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A Step Towards Automated Haematology: DL Models for Blood Cell Detection and Classification

Irfan Sadiq Rahat[1], Mohammed Altaf Ahmed[2], Donepudi Rohini[3], A. Manjula[4], Hritwik Ghosh[1*], Abdus Sobur[5]

[1]School of Computer Science and Engineering (SCOPE), VIT-AP University, Amaravati, Andhra Pradesh
[2]Department of Computer Engineering, College of Computer Engineering & Sciences, Prince Sattam Bin Abdulaziz University, Al-Kharj 11942, Saudi Arabia
[3]Dept. of Computer Science & Engineering, Koneru Lakshmaiah Education Foundation, Vaddeswaram, Guntur Dist,Andhra Pradesh - 522502, India
[4]Department of Computer Science & Engineering, Jyothishmathi Institute of Technology and Science, Karimnagar, Telangana, India
[5]Masters of Information technology, Westcliff University, USA

Abstract

INTRODUCTION: Deep Learning has significantly impacted various domains, including medical imaging and diagnostics, by enabling accurate classification tasks. This research focuses on leveraging deep learning models to automate the classification of different blood cell types, thus advancing hematology practices.
OBJECTIVES: The primary objective of this study is to evaluate the performance of five deep learning models - ResNet50, AlexNet, MobileNetV2, VGG16, and VGG19 - in accurately discerning and classifying distinct blood cell categories: Eosinophils, Lymphocytes, Monocytes, and Neutrophils. The study aims to identify the most effective model for automating hematology processes.
METHODS: A comprehensive dataset containing approximately 8,500 augmented images of the four blood cell types is utilized for training and evaluation. The deep learning models undergo extensive training using this dataset. Performance assessment is conducted using various metrics including accuracy, precision, recall, and F1-score.
RESULTS: The VGG19 model emerges as the top performer, achieving an impressive accuracy of 99% with near-perfect precision and recall across all cell types. This indicates its robustness and effectiveness in automated blood cell classification tasks. Other models, while demonstrating competence, do not match the performance levels attained by VGG19.
CONCLUSION: This research underscores the potential of deep learning in automating and enhancing the accuracy of blood cell classification, thereby addressing the labor-intensive and error-prone nature of traditional methods in hematology. The superiority of the VGG19 model highlights its suitability for practical implementation in real-world scenarios. However, further investigation is warranted to comprehend model performance variations and ensure generalization to unseen data. Overall, this study serves as a crucial step towards broader applications of artificial intelligence in medical diagnostics, particularly in the realm of automated hematology, fostering advancements in healthcare technology.

Keyword: Medical Imaging, Diagnostic Methodologies, Blood Cell Classification, Hematology, ResNet50, AlexNet, MobileNetV2, VGG16, VGG19

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*Corresponding authors Email: me.hritwikghosh@gmail.com

1. Introduction

The field of hematology has been a cornerstone of medical diagnostics for decades. Traditional methods of blood cell detection and classification, however, have been labor-intensive, time-consuming, and prone to human error. With the rapid advancements in artificial intelligence (AI), particularly in the area of DL there is an opportunity to revolutionize this critical aspect of healthcare. DL a subfield of AI, involves the use of artificial neural networks with multiple layers (hence the term "deep") to model and understand complex patterns. In the context of medical imaging, DL models can be trained to recognize and classify different types of cells, diseases, or abnormalities with remarkable accuracy. This capability holds significant potential for the field of hematology, where accurate detection and classification of blood cells are crucial for diagnosing a wide range of conditions. This research paper presents an in-depth exploration of the application of DL models for the detection and classification of blood cells. The study is based on a dataset of approximately 8,500 augmented images of four different types of blood cells: Eosinophils, Lymphocytes, Monocytes, and Neutrophils. These images serve as the input for several DL models, including ResNet50, AlexNet, MobileNetV2, VGG16, and VGG19, which are trained and evaluated based on their ability to accurately classify the blood cell images. The goal of this research is not only to assess the performance of these models but also to contribute to the broader understanding of how DL can be effectively applied in the field of hematology. By automating the process of blood cell detection and classification, we can potentially increase diagnostic accuracy, reduce turnaround times, and ultimately improve patient outcomes. In the subsequent sections, we will navigate through the intricacies of our approach, encompassing the steps taken for data preprocessing, the structure of the employed DL models, and the metrics used for evaluation. We will also unveil and interpret the outcomes, shedding light on the advantages and limitations of each model and discussing the potential impact of these results on the future trajectory of automated hematology. This research serves as a stepping stone towards the broader application of artificial intelligence in medical diagnostics, paving the way for future advancements in automated hematology. It is our hope that this work will inspire further research and development in this area, bringing us closer to the goal of fully automated, highly accurate hematology diagnostics.

2. Literature Review

Deep learning (DL) has been shown to be effective in a variety of research fields, including medical diagnostics, cybersecurity, archaeology, and beyond. This article is driven by the use of DL models in diverse circumstances requiring the detection and categorization of cell pictures. Islam et al. (2022) presented an explainable transformer-based DL model to detect malaria parasites from blood cell images, underscoring the role of DL in parasitic disease diagnostics **[1].**Another research work by Mohamed et al. (2020) aimed at improving white blood cells classification using pre-trained DL models, offering a promising approach for hematological diagnosis **[2].**In the domain of cytology, Dhieb et al. (2019) proposed an automated framework for counting and classifying blood cells using the Mask R-CNN DL model, demonstrating the potential of DL in cellular level diagnostics **[3].**Similarly, Habibzadeh et al. (2018) utilized pre-trained DL models for the classification of white blood cells, further illustrating the effectiveness of transfer learning in this field **[4].**

