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Identification of Leukemia Subtypes from Microscopic Images Using ResNeXt Algorithm

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Abstract: Leukaemia is a severe haematological malignancy characterized by the abnormal proliferation of white blood cells in bone marrow and peripheral blood. Early and accurate identification of leukaemia subtypes is essential for effective diagnosis and treatment planning. This paper proposes a deep learning–based microscopic blood image classification framework using the ResNeXt architecture for automated leukaemia subtype detection. The system formulates leukaemia classification as a multi-class medical image analysis problem, where complex morphological features are extracted from microscopic blood smear images. The proposed framework incorporates preprocessing techniques such as image resizing, normalization, and data augmentation to improve robustness and generalization performance. A ResNeXt backbone with grouped convolutions and residual learning is employed to capture discriminative cellular patterns while maintaining computational efficiency. The model is trained and evaluated on a publicly available leukaemia microscopic image dataset for accurate subtype classification. Experimental results demonstrate improved classification accuracy, feature representation, and prediction reliability compared with conventional convolutional neural network approaches. The proposed system also supports real-time prediction through a Flask-based web interface, enabling accessible and efficient computer-aided diagnosis. The results indicate that the ResNeXt-based framework provides an effective and scalable solution for intelligent leukaemia detection and automated healthcare assistance.

Keywords: Leukaemia Subtype Classification; Microscopic Blood Smear Images; Deep Learning; ResNeXt Architecture; Medical Image Analysis; Automated Disease Detection; Computer-Aided Diagnosis
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I. INTRODUCTION

Leukemia is a serious blood cancer caused by the abnormal growth of white blood cells in the bone marrow and blood. Early and accurate detection of leukaemia subtypes is important for effective treatment and patient survival. Traditional diagnosis methods mainly depend on manual microscopic analysis, which is time-consuming and requires expert knowledge. Our system uses deep learning techniques to automatically classify microscopic blood smear images using the ResNeXt architecture. The proposed framework improves feature extraction, classification accuracy, and diagnostic efficiency while providing real-time prediction through a user-friendly web application.

II. LITERATURE SURVEY

Related Work

Park et al. (2024) developed a deep learning model for differentiating Acute Myeloid Leukemia (AML) and Acute Lymphoblastic Leukemia (ALL) using peripheral blood smear images. The proposed system focused on identifying myeloblast and lymphoblast cells for accurate subtype classification. The model was trained using annotated microscopic blood cell datasets and evaluated using multiple performance metrics. Experimental results demonstrated high classification accuracy and improved diagnostic support for hematologists. However, the model required large annotated datasets and showed reduced performance for complex morphological variations between leukemia cells

Habchi et al. (2024) presented a hybrid leukemia classification framework combining wavelet transform techniques with deep neural networks. The wavelet transform was used to extract texture and frequency-based features from microscopic blood cell images, while the deep neural network performed automated classification. The proposed hybrid model improved feature extraction capability and enhanced classification accuracy compared to traditional approaches. Nevertheless, the integration of wavelet processing increased computational complexity and training time for large-scale medical datasets

Anand et al. (2025) proposed a convolutional neural network–based system for early detection of Acute Lymphoblastic Leukemia using microscopic blood smear images. The study utilized image preprocessing and data augmentation techniques to improve model generalization and classification performance. The developed framework achieved high accuracy in distinguishing leukemia cells from normal blood cells and emphasized the importance of early diagnosis for effective treatment planning. However, the model performance was highly dependent on image quality and dataset diversity, limiting its generalization in real-world clinical environments

Rai et al. (2025) conducted a comparative analysis of various deep learning architectures for leukemia classification using microscopic blood images. The study evaluated multiple CNN-based models in terms of classification accuracy, computational efficiency, and feature extraction performance. Experimental findings indicated that deeper architectures with improved feature learning capabilities produced better classification results. However, several models suffered from increased computational cost, overfitting issues, and reduced efficiency when handling complex medical image datasets

III. EXISTING SYSTEM

The existing leukaemia detection systems mainly rely on manual microscopic examination of peripheral blood smear images by experienced haematologists. In this traditional diagnostic process, medical experts analyse blood cell morphology such as cell shape, size, nucleus structure, and texture to identify abnormalities and classify different leukaemia subtypes. Although manual diagnosis provides reliable results in clinical practice, the process is highly time-consuming, labour-intensive, and dependent on expert knowledge. The increasing volume of medical data and subtle variations between blood cell images further reduce the efficiency and consistency of conventional diagnostic procedures.

