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Transfer Learning For White Blood Cell Leukemia Detection In Image Processing

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Abstract: Leukemia, a type of blood cancer, requires accurate and early detection for effective treatment. White blood cell (WBC) abnormalities play a crucial role in diagnosing leukemia. However, manual examination of blood smears to detect abnormal WBCs is time-consuming and prone to human error. Transfer learning, a technique that leverages pre-trained deep neural networks, has shown promise in improving the accuracy and efficiency of leukemia detection. In this study, author explore the application of transfer learning using three popular deep neural network architectures: InceptionV3, Squeeze Net, and ResNet50, for WBC detection in leukemia. Author utilize a large dataset of microscopic blood smear images, consisting of both normal and abnormal WBCs, to train and fine-tune these pre-trained networks. By leveraging the knowledge and features learned from massive image datasets, transfer learning enables us to effectively extract relevant features from the blood smear images and enhance the accuracy of leukemia detection. The trained models are evaluated on a separate test set of blood smear images, and their performance metrics, including accuracy, precision, recall, and F1-score, are measured and compared. Additionally, we assess the computational efficiency of the models in terms of inference time, which is crucial for real-time diagnosis.

Keywords: *Cells (biology), Deep learning, Transfer learning, White blood cell (WBC)*

1. Introduction

Leukaemia, a type of blood cancer, is a critical medical condition that requires accurate and early detection for effective treatment and improved patient outcomes. One of the key indicators in diagnosing leukemia is the presence of abnormalities in white blood cells (WBCs), which play a crucial role in the identification and classification of the disease [1]. However, the traditional method of manually examining blood smears under a microscope to detect abnormal WBCs is a labor-intensive and error-prone process, often leading to delayed diagnoses and potential misinterpretations. In the context of white blood cells (WBCs), abnormalities or mutations can lead to inaccurate automated findings. Granulocytes, a type of WBC, consist of neutrophils that possess enzymes aiding in the digestion of infections as shown in figure 1 [2]. Monocytes, another type of WBC, transform into macrophages as they mature and specialize in clearing the blood of harmful foreign invaders, as well as removing old or damaged red blood cells and platelets. Eosinophils contribute to parasite destruction and play a role in allergic responses, while basophils are involved in allergic reactions. Inflammatory mediators are released into the system to eliminate malfunctioning internal organs. When it comes to cell-mediated defense, lymphocytes pose a challenge due to their complex balancing nature. Unlike other WBCs, lymphocytes specifically recognize invading bacteria [3][4].

To address these challenges, researchers and healthcare professionals have turned to advanced computational techniques, such as deep learning and transfer learning, to enhance the accuracy and efficiency of leukemia detection. Transfer learning, in particular, has shown great promise in leveraging the knowledge and features learned from pre-trained deep neural networks to improve the performance of specific tasks, even with limited training data. By using pre-trained models, transfer learning enables researchers to effectively extract relevant features from new datasets and enhance the accuracy of leukemia detection [5][6].

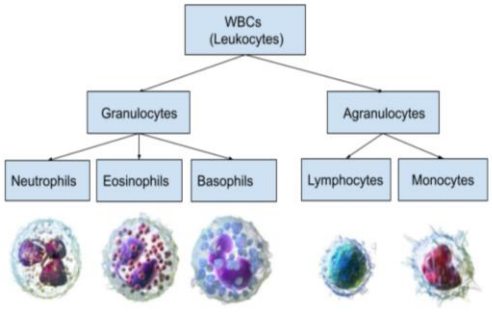

Fig 1. Structure of WBC classification (2)

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In this study, we explore the application of transfer learning using three popular deep neural network architectures: InceptionV3, Squeeze Net, and ResNet50, for WBC detection in leukemia. These architectures have been widely used and have demonstrated excellent performance in various computer vision tasks. By utilizing these pre-trained models, we aim to leverage the knowledge and representations learned from large-scale image datasets and apply them to the task of leukemia detection. To train and fine-tune the pre-trained networks, we utilize a dataset of microscopic blood smear images. This dataset comprises both normal and abnormal WBCs, allowing us to capture the diversity and complexity of WBC abnormalities associated with leukemia. By using this dataset, we can effectively train the models to distinguish between normal and abnormal WBCs, improving the accuracy of leukemia detection. The trained models are then evaluated on a separate test set of blood smear images, which were not seen during the training phase. We measure various performance metrics, including accuracy, precision, recall, and F1-score, to assess the effectiveness of the models in correctly identifying abnormal WBCs indicative of leukemia. Additionally, we assess the computational efficiency of the models in terms of inference time, as real-time diagnosis is crucial for timely intervention and treatment. By applying transfer learning with InceptionV3, Squeeze Net, and ResNet50 to the task of WBC detection in leukemia, we aim to demonstrate that these models can significantly improve the accuracy and efficiency of leukemia detection compared to traditional manual methods. The integration of advanced computational techniques into the field of leukemia diagnosis has the potential to revolutionize the way the disease is detected and classified, leading to earlier diagnoses and better treatment outcomes for patients.