Alzubaidi et al. (2020) employed DL models for the classification of red blood cells to aid in the diagnosis of sickle cell anemia, showing the potential of DL in genetic disorders **[5].** Jha and Dutta (2019) presented a mutual information-based hybrid model and DL for the detection of Acute Lymphocytic Leukemia in single-cell blood smear images, showcasing the versatility of hybrid models in disease detection **[6].** The utility of DL extends beyond cell classification and into disease detection and classification. Deng et al. (2020) proposed a DL approach to detect COVID-19 based on chest X-ray and CT images, exhibiting the power of deep learning in pandemic management **[7]**. Anupama et al. (2022) devised a synergic DL model for the automated detection and classification of brain intracranial hemorrhage images, demonstrating the application of DL in neurology **[8].**

D'Acunto et al. (2018) proposed a DL approach to detect human osteosarcoma cells, indicating the potential of DL in oncology **[9].** In the field of radiology, Sun et al. (2021) used a DL model to improve the performance of radiologists in the detection and classification of breast lesions, further highlighting the efficiency of DL in medical imaging **[10].** Marín et al. (2020) proposed a DL model for the detection and classification of malware traffic, illustrating the adaptability of DL in cybersecurity **[11].** In the field of plant pathology, B R et al. (2021) implemented a DL model for plant disease detection and classification, underlining the potential of DL in agriculture **[12].**

DL has also been utilized in rheumatology, as exhibited by Dulhare and Mubeen (2023) who detected and classified rheumatoid nodules using DL models **[14].** Padma et al. (2022) proposed a DL based detection and classification method for arrhythmias, indicating the potential of DL in cardiology **[15].** Similarly, Madhu et al. (2022) proposed a deep learning model for COVID-19 classification and detection **[16].** In cybersecurity, Ahmed et al. (2022) proposed a DL-based classification model for botnet attack detection, emphasizing the role of DL in ensuring internet security **[17].** A study published in the Obesity, Fitness, & Wellness Week (2022) highlighted the application of DL in the automatic classification of white blood cells **[18].**

Ghosh et al. (2023) conducted an extensive investigation to evaluate water quality using predictive machine learning. Their study demonstrated how machine learning models can be used to accurately evaluate and categorise water quality **[21].** Parameters including pH, dissolved oxygen, BOD, and TDS were included in the dataset that was used for this analysis. The Random Forest model was the most accurate of the models they used, with an impressive accuracy rate of 78.96%. The SVM model, on the other hand, fell behind and had the lowest accuracy of 68.29% **[22].**
In order to help treat lower-grade gliomas, Rahat et al. (2023) **[23]** created a deep learning technique for segmenting FLAIR abnormalities in brain MR images. The study used models such as DeepLabv3 and U-Net **[24]** with a custom loss function to address data imbalance using a genomic dataset.

In a paper published in the International Journal of Creative Research Thoughts, Shobur et al. use machine learning to analyse Walmart data and explore insights.
Mohanty, Ghosh, Rahat, and Reddy **[25]** classify maize leaf diseases in Bangladesh using sophisticated deep learning models in their field study, which provides important insights for agricultural technology. Their groundbreaking method of illness detection is highlighted in the research, which is published in Engineering Proceedings 2023.

In their SSRN paper **[26]** on human rights, Islam, Kazi, and Sobur address how cyberbullying affects children's right to life, highlighting the impact of societal influences. In the International Journal of Creative Research **[27]** Thoughts, Kabir, Sobur, and Amin **[28]** present their machine learning models-based stock price prediction research. In a 2023 paper Rana, Kabir, and Sobur **[29]** compare the error rates of MNIST datasets using different machine learning models.

In summary, the body of literature indicates that DL plays a significant role in cell image detections, classifications, disease detection, and beyond. Its applications range from medical diagnostics and disease detection to cybersecurity and archaeology. This interdisciplinary nature of DL makes it a promising tool for various research fields **[Table.1].**

Table 1. Summary of the Literature Review

Reference	Focus of Study	Techniques Used	Key Findings
Islam et al. (2022) **[1]**	Malaria parasite detection from blood cell images	Explainable transformer-based DL model	DL's role in parasitic disease diagnostics highlighted
Mohamed et al. (2020) **[2]**	White blood cells classification	Pre-trained DL models	Promising approach for hematological diagnosis using DL
Dhieb et al. (2019) **[3]**	Counting and classifying blood cells	Mask R-CNN DL model	Potential of DL in cellular level diagnostics demonstrated using automated framework for blood cell counting and classification
Habibzadeh et al. (2018) **[4]**	White blood cell classification	Pre-trained DL models	Effectiveness of transfer learning in white blood cell classification demonstrated
Alzubaidi et al. (2020) **[5]**	Red blood cell classification for sickle cell anemia	DL models	DL's potential in aiding the diagnosis of genetic disorders, specifically sickle cell anemia
Jha and Dutta (2019) **[6]**	Acute Lymphocytic Leukemia detection	Mutual information-based hybrid model and DL	Versatility of hybrid models in disease detection showcased
Deng et al. (2020) **[7]**	COVID-19 detection based on X-ray and CT images	DL approach	Power of deep learning in pandemic management demonstrated through COVID-19 detection
Anupama et al. (2022) **[8]**	Brain intracranial hemorrhage detection and classification	Synergic DL model	Application of DL in neurology illustrated through automated detection and classification of brain intracranial hemorrhage images
D'Acunto et al. (2018) **[9]**	Human osteosarcoma cell detection	DL approach	Potential of DL in oncology emphasized through the detection of human osteosarcoma cells
Sun et al. (2021) **[10]**	Detection and classification of breast lesions	DL model	Efficiency of DL in improving radiologists' performance in breast lesion detection and classification