Traditional Machine Learning-Based Classification

Several computer-aided diagnostic systems have been developed using traditional machine learning and image processing techniques for leukaemia classification. These systems generally depend on manual feature extraction methods to identify image characteristics such as colour, texture, and morphology before classification. Conventional algorithms are then used for disease prediction based on the extracted features. Although these methods can reduce the workload of medical professionals to some extent, they often fail to capture complex microscopic patterns and subtle morphological variations present in blood smear images, resulting in limited classification accuracy and reduced robustness.

Microscopic Image Preprocessing Techniques

Existing systems also utilise basic image preprocessing techniques to improve the quality of microscopic blood smear images before analysis. Common preprocessing operations include image resizing, normalization, noise removal, and contrast enhancement to standardize the input images for classification models. While preprocessing improves image clarity and consistency, traditional systems still struggle to achieve high diagnostic performance in complex clinical scenarios due to limitations in feature extraction capability and model generalization.

Limitations of Existing Systems

Many conventional leukaemia detection systems are not fully automated and lack integration with modern web-based healthcare platforms. Most existing approaches require continuous human intervention and do not provide real-time diagnostic support. In addition, traditional machine learning models often suffer from lower scalability, high computational complexity, and reduced efficiency when processing large medical datasets. Therefore, there is a need for an advanced deep learning–based automated diagnostic system capable of providing accurate, efficient, and real-time leukaemia classification with improved accessibility and healthcare support.

IV. PROPOSED SYSTEM

The proposed system is a web-based application designed to automate the detection and classification of blood-related diseases using deep learning techniques. It integrates a trained ResNeXt convolutional neural network model with a Flask-based web interface, enabling users to upload blood cell images for analysis. The system processes the input images through preprocessing steps such as resizing, normalization, and tensor conversion before feeding them into the model for prediction. It classifies the images into four categories—Benign, Early, Pre, and Pro—representing different stages or conditions of the disease.

The core strength of the proposed system lies in the use of the ResNeXt architecture, which enhances feature extraction through grouped convolutions and residual learning. This allows the model to capture complex patterns in medical images with higher accuracy and efficiency compared to traditional methods. The system is also designed to leverage GPU acceleration when available, ensuring faster processing and real-time predictions. Additionally, secure file handling mechanisms are implemented to safely manage uploaded images.

The application provides a simple and user-friendly interface, making it accessible to both medical professionals and non-technical users. By deploying the model on a web platform, the system enables remote access and real-time diagnosis support, reducing the need for manual intervention. Overall, the proposed system aims to improve diagnostic accuracy, reduce workload on healthcare professionals, and provide a scalable solution for early detection of blood diseases.

V. SYSTEM ARCHTECTURE

The system architecture of the proposed leukaemia subtype classification framework is designed to provide accurate, efficient, and automated medical image analysis using deep learning techniques. The architecture integrates microscopic blood smear image processing with the ResNeXt deep learning model to support reliable disease detection and classification. The system follows a modular architecture in which each component performs specific operations independently while contributing to the complete diagnostic workflow. The architecture includes image acquisition, preprocessing, feature extraction, classification, result visualization, and database management modules. This structured design improves scalability, computational efficiency, and ease of integration with future medical imaging technologies.

User Interaction and Front-End Interface

The user interacts with the system through a user-friendly web-based interface designed for easy image upload and result visualization. The interface allows medical professionals or laboratory technicians to upload microscopic blood smear images for analysis. It also provides options to view classification results, predicted leukaemia subtype, and performance details of the diagnostic model. The front-end interface ensures smooth communication between users and the backend processing system, enabling fast and convenient disease diagnosis support.