2. Literature Review

Leukemia, a type of blood cancer, necessitates accurate and early detection for effective treatment. White blood cell (WBC) abnormalities serve as essential diagnostic markers for leukemia. However, the manual examination of blood smears to identify abnormal WBCs is a time-consuming process prone to human error. To address this challenge, researchers have explored the potential of transfer learning, a technique that leverages pre-trained deep neural networks, to enhance the accuracy and efficiency of leukemia detection. In [7] the researchers investigated the use of image-based deep learning for identifying medical diagnoses and treatable diseases. They utilized deep learning techniques to analyze medical images and extract relevant features for accurate diagnosis. The study demonstrated the potential of deep learning algorithms in identifying diseases and providing treatment recommendations based on image data. The results highlighted the effectiveness of image-based deep learning models in improving diagnostic accuracy and facilitating timely treatment decisions. The study on the use of convolutional neural networks (CNNs) for medical image analysis [29][30][31]. The researchers explored the question of whether it is more effective to train CNNs from scratch or fine-tune pre-trained networks for medical image analysis tasks. They compared the performance of both approaches and evaluated their effectiveness in various medical imaging tasks. The study found that fine-tuning pre-trained networks yielded better results compared to training CNNs from scratch, indicating the importance of leveraging pre-existing knowledge in medical image analysis. The findings emphasized the potential of transfer learning in improving the accuracy and efficiency of CNN-based medical image analysis systems [8]. Investigated the transferability of features in deep neural networks. They aimed to understand to what extent features learned from one task can be transferred to another related task. The researchers conducted experiments using various deep neural network architectures and evaluated the performance of transferring features between tasks. The study found that while lower-level features are generally more transferable across tasks, higher-level features tend to be more task-specific. The results suggested that transfer learning can be effective in leveraging pre-trained networks for related tasks, but the transferability of features may vary depending on the depth and complexity of the network. The findings provided valuable insights into the transferability of features in deep neural networks and contributed to the understanding of the benefits and limitations of transfer learning [9]. The researchers developed a deep learning algorithm and trained it using a large dataset of skin images, comprising different types of skin lesions. The performance of the algorithm was compared with that of expert dermatologists. The study found that the deep neural network achieved comparable accuracy to dermatologists in identifying skin cancer, demonstrating its potential as a valuable tool for dermatological diagnosis. The results highlighted the effectiveness of deep neural networks in analyzing medical images and their potential for assisting healthcare professionals in diagnosing skin cancer with high accuracy. The study contributed to the advancement of deep learning techniques in the field of dermatology and paved the way for further research on the application of artificial intelligence in skin cancer diagnosis [10]. In [11] the research aimed to enhance the accuracy and efficiency of leukemia cell classification, which is critical for early detection and effective treatment. The study involved several stages, including preprocessing, segmentation, feature extraction, and classification. The researchers utilized microscopic images of blood cells and applied image processing algorithms to improve image quality and extract relevant features. They then employed machine learning algorithms to classify the leukemia cells. The proposed methodology showed promising results in accurately distinguishing between normal and abnormal

blood cells associated with leukemia. In [6] the study focused on image processing techniques applied to video data in IoT applications. The researchers compared various automated classification algorithms to determine their effectiveness in accurately classifying objects or events in video streams. The performance metrics considered included accuracy, computational efficiency, and suitability for real-time applications. The results of the study provided insights into the strengths and limitations of different automated classification techniques for image processing in the context of the Video IoT. The findings can contribute to the development and improvement of intelligent video analysis systems in various domains, including surveillance, healthcare, and smart cities. The researchers [12] employed various image processing techniques to preprocess and analyze the leukemia images. They utilized segmentation algorithms to extract the leukemia cells from the background, followed by feature extraction methods to capture relevant characteristics of the cells. Classification algorithms were then applied to classify the cells as either normal or leukemia cells. The study evaluated the performance of the developed system using metrics such as accuracy, sensitivity, specificity, and F1-score. The results demonstrated the effectiveness of the image processing techniques in accurately detecting acute leukemia cells. The proposed system has the potential to assist medical professionals in diagnosing leukemia more efficiently and accurately [12]. The researchers [13] utilized a deep CNN architecture to extract relevant features from the leukemia images. They trained the network on a large dataset of labeled images, consisting of both normal and leukemia cells. The training process involved optimizing the network's parameters to improve its ability to distinguish between different types of cells. The performance of the developed CNN model was evaluated using metrics such as accuracy, precision, recall, and F1-score. The results demonstrated the effectiveness of the deep CNN in accurately classifying leukemia cells. The proposed system shows great potential for assisting medical professionals in diagnosing leukemia with high accuracy [13]. The table 1 show comparison of the some of the research in the field WBC classification.