Marín et al. (2020) **[11]**	Malware traffic detection and classification	DL model	Adaptability of DL showcased in the field of cybersecurity through the detection and classification of malware traffic
B R et al. (2021) **[12]**	Plant disease detection and classification	DL model	Potential of DL in agriculture demonstrated through the implementation of a model for plant disease detection and classification
Dulhare and Mubeen (2023) **[14]**	Rheumatoid nodule detection and classification	DL models	Utilization of DL in rheumatology for detecting and classifying rheumatoid nodules
Padma et al. (2022) **[15]**	Arrhythmias detection and classification	DL-based method	Potential of DL in cardiology illustrated through the proposed method for arrhythmias detection and classification
Madhu et al. (2022) **[16]**	COVID-19 classification and detection	Deep learning model	Contribution of DL in the fight against COVID-19 highlighted through the proposed classification and detection model
Ahmed et al. (2022) **[17]**	Botnet attack detection in cybersecurity	DL-based classification model	Emphasis on DL's role in ensuring internet security through the proposed model for botnet attack detection
Obesity, Fitness, & Wellness Week (2022) **[18]**	White blood cell classification	DL application in automatic classification	Application of DL in the automatic classification of white blood cells highlighted
Ghosh et al. (2023) **[21]**	Water quality evaluation with predictive machine learning	Random Forest and SVM models	Machine learning models, particularly Random Forest, can accurately evaluate and categorize water quality parameters

3. Dataset Overview

The foundation of this research lies in a robust and diverse dataset, which is instrumental in training and evaluating the deep learning models. The dataset has at least 8,500 augmented images of blood cells, enough for training our models for the purpose of this researcher. These images represent four distinct blood cells: Eosinophils, Lymphocytes, Monocytes, and Neutrophils. Each of these cell types plays a unique role in the human immune system. Thus, being able to correctly identify and classify them is vital for diagnosing various health conditions. To ensure that the models make accurate predictions that are not affected by bias, we distributed around 2000 images for each of the different types of cells in our dataset. This gives the models an equal opportunity to learn the characteristics of each cell. The images are stored in JPEG format, a commonly used format for storing digital images. This format is compatible with most image processing and ML libraries, making it convenient for land-based processing of the images. In addition to the augmented images, the dataset also includes an additional set of 410 original images (pre-augmentation). The dataset provided includes images of various types of blood cells, organized into two folders: 'dataset-master' and 'dataset2-master'. In the 'dataset-master' folder, you will find 410 original images of blood cells, accompanied by additional information about the characteristics of each cell. The 'dataset2-master' folder contains a larger set of 8,500 augmented images, further expanding the dataset. With its diverse range of images and accompanying details, this dataset serves as a valuable resource for training DL models for the classification of blood cells. Its diversity ensures that the models are exposed to a wide range of cell images, enabling them to learn the nuanced differences between the cell types. The inclusion of both original and augmented images also allows for the exploration of different training strategies, such as training on the original images and validating on the augmented images, or vice versa **[Fig. 1]**.

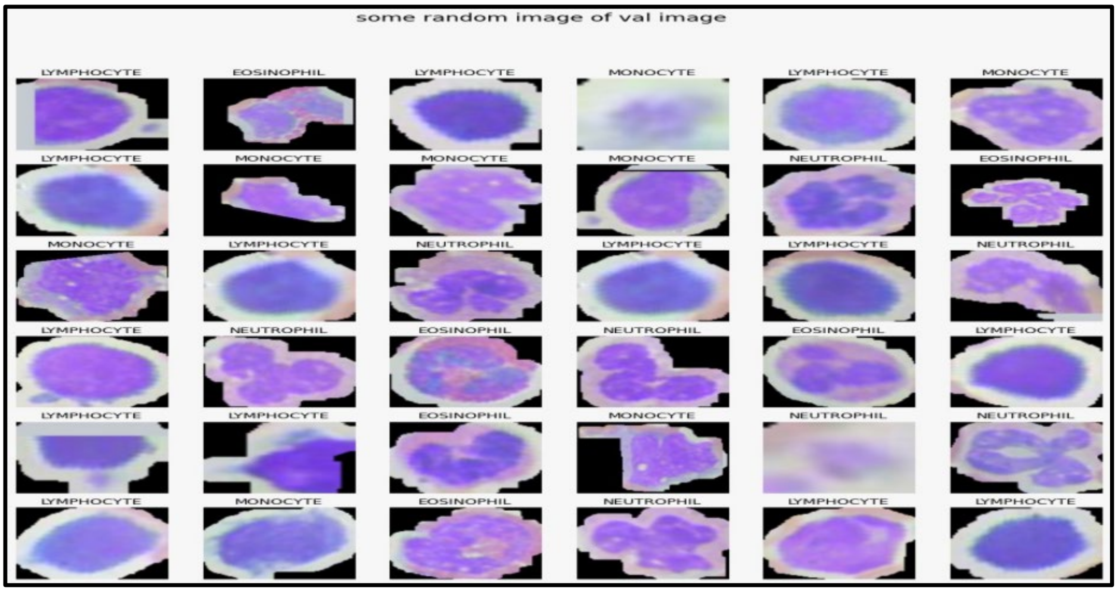


Fig 1: Sample image of dataset

3.1 Data Preprocessing

The initial phase of our methodology is centered around readying the dataset for the DL models. Our dataset, a collection of roughly 8,500 augmented images representing four distinct types of blood cells, undergoes a series of preprocessing steps. Our data preprocessing pipeline includes important steps that aim to ensure consistency and optimize the performance of our deep learning models. To preserve consistency, we first change the image size based on the input layer specifications. Furthermore, we normalize the image pixel values, often rescaling them to a predefined range between 0 and 1, which improves the models' learning capacity. In addition, we divide the dataset into two subsets: training and validation. The validation set is used to fine-tune hyperparameters and reduce the danger of overfitting, resulting in more robust and effective models. Our models are trained using the training set.