ResNeXt Model Interface and Deep Learning Processing

After image upload, the microscopic blood smear images are forwarded to the preprocessing and deep learning module. In this stage, the images undergo resizing, normalization, noise reduction, and data augmentation to improve image quality and model generalization. The processed images are then supplied to the ResNeXt architecture for automated feature extraction and classification. The ResNeXt model uses grouped convolutions and residual connections to learn complex morphological features such as nucleus shape, cytoplasm texture, and cell boundaries. The extracted deep features are passed through fully connected layers and a softmax classifier to accurately identify different leukaemia subtypes including Acute Lymphoblastic Leukaemia (ALL), Acute Myeloid Leukaemia (AML), and normal blood cells.

Result Delivery and Visualization

Once the classification process is completed, the prediction results are transferred to the backend system for result formatting and visualization. The system displays the classified leukaemia subtype along with prediction confidence and performance metrics. Users can analyse the generated results through graphs, confusion matrices, ROC curves, and classification accuracy outputs. This visualization module helps medical professionals interpret diagnostic outcomes clearly and supports effective clinical decision-making.

Database Management and System Scalability

The proposed system stores uploaded microscopic images, preprocessing information, classification outputs, and user records within a structured database management system. This storage mechanism enables efficient data retrieval, result tracking, and future analysis of medical records. The modular architecture also supports scalability, allowing integration of larger medical datasets, advanced preprocessing methods, and improved deep learning architectures in future

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developments. The scalable framework ensures long-term adaptability and supports the development of intelligent computer-aided diagnostic systems for haematological disease detection.

VI. WORKING SCENARIO

The proposed leukaemia subtype classification system operates as an automated deep learning–based medical image analysis framework designed to assist in accurate and efficient disease diagnosis. The workflow begins when the user uploads microscopic blood smear images through the web-based interface. These uploaded images contain important morphological information of blood cells, including nucleus shape, cytoplasm texture, and cell structure, which are essential for identifying different leukaemia subtypes such as Acute Lymphoblastic Leukaemia (ALL), Acute Myeloid Leukaemia (AML), and normal blood cells.