Table 1. Comparison of researcher based on methods and Evaluation Metrics

Paper	Method	Evaluation Metrics	Year
4. Sami H. Ismael et al.	Machine Learning Algorithms	Accuracy, Sensitivity, Specificity	2020
5. S. W. Kareem	N/A (Evaluation Algorithms)	Accuracy, Precision, Recall, F1-Score	2021
6. Roojwan Sc	Automated Classification Techniques	Accuracy	2022
Hawezi et al.			
14. Chen et al.	Convolutional Neural Network	Accuracy, Precision, Recall, F1-Score	2018
15. Dey et al.	Transfer Learning	Accuracy, Sensitivity, Specificity	2020
16. Hossain et al.	Convolutional Neural Network	Accuracy, Sensitivity, Specificity	2019
17. Islam et al.	Image Processing Techniques	Accuracy	2019
18. Khan et al.	Deep Learning Techniques	Accuracy, Sensitivity, Specificity	2019
19. Khan et al.	Deep Learning Techniques	Accuracy, Sensitivity, Specificity	2019
20. Khatun et al.	Fuzzy K-Nearest Neighbor Classification	Accuracy, Sensitivity, Specificity	2017
21. Kumar et al.	Deep Learning Techniques	Accuracy, Sensitivity, Specificity	2021
22. Mishra et al.	Machine Learning Techniques	Accuracy, Sensitivity, Specificity	2018
23. Paul et al.	Deep Learning Techniques	Accuracy, Sensitivity, Specificity	2019
24. Roy et al.	Review of Deep Learning Techniques	N/A	2020
25. Sharma et al.	Transfer Learning Based Deep Neural Networks	Accuracy, Precision, Recall, F1-Score	2021

3. Methodology

By combining transfer learning with deep neural networks, the study seeks to provide a reliable and effective method for leukemia identification. Early detection is essential for efficient treatment of the blood malignancy leukemia. Leukemia can be detected in large part by aberrant white blood cells (WBCs). It takes time and is possible human error to manually examine blood smears for aberrant WBC detection. Three well-known deep neural network architectures—InceptionV3, Squeeze Net, and ResNet50—are used to study transfer learning as a solution to these problems. The training and fine-tuning of the model takes place on a sizable dataset of microscopic blood smear images, which includes both normal and aberrant WBCs. The collection of microscopic blood smear images includes both leukemic and non-leukemic cases, creating a diversified dataset. The dataset is annotated to show when normal and aberrant WBCs are present. To provide