3.1.2 Model Selection and Training

The next stage involves the selection and training of the deep learning models. We carefully selected five unique models known for their remarkable performance in picture classification tasks for this study: ResNet50, AlexNet, MobileNetV2, VGG16, and VGG19. Each model is trained on the given training set using an appropriate optimization technique, such as stochastic gradient descent or Adam, to ensure thorough training. Critical model performance parameters, such as learning rate and batch size, are fine-tuned depending on their performance on the validation set.

3.1.3 Model Evaluation

The final stage involves evaluating the performance of the trained models. A separate test set, unseen during training or validation, is used to evaluate the models' performance. The models are thoroughly evaluated using a variety of measures such as accuracy, precision, recall, and F1-score. These metrics provide a thorough assessment of the models' capabilities, taking into account their accuracy in picture categorization and ability to decrease misclassifications. Throughout this process, the research adheres to rigorous standards of reproducibility and transparency. All steps, from data preprocessing to model evaluation, are documented in detail, and the code used for the models is made available for review. This ensures that the research can be independently verified and built upon by other researchers in the field. In summary, this paper employs a robust dataset, state-of-the-art models, and rigorous evaluation techniques to comprehensively investigate the potential of DL models for blood cell detection and classification. The findings of this study contribute valuable insights to the field of automated hematology.

3.2 Image Resizing

In the realm of image classification tasks, particularly when employing deep learning models, image resizing is a crucial preprocessing step. This process involves modifying the dimensions of an image to align with the input requirements of the model. The selection of image size can significantly impact both the computational efficiency and the performance of the model. Here, we discuss some of the most prevalent techniques for image resizing:

- **Nearest-Neighbor Interpolation:** This method is a simple approach to image scaling. It operates by reproducing the value of the pixel in the scaled image that is closest to the matching pixel. While it is computationally efficient, it may provide a blocky or pixelated appearance when applied to greater scaling scales or when there is a significant difference in size between the original and scaled image.

- **Bilinear Interpolation:** This technique employs a calculation method where a new pixel's value is determined by taking into account the weighted average of the four closest pixels arranged in a 2x2 grid. This particular method yields a more polished result compared to using the nearest-neighbor interpolation. It becomes a more appropriate choice, especially when dealing with substantial resizing scales, as it produces smoother outcomes.

- **Bicubic Interpolation:** This advanced method uses the values of the nearest 16 pixels (in a 4x4 neighborhood) to determine the value of a new pixel. It provides even smoother results than bilinear interpolation, but it is also more computationally intensive.

- **Lanczos Resampling:** This method employs a high-quality Lanczos filter to calculate the value of a new pixel based on a larger neighborhood. It provides very high-quality results but is also the most computationally intensive method.

The choice of image resizing technique is contingent on the specific requirements of the task. For tasks necessitating high-quality images, bicubic interpolation or Lanczos resampling might be the optimal choice. For tasks demanding computational efficiency, nearest-neighbor or bilinear interpolation might be more suitable. It's also crucial to consider the size of the images. Larger images contain more details but require more computational resources, while smaller images are quicker to process but may lack crucial details. Common sizes for image classification tasks include 224x224, 256x256, and 512x512 pixels.

3.3 Image Data Augmentation

Augmenting picture data is a widely used strategy in deep learning problems, with a view of increasing the diversity and quantity of the training dataset to improve model performance. As a result, the model's performance and generalization capabilities are improved. This paper looks at various data augmentation techniques to enrich our dataset of blood cell images. Here are some of the most commonly used data augmentation techniques in image classification tasks:

- **Rotation:** This technique includes rotating the image. It improves the model's ability to distinguish objects in different orientations. The rotation angle is typically chosen randomly within a certain range (e.g., -20 to 20 degrees).

- **Translation:** This technique involves shifting the image along the x or y direction by a certain number of pixels. This increases the model's positional resilience and its ability to handle objects appearing in diverse places within the image.

- **Scaling:** This technique involves resizing the image by a certain factor, either enlarging it (zooming in) or reducing it (zooming out). It improves scalability and generalization by increasing the model's adaptability in detecting objects at different scales.

- **Flipping:** This technique involves mirroring the image along the horizontally or vertically axis. It helps the model recognize the object in a variety of angles.

- **Shearing:** This technique introduces controlled distortions along a specified axis. It allows the model to detect objects under different forms of deformations and enhancing adaptability.

- **Brightness and Contrast Adjustment:** This technique involves altering the brightness and contrast of the image. It helps the model to recognize the object under different lighting conditions.

The selection of data augmentation techniques is contingent on the unique demands of the task and the intrinsic characteristics of the images. It's equally crucial to weigh the computational considerations and the prospective influence of these techniques on the model's performance. Through the application of these techniques, we managed to substantially amplify the quantity and variety of our training dataset. This, in turn, facilitated the creation of more resilient and precise models for the classification of blood cells.

3.4 Image Normalization

Image normalization is an essential preprocessing step in image classification tasks. Its primary objective is to modify the pixel values throughout the image to a designated range, resulting in notable improvements in both computational efficiency and model performance. Here are some of the most commonly employed techniques for image normalization:

- **Min-Max Normalization:** Also known as feature scaling, this technique aims to adjust pixel values to a predetermined range, typically between 0 and 1 or -1 and 1. It accomplishes this by subtracting the minimum pixel value and dividing the result by the range of pixel values.