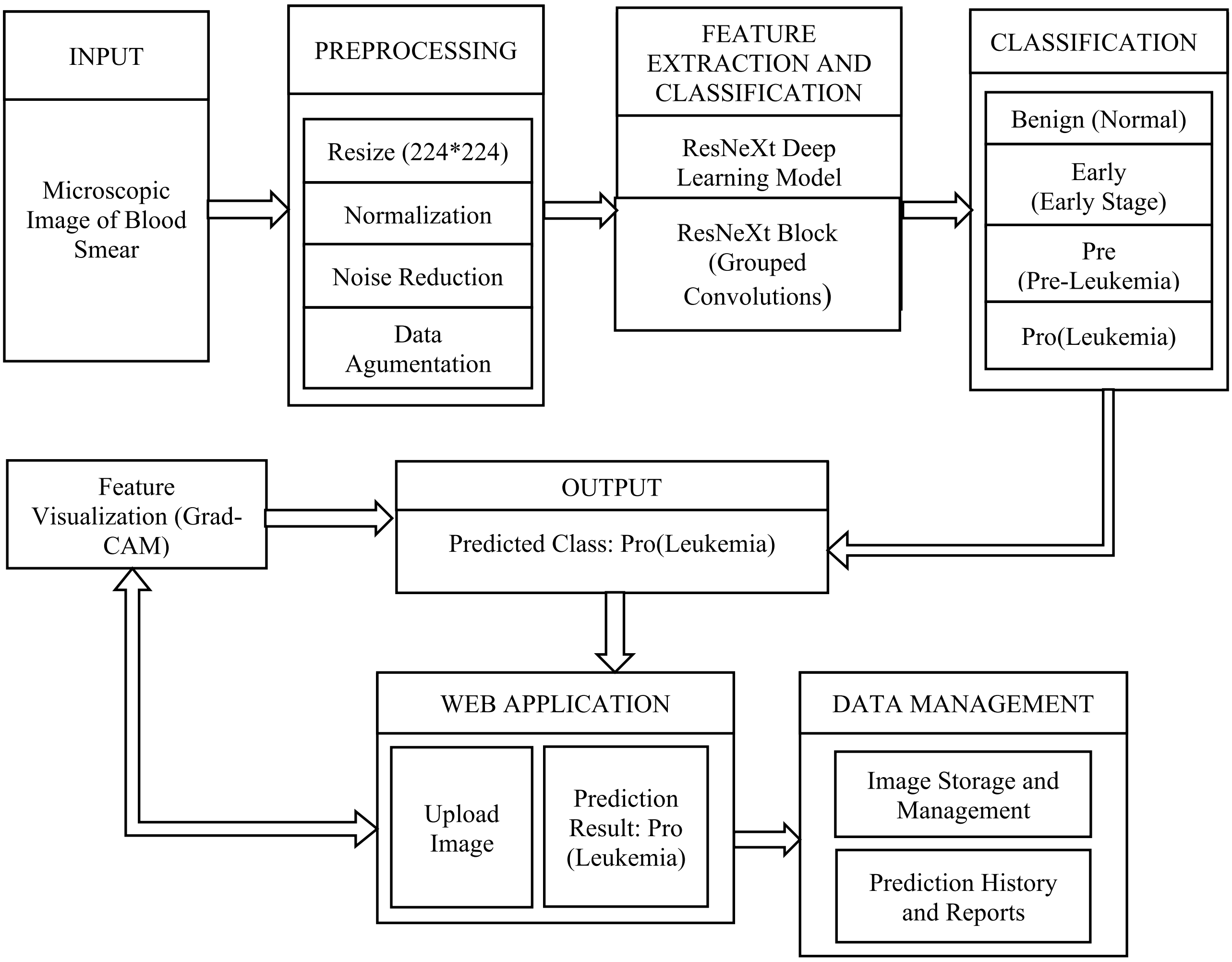


Fig 1. Workflow of Identification of Leukemia Subtypes from Microscopic Images using ResNeXt Algorithm

Initially, the uploaded microscopic images undergo preprocessing operations to improve image quality and standardize the dataset for deep learning analysis. The preprocessing stage includes image resizing, normalization, noise removal, and contrast enhancement to ensure uniform image dimensions and stable model performance. In addition, data augmentation techniques such as rotation, flipping, zooming, and cropping are applied to increase dataset diversity and reduce overfitting. These preprocessing techniques help the system handle variations in staining conditions, lighting, and cell orientation present in microscopic blood smear images.

After preprocessing, the refined images are transferred to the ResNeXt-based deep learning model for automated feature extraction and classification. The ResNeXt architecture uses grouped convolutions and residual connections to capture complex morphological patterns from blood cell images efficiently. The model automatically learns discriminative features such as abnormal nucleus size, irregular cell boundaries, chromatin density, and cytoplasm characteristics associated with different leukaemia subtypes. The extracted features are processed through fully connected layers and a softmax classifier to predict the corresponding disease category with high accuracy.

The proposed automated framework significantly reduces manual workload and improves diagnostic efficiency by providing rapid and reliable leukaemia subtype classification from microscopic blood smear images. The modular architecture of the system also supports future integration of advanced deep learning models, larger medical datasets, and intelligent healthcare applications for enhanced haematological disease diagnosis.