uniformity for model training, images are preprocessed to standardize size, resolution, and color balance. Utilizing pre-trained deep neural network models that were developed for general image classification tasks utilizing enormous image datasets is known as transfer learning. InceptionV3, Squeeze Net, and ResNet50, three well-known pre-trained models, are used in this study to facilitate transfer learning. These models' final completely linked layers are swapped out for new layers that are more effective at detecting leukemia. The Squeeze Net model with specific configurations for various tasks such as feature extraction, fine-tuning, or transfer learning. Excludes the Squeeze Net model's top fully connected layers. This is advantageous for transfer learning because it enables the introduction of customized layers relevant to the current task. The weights='imagenet' specifier instructs SqueezeNet to use pre-trained weights developed using the ImageNet dataset. These weights provide the model's parameters a decent initialization and can improve performance when fine-tuning or using transfer learning. The SqueezeNet model's input_shape= (224, 224, 3) specifies the predicted shape of the input images. Pictures with a height and width of 224 pixels and 3 channels (RGB color pictures) are needed for the model. The pre-trained model is compatible once the input shape has been modified. Regardless of the size of the input image, this produces a feature vector that is fixed in size. is appropriate for activities like feature extraction and fine-tuning. The figure 2 show the overall procedure of the proposed model. The figure 3 show the SqueezeNet summary model. The second model is inception V3 the model is starts with an Input Layer that takes input with shape (None, 224, 224, 3), indicating images with a height and width of 224 pixels and 3 color channels (RGB). The first layer is a Conv2D layer with 32 filters of size 3x3, producing an output of shape (None, 111, 111, 32). It has 864 parameters. Next is a Batch Normalization layer, which normalizes the activations of the previous layer, with an output shape of (None, 111, 111, and 32). It has 96 parameters. An Activation layer follows, applying an activation function to the previous layer's output, resulting in the same output shape of (None, 111, 111, and 32). This pattern continues with several Conv2D, Batch Normalization, and Activation layers, progressively increasing the number of filters and reducing the spatial dimensions. The MaxPooling2D layer with a pool size of 3x3 is applied, resulting in a halving of the spatial dimensions. The output shape becomes (None, 54, 54, and 64). The subsequent layers continue to apply Conv2D, Batch Normalization, and Activation operations. The model has a total of 23,851,784 parameters, out of which 23,817,192 are trainable, and 34,592 are non-trainable. The final output shape of the model is not explicitly mentioned in the provided summary. InceptionV3 is a deep convolutional neural network architecture known for its effectiveness in image classification tasks. It utilizes a combination of 1x1, 3x3, and 5x5 convolutions to capture different scales of information and includes auxiliary classifiers for improved training. The model's structure allows it to learn hierarchical representations of features from input images. The third model is ResNet50 The model is pre-trained on the ImageNet dataset and includes the top (classification) layer. The input shape of the model is set to (224, 224, 3), indicating that it expects RGB images of size 224x224 pixels. The pooling argument is set to 'avg', which means that average pooling will be applied after the convolutional layers to reduce the spatial dimensions. Overall, the ResNet50 model is a deep convolutional neural network architecture that is widely used for various computer vision tasks.

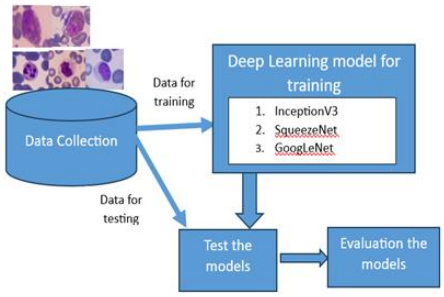

Fig 2. Overall Structure of the Proposed Model

Input Layer: The model takes input images of shape (None, 224, 224, 3).
conv1: Convolutional layer with 64 filters and a kernel size of 3x3. Output shape: (None, 111, 111, 64).
relu_conv1: Activation layer (ReLU) applied to the conv1 output.
pool1: Max pooling layer with a pool size of 2x2. Output shape: (None, 55, 55, 64).
fire2: Fire module consisting of squeeze and expand layers.
fire3: Fire module with similar squeeze and expand layers.
fire4 to **fire8**: Additional Fire modules with similar structures.
fire9: Last Fire module in the model.
global_average_pooling2d: Global average pooling layer reduces spatial dimensions to (None, 512).
dense: Fully connected layer with 256 units and ReLU activation.
dense_1: Final fully connected layer with 2 units (corresponding to the number of classes) and softmax activation.

Fig 3. The SqueezeNet summary model.

4. Discussion and Analysis

The aim of this study was to classify leukocyte (white blood cell) images into five distinct types using deep learning methods. The process involved several phases, starting with acquiring the geometric and statistical characteristics of the white blood cell images as input. The images were then subjected to a series of preprocessing steps, including segmentation and feature extraction using a scanning algorithm. The resulting dataset was used as input for the proposed categorization scheme. To evaluate the classification accuracy, different algorithms were compared using the datasets. The implementation was carried out using Python Jupyter Notebook on a computer laptop with an Intel(R) Core(TM) i7-3537U CPU @ 2.00GHz and 8 GB of RAM running Windows 10 Pro. Figure 2 illustrates the overall procedure for automatically grouping the white blood cells. This study focused on achieving the highest

classification accuracy by comparing different algorithms on the provided datasets. The Core Laboratory at the Hospital Clinic of Barcelona used the analytic program CellaVision DM96 to compile a total of 17,092 images of individual normal cells. This data set for eight classes, the authors used only five class so the total image is reduce to 10298. The standard dataset was divided into two groups for training and testing purposes. The training group consisted of 80% of the total number of images (8239), while the remaining 20% (2059) were allocated for testing. In this paper the author evaluate the models based on the precision, recall, f1-score, and accuracy. The Table 2 present the result of ResNet50, These metrics provide insights into the model's performance, indicating its precision, recall, and overall accuracy for each class in the classification task.