- **Decimal Scaling:** This alternative method of rescaling pixel values involves modifying the decimal point position based on the pixels' greatest absolute value. The amount of this maximum value determines the degree of modification. This approach is less frequent, although it might be useful when dealing with photos with big or changing pixel values.

The selection of an image normalization technique is contingent on the unique demands of the task at hand and the inherent properties of the images. If the task necessitates the maintenance of the original features and structure of the images, Min-Max normalization could be the optimal choice. Conversely, for tasks dealing with images where pixel values follow a Gaussian distribution, Z-score normalization might be more appropriate. It's also crucial to weigh the computational efficiency of the normalization method against its potential influence on the model's performance. In our research, we carefully considered these factors and chose the most appropriate image normalization technique for our dataset of blood cell images.

4. Performance of all Models

Below are diagrammatic representations illustrating the performance of each model employed in our study: ResNet50, AlexNet, MobileNetV2, VGG16, and VGG19.

- **ResNet50:** This model showed a varied performance across different cell types. For Eosinophils, it had a precision of 0.73, recall of 0.32, and an F1-score of 0.45. For Lymphocytes and Monocytes, the precision was perfect (1.00), with recalls of 0.95 and 0.75, respectively. Neutrophils had the lowest precision (0.50) but the highest recall (0.92). The overall accuracy of the model was 0.74, indicating a fairly good performance **[Fig.2,3].**

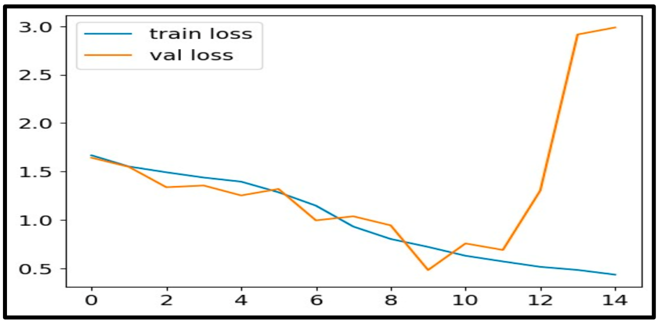


Fig 2: Model Loss for ResNet50 model

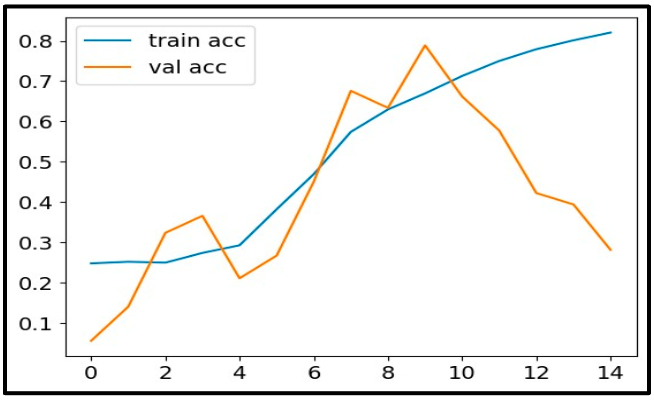


Fig 3: Model Accuracy for ResNet50 model

- **AlexNet:** The model exhibited a loss of 0.1741, signifying a favorable fit to the training data. It achieved a high accuracy of 0.9465, indicating its proficiency in correctly classifying a significant portion of the images. Furthermore, the model demonstrated robust generalization to unseen data with a test accuracy of 0.9465020298957825**[Fig.4].**

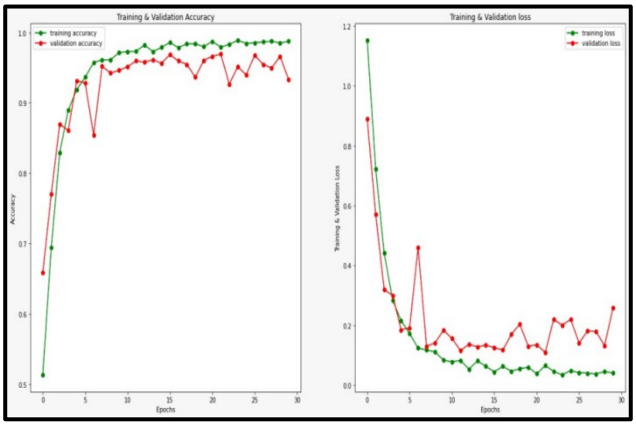


Fig 4: Model Accuracy and Loss for AlexNet

- **MobileNetV2:** This model demonstrated a balanced performance across all classes, with precision ranging from 0.73 to 0.85 and recall from 0.64 to 0.95. The overall accuracy of the model was 0.78, indicating a good performance **[Fig.5,6].**