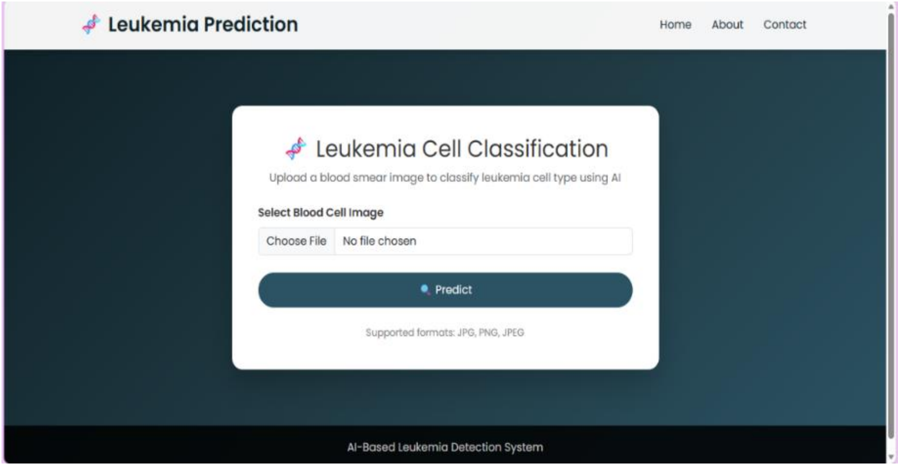
VII. TECHNICAL METHODOLOGY

The proposed Leukemia Subtype Classification System begins with microscopic blood smear image acquisition and preprocessing. When a user uploads a microscopic blood smear image, the backend validates the image format, resolution, and quality before forwarding it to the preprocessing module. Image preprocessing techniques such as resizing, normalization, noise removal, and contrast enhancement are performed to improve image quality and maintain uniformity across the dataset. Data augmentation methods including rotation, flipping, zooming, and cropping are also applied to increase dataset diversity and improve model generalization during deep learning training.

Once preprocessing is completed, the system forwards the processed microscopic images to the ResNeXt deep learning architecture for automated feature extraction and classification. The ResNeXt model uses grouped convolutions and residual connections to learn complex morphological patterns present in blood cells. The model extracts important discriminative features such as nucleus shape, chromatin density, cytoplasm texture, and cell boundaries, which are essential for identifying different leukemia subtypes. The extracted deep features are then passed through fully connected layers and a softmax classifier to predict the corresponding disease category, including Acute Lymphoblastic Leukaemia (ALL), Acute Myeloid Leukemia (AML), and normal blood cells.

During model training, optimization algorithms such as Adam and stochastic gradient descent are used to minimize classification loss and improve prediction accuracy. The ResNeXt architecture performs hierarchical feature learning through multiple transformation paths, enabling efficient classification with reduced computational complexity. The trained model analyses microscopic blood smear images and generates prediction outputs with high diagnostic accuracy and reliability.

After classification, the generated prediction results undergo result visualization and performance evaluation. The final output, along with classification confidence, confusion matrix analysis, ROC curve, accuracy graph, precision, recall, and F1-score metrics, is displayed through the user interface. The classified images, prediction reports, and user records are stored in the database system for future reference and clinical analysis. The backend API then transmits the final results to the frontend interface, where users can visualize, compare, and analyse the diagnostic outputs. This technical methodology ensures scalability, computational efficiency, reliable automated diagnosis, and effective integration of deep learning models for intelligent leukemia subtype classification.



Leukemia Cell Classification

Upload a blood smear image to classify leukemia cell type using AI

Select Blood Cell Image

No file chosen

Supported formats: JPG, PNG, JPEG

AI-Based Leukemia Detection System

Fig.2 Home page – AI-Based Leukemia

This Fig.2 shows a web-based Leukemia Prediction System where users can upload blood smear images and use AI to classify leukemia cell types through an easy-to-use interface.