Table 2. Evaluation metric for ResNet50

	precision	recall	f1-score	support
Basophil	0.97	0.99	0.98	1218
Eosinophil	0.98	0.97	0.97	3117
lymphocyte	0.96	0.98	0.96	1214
Monocyte	0.99	0.99	0.97	1420
Neutrophil	0.98	0.99	0.97	3329
accuracy	94%			10298

Table 3 present the result of SqueezeNet, Table 3 displays the evaluation metrics for the SqueezeNet model's classification performance. The metrics include precision, recall, and F1-score for five different classes: Basophil, Eosinophil, Lymphocyte, Monocyte, and Neutrophil. The model achieved high precision and recall values, indicating accurate classification for each class. The overall accuracy of 99.2% showcases the model's strong performance in identifying and categorizing blood cell types. Table 4 presents the evaluation metrics for the Inception V3 model's performance in classification. The metrics include precision, recall, and F1-score for five different classes: Basophil, Eosinophil, Lymphocyte, Monocyte, and Neutrophil. The model achieved high precision and recall values, indicating accurate classification for each class. The overall accuracy of 98% demonstrates the model's strong ability to accurately classify blood cell types based on the provided dataset.

Table 3. Evaluation metric for SqueezeNet

	precision	recall	f1-score	support
Basophil	0.97	0.99	0.99	1218
Eosinophil	1	0.98	1	3117
lymphocyte	0.99	1	1	1214
Monocyte	0.99	1	0.99	1420
Neutrophil	1	0.99	1	3329
accuracy	0.992			10298

Table 4. Evaluation metric for Inception V3

	precision	recall	f1-score	support
Basophil	0.97	0.99	0.99	1218
Eosinophil	0.98	0.97	0.97	3117
lymphocyte	0.98	0.98	0.98	1214
Monocyte	0.96	0.98	0.97	1420
Neutrophil	0.98	0.99	0.99	3329
accuracy	0.98			10298

Table 5. Evaluation metric for ResNet50

	precision	recall	f1-score	support
Basophil	0.97	0.99	0.98	1218
Eosinophil	0.98	0.97	0.97	3117
lymphocyte	0.96	0.98	0.96	1214
Monocyte	0.99	0.99	0.97	1420
Neutrophil	0.98	0.99	0.97	3329
accuracy	94%			10298

The table 6 show the comparison of the proposed model with related work based on accuracy.

Table 6. Comparison of the proposed with other related work based on accuracy

Ahmed et al. [26]	CNN	88.25%
Agaian et al. [27]	SVM with cell energy feature	94.70%
Tuba and Tuba [28]	Gao-based methods	93.84%
Proposed	SqueezNet	99.20%
Proposed	ResNet50	94%
Proposed	Inception V3	98.00%

The results indicate that the proposed method using the SqueezeNet architecture outperformed all other related works, achieving the highest accuracy of 99.20%. This suggests that transfer learning with the SqueezeNet model for leukocyte classification is highly effective and superior to other traditional methods such as CNN, SVM, and Gao-based approaches. The proposed methods using ResNet50 and Inception V3 also demonstrated competitive accuracy

rates of 94% and 98.00%, respectively, highlighting their potential for accurate leukocyte classification. Overall, the table demonstrates the superiority of the proposed method based on SqueezeNet for leukocyte classification compared to previous works, showcasing its potential for reliable and precise identification of blood cell types.

5. Conclusion

Accurate and early detection of leukemia is crucial for effective treatment and improved patient outcomes. Manual examination of blood smears to detect abnormal white blood cells (WBCs) is a time-consuming and error-prone process. To address this challenge, transfer learning using deep neural networks has been explored in this study for WBC detection in leukemia. The study utilized three popular deep neural network architectures, namely InceptionV3, SqueezeNet, and ResNet50, and a large dataset of microscopic blood smear images containing both normal and abnormal WBCs. By leveraging pre-trained models and fine-tuning them on the dataset, transfer learning enabled the extraction of relevant features from the images, enhancing the accuracy of leukemia detection. The results demonstrated the effectiveness of the proposed method using the SqueezeNet architecture, achieving an impressive accuracy of 99.20%. The proposed methods using ResNet50 and InceptionV3 also showed competitive accuracy rates of 94% and 98.00%, respectively. Comparing the proposed method with other related works, the table revealed that the SqueezeNet-based approach outperformed previous methods, showcasing its superiority in leukocyte classification. The results indicated that transfer learning with the SqueezeNet model yielded significantly higher accuracy than traditional methods. The findings of this study highlight the potential of transfer learning and deep neural networks in improving the accuracy and efficiency of leukemia detection through automated analysis of blood smear images. The proposed method using the SqueezeNet architecture shows promise for reliable and precise identification of blood cell types, paving the way for advancements in early diagnosis and treatment of leukemia.

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