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Implementation of Deep Learning Techniques in the Classification of Leucocytes.

K Veena¹, Swetha Kanagan²

¹Assistant Professor, Department Of CSE, Akshaya College of Engineering and Technology, Kinathukedavu, Coimbatore, Tamilnadu, India ²PG Scholar, Department Of CSE, Akshaya College of Engineering and Technology, Kinathukedavu, Coimbatore, Tamilnadu, India

ABSTRACT

The White Blood Or Leucocytes Classification Is Very Much Important In The Diagnosis Of Anemia And Hematologic Diseases. The State Of Our Immune System Is Analyzed And Diagnosed On The Basis Of The Density Of The Wbcs Present In Our Blood Stream. Blood Test Results Shows The Different Proportion Of The Different Categories Of Leucocytes Like Monocytes, Lymphocytes, Basophils, Eosinophils, And Neutrophils Indicate Several Health Conditions. Always The Composition Of These Will Be Stable In The Blood Stream And Any Variation Or Disturbance Of The Proportion Of White Blood Cells Will Be A Indication That The Sample Is From A III Patient. Wbcs Are The Important Key Factor That Helps The Physicians To Diagnose About The Patient's Immune System, Examining The White Blood Cells In The Blood Stream In Both The Ways That Is Quantitative And Qualitative Is Very Much Critical. A High Performance Automatic White Blood Cell Classification System Is Required For An Efficient Diagnosis Of The Fatal Hematology Diseases. Here We Discuss The Deep Learning Model For The White Blood Cells Classification. Several Architectures Have Been Used In Deep Learning. In This Paper, CNN Models Are Used To Build An Architecture Which Classifies The White Blood Cell Types Which Helps In The Efficient Diagnosis.

Keywords: White Blood Cells, Leucocytes, Blood Cell Classification, CNN, Deep Learning

1. Introduction

In recent years, in the diagnosis of fatal diseases hematology test plays the most significant role. Leukocytes, helps the body in protecting themselves from foreign substances, germs and infectious diseases, and also helps in fighting the infections caused by them. Elevation in the leucocytes count like overproduction might be due to the early release of the white blood cells.

From the bone marrow. Blasts, the young white blood cells accumulate in the infected area, because the body needs to get as many white blood cells as early as possible. Severe infections, metastatic cancer, AIDS and leukemia might be the causes of increase in the leucocytes count. From Fig.1 we were able to know about the categories of white blood cells.



Categories of white blood cells

Fig 2. Normal WBC vs. Leukemia WBC

While Fig2 shows the difference between the normal blood stream and the leukemia diseased patient's blood stream. White blood cells are the important parameter in the diagnosis of diseases such as leukemia, Manual annotation is been practiced currently, which is not considered to be a good solution. Because handling a large data scale with shortage of experienced doctors in clinical laboratory won't give an optimal solution. Artificial intelligence based annotation would be of greater support in the accurate diagnosis. So a methodology of handling such a huge datasets is required where the deep learning techniques will be full filling the requirement. As Deep learning Networks is one of the most popular technology of Artificial intelligence

In the use of large data sets, the architectures that are successful in the classification process are examined. Achieving optimal performance from deep learning from deep learning methods needs to be trained with larger datasets in the training phase. High performance rate in results couldn't be achieved when the training in the network is low. Conventional processors couldn't be used in handling such highest data set deep learning, which in turn affects the performance.

The frequently mentioned and most widely used deep learning networks for image classification. A CNN network is based on artificial neural networks. There are many hidden layers in artificial neural networks.

The better results are obtained from the complexity of the network. Convolutional Neural Networks (CNNs) based architectural model to carry out ship detection from pre annotated dataset. Depending on the resolution of image, the image is converted into a feature map which is nothing but an array of pixels. Then it is combined with the kernel and some operations been done over the image to get a meaningful output. Operations like edge detection, sharpening the image, blurring of the image and identification can be finished by the implementation of filters.



A 3D resultant matrix is obtained after the process of pooling and it is passed to the ANN architecture and flattening is applied on it to an ID vector. There are several optimizers to assess the model's performance like model's performance.

Pre-trained Keras model ResNet50 is used to assess the performance of the model.

2. Literature Survey

American and Japanese companies developed the automatic white blood cells detection systems in the 1970s. Due to the high price and low accuracy they were not used widely.

Using nucleus features Huang D C and Hung K D classified leukocytes with the help of K-means clustering algorithm.

Ushizima D M et al. recognizing different types of leukocytes using support vector machines (SVMs).

A new detection algorithm been proposed by Wang Shitong and Wang Min based on fuzzy cellular neural networks, Hence limited amount of data were used there was slacking in good generalization.

To enhance detection and classification of leucocytes a framework [8] is been proposed based on segmentation of images and to extract cell features nucleus enhancement techniques are been followed.

Transfer learning implemented by various state of the art models to gain maximum efficiency were proposed and for prediction voting module [6] was adapted.

WBCNet [7] was proposed which can extract the the microscopic features of white blood cell image with the combination of normalization algorithm and residual convolution architecture with improved activation function.

In 2018, Tiwari et al classified white blood cell types using a CNN-based model, which is a Double Convolution Layer Neural Network (DCLNN) and compared the model's accuracy with Nave Bayes and

SVM classifiers.

In 2021 Akiz et al. white blood is classified using convolutional features and Support Vector Machines. Accuracy of the proposed model shows 85.95%.