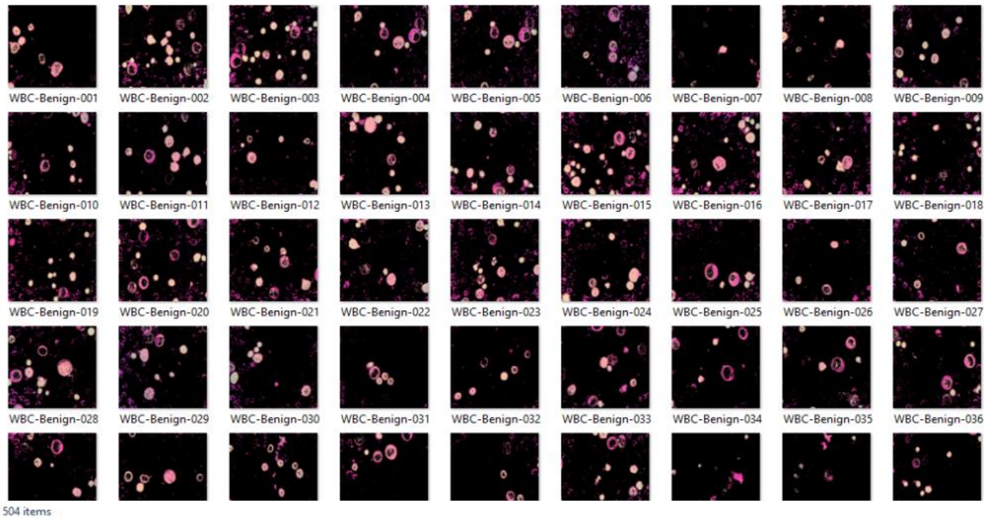
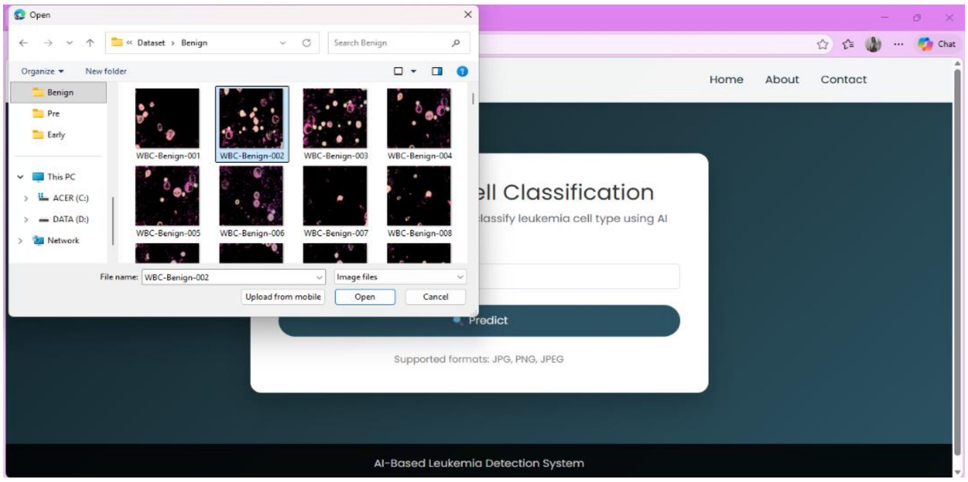


Fig.3 Leukemia Images Data Collection

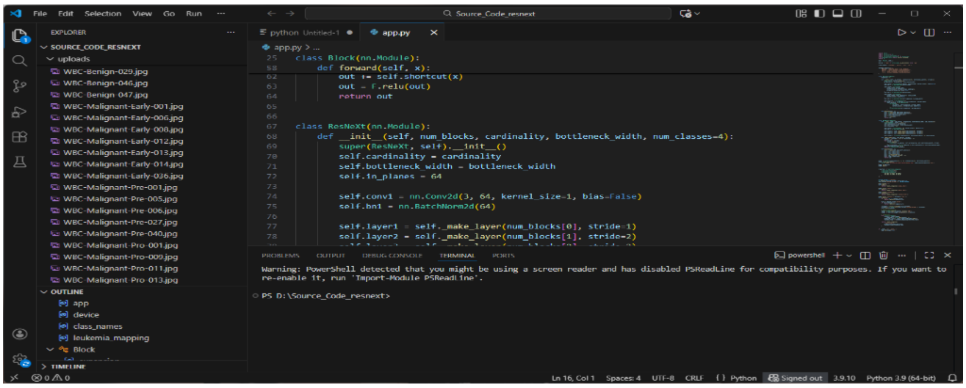
This Fig.3 shows blood smear image samples used for training and testing the leukemia detection model to identify normal white blood cell patterns.