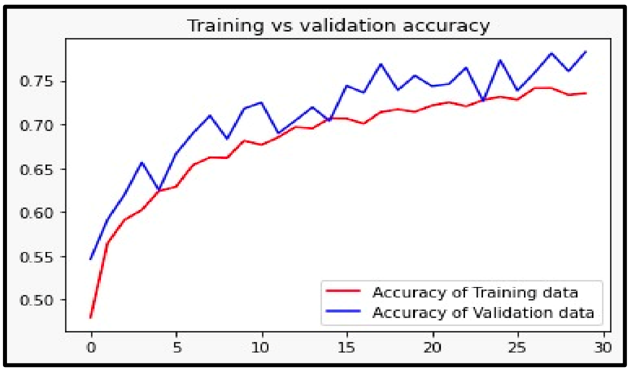


Fig 5: Model Accuracy for MobileNetV2

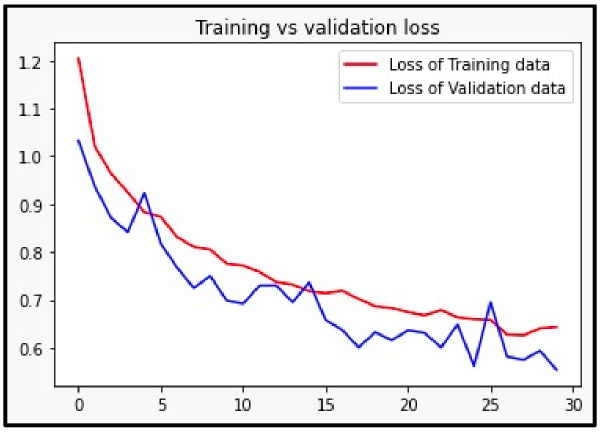


Fig 6: Model Loss for MobileNetV2

- ✧ **VGG16:** This model has a loss of 0.1904, which is a decent fit for the training data. The accuracy was high at 0.9421, and the validation accuracy was even better at 0.9915, showing that the model performed well on both the training and validation sets. **[Fig.7,8].**

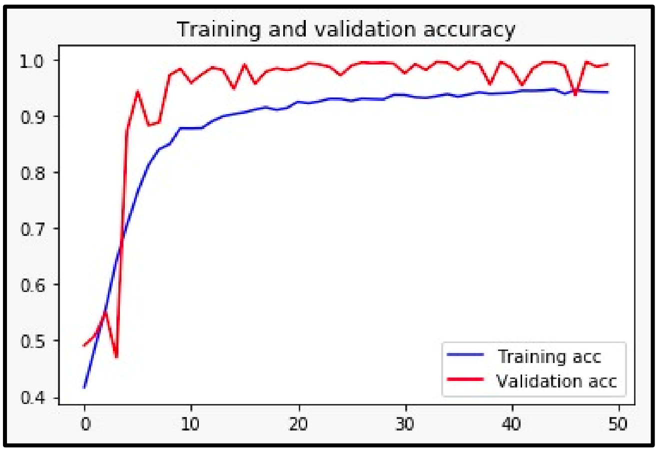


Fig 7: Model Accuracy for VGG16

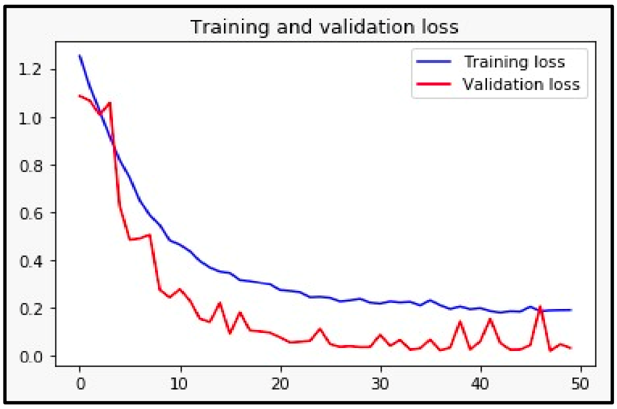


Fig 8: Model Loss for VGG16

- ✧ **VGG19:** This model outperformed all other models with a near-perfect precision, recall, and F1-score for all cell types. The overall accuracy of the model was 0.99, making it the best model for this task **[Fig.9,10].**

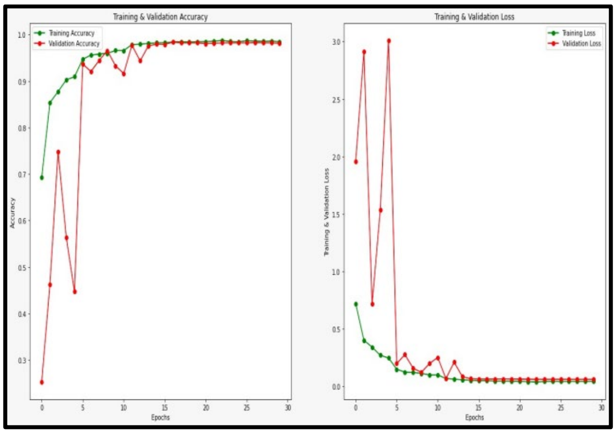
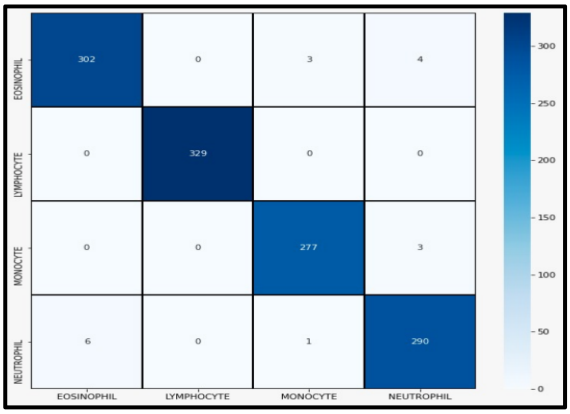


Fig 9: Model Loss and Accuracy for VGG19



	EOSINOPHIL	LYMPHOCYTE	MONOCYTE	NEUTROPHIL
EOSINOPHIL	302	0	3	4
LYMPHOCYTE	0	329	0	0
MONOCYTE	0	0	277	3
NEUTROPHIL	6	0	1	290

Fig 10: Confusion Matrix for VGG19

Conclusion: While all models correctly categorised blood cells, VGG19 stood out as the top predictor due to its high accuracy. It's crucial to remember that these outcomes depend on a number of variables, including the calibre and variety of the training data, the complexity of the model architecture, and the selection of the hyperparameters. Additional research is required to verify these findings.