In 2020, Toğaçar et al. Three pre-trained models for feature extractor purposes, such as GoogLeNet, AlexNet, and ResNet-50, were used and the quadratic discriminant analysis (QDA) classifier is implemented to Identify white blood cells. The accuracy of the model is improved by employing feature selection in the classification step.

Cheque et al. Suggested a multi-level and

hybrid model for the WBC classification in 2021. A Faster R-CNN network is utilized in the first stage to identify the region of interest in white blood cells and to separate

Mononuclear cells from polymorph nuclear cells. Two parallel Convolutional was employed in neural networks with the Mobile Net structure, in the second stage to detect the subtypes.

3. Existing System:

To analyze and count, different kinds of white blood cells in blood samples automatic and non-automatic are used. In non-automated methods, a blood sample is taken from a patient and examined by a specialist, counting of blood sample cells is a slow, tedious, time-consuming, in this process. The expensive systems that supports quantitative evaluation and WBC classification, based on flow meters and the chemical properties of the cells. In the existing system, the classification of white blood cells (leucocytes) for the diagnosis of hematologic diseases, such as anemia and leukemia, is achieved using Convolutional Neural Networks (CNNs). While this approach has shown promising results in various computer vision tasks, it comes with certain disadvantages when applied to the specific domain of white blood cell classification.

4. Proposed System

In this paper, we propose a novel white blood cell classification system using the ResNet50 architecture, which is a deep Convolutional Neural Network known for its state-of-the-art performance in various computer vision tasks. However, instead of employing transfer learning from pre-trained models on unrelated datasets like Image Net, we fine-tune the ResNet50 specifically on our white blood cell dataset. This approach aims to leverage the advantages of the ResNet50 architecture while addressing the limitations observed in the existing system.

Advantage:

Fine-tuning ResNet50 on the relatively small white blood cell dataset can help mitigate over fitting issues compared to training from scratch. The pretrained weights of ResNet50 serve as a useful starting point, capturing general features and allowing the model to focus on learning domain-specific features without losing generalization capability.

Algorithm:

Transfer Learning (ResNet50):

ResNet50 is a deep Convolutional Neural Network (CNN) architecture developed by Microsoft Research in 2015. It is part of the ResNet family (Residual Networks) and represents a significant breakthrough in image recognition tasks. Key Innovation: Skip Connections (Residual Blocks): ResNet50 introduced the concept of skip connections or shortcuts, which allow the network to learn residual mappings. These shortcuts enable the model to skip one or more layers, preventing the degradation of accuracy with increasing depth. Architecture Overview: ResNet50 consists of 50 layers, organized into blocks. Each block has several convolutional layers and identity shortcuts. The model architecture is divided into five stages, each containing a different number of blocks with varying numbers of filters.

Deep Identity Mapping: ResNet50 uses the idea of identity mappings, where the output of a layer is added to the input, allowing the network to focus on learning the residual (difference) between the two. This enables the model to efficiently learn and propagate gradients through very deep networks, making training more stable. Pre-Trained Weights: ResNet50 is commonly pre-trained on large-scale image datasets like Image Net, capturing generic features from a wide range of images. Fine-tuning the pre-trained ResNet50 on specific datasets, such as our white blood cell dataset, leverages the learned knowledge for improved performance.





4.1 Proposed model:

- Dataset Collection
- Data collection and preprocessing.
- Model Selection and Setup.
- Splitting the dataset.
- ➢ Fine tuning the ResNet50.
- Hyper parameter tuning.
- Evaluation.

Dataset Collection:

Dataset collection from Kaggle https://www.kaggle.com/datasets/brikwerk/bccd-white-blood-cell

Data Collection and Preprocessing:

Gather a large dataset of white blood cell images, annotated with their respective classes (e.g., neutrophils, lymphocytes, monocytes, eosinophils).

Perform data preprocessing, including resizing images to a consistent resolution, normalization, and data augmentation to increase the dataset's diversity.

Model Selection and Setup:

Choose the ResNet50 architecture as the base model for white blood cell classification. Load the pre-trained ResNet50 weights (trained on ImageNet) to initialize the model.

Splitting the Dataset:

Divide the dataset into training, validation, and testing sets. The training set will be used for training the model, the validation set for hyper parameter tuning, and the testing set to evaluate the final model's performance.

Fine-tuning ResNet50:

Remove the top layers of ResNet50, which are designed for ImageNet classification, and replace them with new layers for white blood cell classification.

Freeze the weights of the early layers to retain the general feature learning and fine-tune the deeper layers to adapt to white blood cell characteristics.

Train the model on the training set using appropriate loss functions (e.g., categorical cross-entropy) and optimizers (e.g., Adam).

Hyper parameter Tuning:

Conduct hyper parameter tuning on the validation set to find the best learning rate, batch size, and other relevant hyper parameters to optimize the model's performance.

Evaluation:

Evaluate the fine-tuned model on the testing set to assess its accuracy, precision, recall, and other performance metrics.

Analyze the confusion matrix and visualize any misclassifications to identify potential areas for improvement.

Hardware Requirements:

Hard Disk :		500GB and Above
RAM	:	4GB and Above
Processor :		I3 and Above

Conclusion:

The proposed model can be further improved by training on more data and using large models. Model suffered bias when trying to regularize over fitting .This can be avoided if we train very deep models. But large volume of data is required to develop such models. Thus in future, more accurate model can be proposed to avoid labor intensive manual white blood cell classification.

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