File name: WBC-Benign-002

Fig.4 Blood Smear Image Upload for Leukemia Classification

This Fig.4 shows the process of uploading a blood smear image into the Leukemia Prediction System for AI-based leukemia cell classification and stage detection

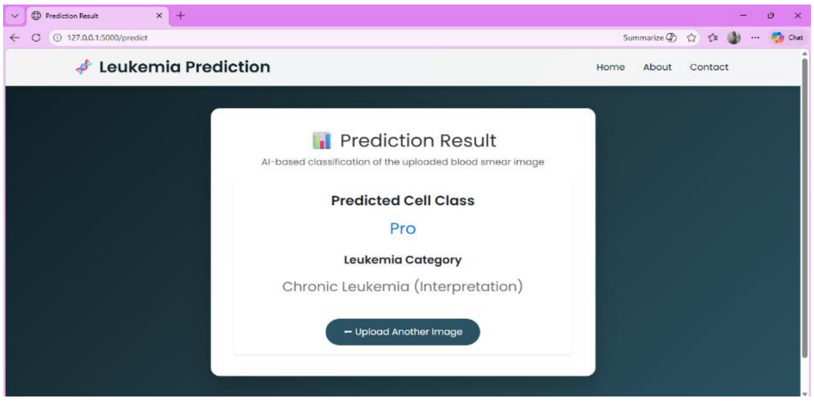


```
class Block(nn.Module):
    def forward(self, x):
            out += self.shortcut(x)
            out = F.relu(out)
            return out


class ResNeXt(nn.Module):
    def __init__(self, num_blocks, cardinality, bottleneck_width, num_classes=4):
        super(ResNeXt, self).__init__()
        self.cardinality = cardinality
        self.bottleneck_width = bottleneck_width
        self.in_planes = 64

        self.conv1 = nn.Conv2d(3, 64, kernel_size=1, bias=False)
        self.bn1 = nn.BatchNorm2d(64)

        self.layer1 = self._make_layer(num_blocks[0], stride=1)
        self.layer2 = self._make_layer(num_blocks[1], stride=2)
```

```
Warning: PowerShell detected that you might be using a screen reader and has disabled PSReadLine for compatibility purposes. If you want to
re-enable it, run 'Import-Module PSReadLine'.

PS D:\Source_Code_resnext>
```

Fig.5 Python-Based ResNeXt Architecture for Leukemia Detection

This Fig.5 shows the Python-based ResNeXt model implementation used for AI-based leukemia detection and classification



Prediction Result

AI-based classification of the uploaded blood smear image

Predicted Cell Class

Pro

Leukemia Category

Chronic Leukemia (Interpretation)

Fig.6 Leukemia Prediction Result Page

This Fig.6 Shows AI-based leukemia prediction result showing the detected leukemia stage and classification from the uploaded blood smear image.

VIII. CONCLUSION

This study presented a deep learning-based framework for the automated identification of leukaemia subtypes from microscopic blood smear images using the ResNeXt architecture. Early and accurate detection of leukaemia is important for powerful treatment planning and improving patient viability rates. The classical methods of diagnosis are based on manual examination by a microscope, a time-consuming process that is still subject to interpretation by specialists. In order to address these shortcomings, the suggested system uses a deep learning model, which is based on ResNeXt and has the ability to obtain discriminative features in microscopic images by default. Preprocessing of the dataset, normalising images, resizing, and augmenting the data helped to improve the quality and diversity of the dataset, improving the model's generalisation ability. The ResNeXt structure can use a grouped convolution and residual linkages to identify any intricate morphological structure in blood cells. The experimental data shows that the proposed model can attain high classification efficiency with an overall accuracy of 98.70%, a precision of 97.50%, a recall of 96.90% and an F1 of 97.20%. The ROC analysis and confusion matrix also prove the high level of discriminative ability of the model to differentiate between leukaemia subtypes, including ALL, AML, and normal cells. Overall, the proposed system provides an efficient and reliable approach for leukaemia subtype classification. This automated framework can support medical professionals in rapid and accurate diagnosis while reducing manual workload, thereby contributing to the development of intelligent computer-aided diagnostic systems for haematological diseases.

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