5. Results and Discussion

The findings of our study are presented and interpreted. The evaluation of five DL models, namely ResNet50, AlexNet, MobileNetV2, VGG16, and VGG19, is conducted. These models are trained and tested on a dataset consisting of 8,500 augmented images of four distinct types of blood cells. The performance of each model is assessed using various metrics, including accuracy, precision, recall, and F1-score. The analysis reveals varying levels of performance among the models. For instance, ResNet50 demonstrates a solid ability to differentiate between different blood cell types, achieving an accuracy of 74%. On the other hand, AlexNet exhibits superior performance in the classification task, with an accuracy of 94.65%. MobileNetV2 and VGG16 also show promising results, with accuracies of 78% and 94.21% respectively. Notably, VGG19 emerges as the top-performing model, achieving an impressive accuracy of 99%. These results offer valuable insights into the capabilities of different deep learning models in the context of blood cell classification. The exceptional performance of VGG19 suggests its potential for further exploration and application in automated hematology. However, it is important to consider factors such as computational efficiency and complexity when selecting a model. In the discussion, a deeper analysis of these results is provided, including an exploration of the reasons behind the varying performance of the models and a discussion of the implications for future research and application in automated hematology. Additionally, the potential limitations of the study are discussed, and directions for future research are proposed.

6. Conclusion and Future Work

In conclusion, our research findings showcase the efficacy of DL models in accurately classifying blood cell images. VGG19 exhibited the most promising outcomes, achieving an impressive accuracy rate of 99%, positioning it as the optimal model for this specific task. However, it is important to recognize that several factors can influence model performance, including the quality and diversity of the training dataset, the selection of image preprocessing and augmentation techniques, and model complexity. Moving forward, there are several potential avenues for further exploration. One possibility is to investigate more advanced DL models or ensemble methods to enhance classification performance. Additionally, exploring the application of these models to other types of medical images or more complex tasks like object detection or semantic segmentation would be worthwhile. Incorporating additional data, such as patient demographics or clinical history, could also contribute to developing a more comprehensive predictive model. Lastly, conducting a thorough analysis of misclassified images would provide valuable insights into the limitations of current models and guide the development of more robust and accurate models in the future.

References

[1] Islam, M. R., Nahiduzzaman, M., Goni, M. O. F., Sayeed, A., Anower, M. S., Ahsan, M., & Haider, J. (2022). Explainable Transformer-Based Deep Learning Model for the Detection of Malaria Parasites from Blood Cell Images. Sensors (Basel, Switzerland), 22(12), 4358. https://doi.org/10.3390/s22124358

[2] Mohamed, E., H. El-Behaidy, W., Khoriba, G., & Li, J. (2020). Improved White Blood Cells Classification based on Pre-trained Deep Learning Models. Journal of Communications Software and Systems, 16(1), 37–45. https://doi.org/10.24138/jcomss.v16i1.818

[3] Dhieb, N., Ghazzai, H., Besbes, H., & Massoud, Y. (2019). An Automated Blood Cells Counting and Classification Framework using Mask R-CNN Deep Learning Model. 2019 31st International Conference on Microelectronics (ICM), 300–303. https://doi.org/10.1109/ICM48031.2019.9021862

[4] Habibzadeh, M., Jannesari, M., Rezaei, Z., Baharvand, H., & Totonchi, M. (2018). Automatic white blood cell classification using pre-trained deep learning models: ResNet and Inception. 10696, 1069612–1069612–8. https://doi.org/10.1117/12.2311282

[5] Alzubaidi, L., Fadhel, M. A., Al-Shamma, O., Zhang, J., & Duan, Y. (2020). Deep Learning Models for Classification of Red Blood Cells in Microscopy Images to Aid in Sickle Cell Anemia Diagnosis. Electronics (Basel), 9(3), 427. https://doi.org/10.3390/electronics9030427

[6] Jha, K. K., & Dutta, H. S. (2019). Mutual Information based hybrid model and deep learning for Acute Lymphocytic Leukemia detection in single cell blood smear images. Computer Methods and Programs in Biomedicine, 179, 104987–104987. https://doi.org/10.1016/j.cmpb.2019.104987

[7] Deng, X., Shao, H., Shi, L., Wang, X., & Xie, T. (2020). A Classification–Detection Approach of COVID-19 Based on Chest X-ray and CT by Using Keras Pre-Trained Deep Learning Models. Computer Modeling in Engineering & Sciences, 125(2), 579.https://doi.org/10.32604/cmes.2020.011920

[8] Anupama, C. S. S., Sivaram, M., Lydia, E. L., Gupta, D., & Shankar, K. (2022). Synergic deep learning model–based automated detection and classification of brain intracranial hemorrhage images in wearable networks. Personal and Ubiquitous Computing, 26(1), 1–10. https://doi.org/10.1007/s00779-020-01492-2

[9] D'Acunto, M., Martinelli, M., & Moroni, D. (2018). Deep Learning Approach to Human Osteosarcoma Cell Detection and Classification. Multimedia and Network Information Systems, 353–361. https://doi.org/10.1007/978-3-319-98678-4_36

[10] Sun, Y., Qu, Y., Wang, D., Li, Y., Ye, L., Du, J., Xu, B., Li, B., Li, X., Zhang, K., Shi, Y., Sun, R., Wang, Y., Long, R., Chen, D., Li, H., Wang, L., & Cao, M. (2021). Deep learning model improves radiologists' performance in detection and classification of breast lesions. Chinese Journal of Cancer Research, 33(6), 682–693. https://doi.org/10.21147/j.issn.1000-9604.2021.06.05

[11] Marín, G., Casas, P., & Capdehourat, G. (2020). DeepMAL -- Deep Learning Models for Malware Traffic Detection and Classification. https://doi.org/10.48550/arxiv.2003.04079

