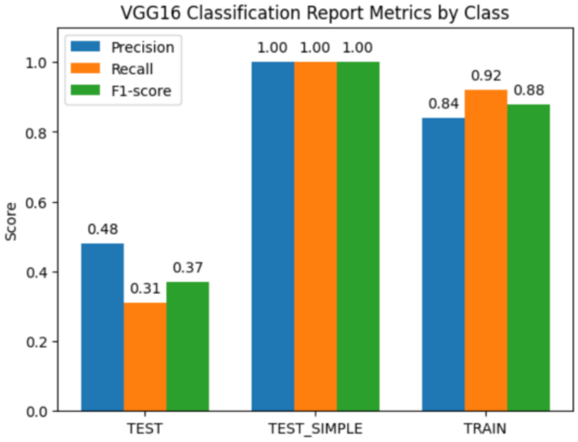

Fig. 6. Classification report of the VGG-16 model

3.3. Performance analysis of the classic CNN

The classic CNN model exhibits the most significant overfitting among the three architectures, as shown by its accuracy and loss curves (Fig. 8). The training accuracy rapidly reaches near-perfect levels (close to 1.00), while the validation accuracy stabilizes at approximately 76–78%, resulting in the largest gap between training and validation performance. This indicates that the classic CNN memorizes the training data rather than learning generalizable patterns, making it the least reliable model for this classification task.

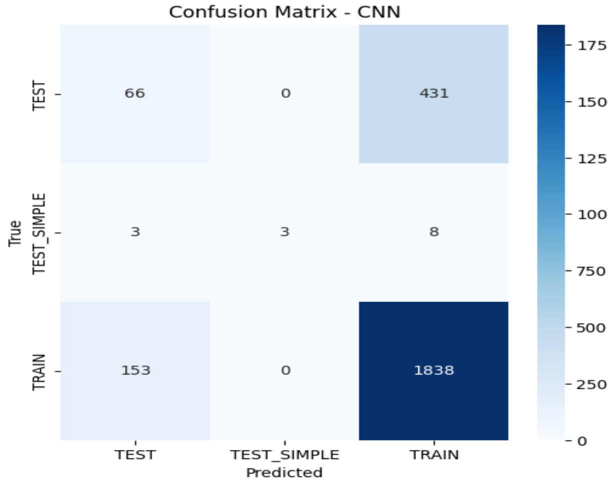

Fig. 7. Confusion matrix of the CNN model

The confusion matrix for the classic CNN (Fig. 7) reveals significant misclassification issues. Out of 497 TEST samples, only 66 were correctly classified, with 431 misclassified as TRAIN. The TEST_SIMPLE class performed worst, with only 3 out of 14 correctly identified, while 3 were misclassified as TEST and 8 as TRAIN. The TRAIN class achieved 1,838 correct predictions out of 1,991, with 153 misclassified as TEST. These results indicate a strong bias toward the majority TRAIN class and poor discrimination ability for minority classes. The classification report (Figure 9) highlights the classic CNN's limitations, achieving an overall accuracy of approximately 76.2%, the lowest among the three models. The TEST class performed poorly with precision of 0.30, recall of 0.13, and F1-score of 0.18. The TEST_SIMPLE class achieved perfect precision (1.00) but very low recall (0.21) and F1-score (0.35), indicating that while its predictions for this class were accurate, it failed to detect most TEST_SIMPLE samples. The TRAIN class showed precision of 0.81, recall of 0.92, and F1-score of 0.86, confirming the model's bias toward the majority class.

The classic CNN exhibits the most severe overfitting among the three architectures, with a large gap between training accuracy (near 100%) and validation accuracy (approximately 76–78%). Its poor performance on minority classes (TEST and TEST_SIMPLE) and heavy bias toward the TRAIN class make it the least suitable model for this imbalanced classification task. Improvements through regularization techniques, data augmentation, and class-weighted loss functions would be necessary to enhance its generalization capabilities.

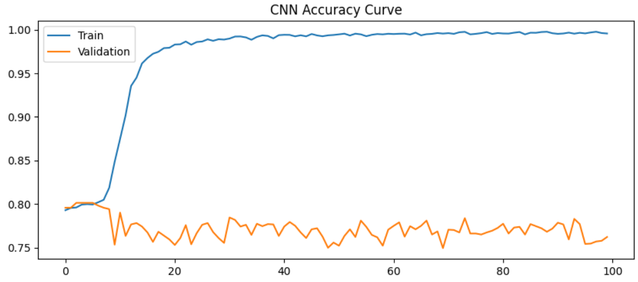

Fig. 8. Accuracy and error curves of the CNN model

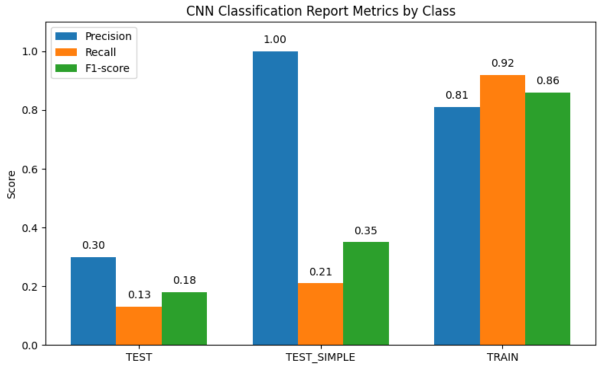

Fig. 9. Classification report of the CNN model

4. Conclusion

This study evaluated the performance of three deep learning architectures – ResNet-50, VGG-16, and a classic CNN – for classifying blood cell image categories using a Kaggle dataset with three classes (TEST, TEST_SIMPLE, and TRAIN). The analysis revealed that ResNet-50 achieved the highest validation accuracy of approximately 80%, followed by VGG-16 at 79.6% and the classic CNN at 76.2%. A key finding was the significant overfitting exhibited by both VGG-16 and the classic CNN, where training accuracy approached 100% while validation accuracy remained around 76–80%. ResNet-50 demonstrated the most balanced performance with minimal overfitting. The confusion matrices revealed that all models struggled with the highly imbalanced dataset, particularly in correctly classifying the minority TEST and TEST_SIMPLE classes. The classification reports confirmed these challenges, with low precision and recall for underrepresented classes across all models. These results highlight the importance of addressing class imbalance through techniques such as oversampling, data augmentation, and class-weighted loss functions. Future work should focus on balancing the dataset, exploring ensemble methods, and applying transfer learning strategies to improve generalization across all classes.

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Prof. Achraf Benba
e-mail: a.benba@um5r.ac.ma

Received the Ph.D. degree in electrical engineering from National Higher School of Arts and Crafts, Mohammed V University, Rabat, Morocco, in 2017. He is a member of Electronic Systems, Sensors and Nanobiotechnologies teams at National Higher School Of Arts And Crafts, Mohammed V University. His interests are in speech processing for detecting people with neurological disorders and cardiac.

https://orcid.org/0000-0001-7939-0790

Prof. Sara Sandabad
e-mail: sandabad@isem.ac.ma

Received the B.Sc. and the M.Sc. degrees in Electrical Engineering from Higher Teacher Training College For Technical Education, Mohamed V University of Rabat (Morocco) and the Ph.D. degree from National Higher School For Computer Science and Systems Analysis from the Mohamed V University of Rabat, all in Electrical Engineering, in 2010, 2012, and 2016, respectively. Currently, she is a professor of Electrical Engineering at Higher Institute of Maritime Studies (ISEM), Casablanca, Morocco.

https://orcid.org/0000-0002-0813-6178