[12] B R, P., Ashok, A., & A V, S. H. (2021). Plant Disease Detection and Classification Using Deep Learning Model. 2021 Third International Conference on Inventive Research in Computing Applications (ICIRCA), 1285–1291. https://doi.org/10.1109/ICIRCA51532.2021.9544729

[13] Dulhare, U. N., & Mubeen, A. (2023). Detection and Classification of Rheumatoid Nodule using Deep Learning Models. Procedia Computer Science, 218, 2401–2410. https://doi.org/10.1016/j.procs.2023.01.215

[14] Padma, T., Uday Kiran, A., Jahnavi, C., Rahul, S., Raja, N., & Kamal Kumar, M. (2022). Detection and Classification of Arrhythmias by Deploying Deep Learning Models. Journal of Physics. Conference Series, 2325(1), 12053. https://doi.org/10.1088/1742-6596/2325/1/012053

[15] Madhu, M., Xavier, A., & Jayapandian, N. (2022). Covid-19 Classification and Detection Model using Deep Learning. 2022 International Conference on Electronics and Renewable Systems (ICEARS), 1457–1462. https://doi.org/10.1109/ICEARS53579.2022.9752290

[16] Ahmed, A. A., Jabbar, W. A., Sadiq, A. S., & Patel, H. (2022). Deep learning-based classification model for botnet attack detection. Journal of Ambient Intelligence and Humanized Computing, 13(7), 3457–3466. https://doi.org/10.1007/s12652-020-01848-9

[17] Researchers at Chitkara University Have Published New Study Findings on Computational Intelligence and Neuroscience (Deep Learning Model for the Automatic Classification of White Blood Cells). (2022). Obesity, Fitness, & Wellness Week, 3844.

[18] Veeranampalayam Sivakumar, A. N., Li, J., Scott, S., Psota, E., J. Jhala, A., Luck, J. D., & Shi, Y. (2020). Comparison of Object Detection and Patch-Based Classification Deep Learning Models on Mid- to Late-Season Weed Detection in UAV Imagery. Remote Sensing (Basel, Switzerland), 12(13), 2136. https://doi.org/10.3390/rs12132136

[19] Berganzo-Besga, I., Orengo, H. A., Lumbreras, F., Aliende, P., & Ramsey, M. N. (2022). Automated detection and classification of multi-cell Phytoliths using Deep Learning-Based Algorithms. Journal of Archaeological Science, 148, 105654. https://doi.org/10.1016/j.jas.2022.105654

[20] Wang, C.-W., Huang, S.-C., Lee, Y.-C., Shen, Y.-J., Meng, S.-I., & Gaol, J. L. (2022). Deep learning for bone marrow cell detection and classification on whole-slide images. Medical Image Analysis, 75, 102270–102270. https://doi.org/10.1016/j.media.2021.102270

[21] Ghosh, H., Tusher, M.A., Rahat, I.S., Khasim, S., Mohanty, S.N. (2023). Water Quality Assessment Through Predictive Machine Learning. In: Intelligent Computing and Networking. IC-ICN 2023. Lecture Notes in Networks and Systems, vol 699. Springer, Singapore. https://doi.org/10.1007/978-981-99-3177-4_6

[22] Ghosh H, Rahat IS, Shaik K, Khasim S, Yesubabu M. Potato Leaf Disease Recognition and Prediction using Convolutional Neural Networks. EAI Endorsed Scal Inf Syst [Internet]. 2023 Sep. 21 [cited 2023 Sep. 22];.https://doi.org/10.4108/eetsis.3937

[23] Rahat IS, Ghosh H, Shaik K, Khasim S, Rajaram G. Unraveling the Heterogeneity of Lower-Grade Gliomas: Deep Learning-Assisted Flair Segmentation and Genomic Analysis of Brain MR Images. EAI Endorsed Trans Perv Health Tech [Internet]. 2023 Sep. 29 [cited 2023 Oct. 2];9.https://doi.org/10.4108/eetpht.9.4016

[24] M. Mandava, S. R. Vinta, H. Ghosh, and I. S. Rahat, “An All-Inclusive Machine Learning and Deep Learning Method for Forecasting Cardiovascular Disease in Bangladeshi Population”, EAI Endorsed Trans Perv Health Tech, vol. 9, Oct. 2023.https://doi.org/10.4108/eetpht.9.4052

[25] Mohanty, S.N.; Ghosh, H.; Rahat, I.S.; Reddy, C.V.R. Advanced Deep Learning Models for Corn Leaf Disease Classification: A Field Study in Bangladesh. Eng. Proc. 2023, 59, 69. https://doi.org/10.3390/engproc2023059069

[26] Md Abdus Shobur,Abdus Sobur,Md Ruhul Amin, "Walmart Data Analysis Using Machine Learning", International Journal of Creative Research Thoughts (IJCRT), ISSN:2320-2882, Volume.11, Issue 7, pp.f894-f898, July 2023, Available at :http://www.ijcrt.org/papers/IJCRT2307693

[27] Nazrul Islam, Kazi and Sobur, Abdus and Kabir, Md Humayun, The Right to Life of Children and Cyberbullying Dominates Human Rights: Society Impacts (August 8, 2023). Available at SSRN: https://ssrn.com/abstract=4537139

[28] Md Humayun Kabir,Abdus Sobur,Md Ruhul Amin, "Stock Price Prediction Using the Machine Learning Model", International Journal of Creative Research Thoughts (IJCRT), ISSN:2320-2882, Volume.11, Issue 7, pp.f946-f950, July 2023, Available at :http://www.ijcrt.org/papers/IJCRT2307700

[29] Md Suhel Rana, Md Humayun Kabir, & Abdus Sobur. (2023). Comparison of the Error Rates of MNIST Datasets Using Different Type of Machine Learning Model. https://doi.org/10.5281/zenodo.8010602