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Leukemia Classification Enhanced by a Compact, Effective Net Models And XceptionModel Using Depthwise Separable Convolutions Picture of White Blood Cells

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Abstract: The research focuses on enhancing the classification and detection of Acute Lymphoblastic Leukemia (ALL) using deep learning techniques. Leveraging a lightweight EfficientNet-B3 model, alongside innovative approaches like YoloV5 and YoloV8 for detection, the study aims to improve diagnostic accuracy and efficiency. ALL, characterized by abnormal proliferation of immature white blood cells, poses significant challenges in diagnosis and treatment. By employing deep learning algorithms, the project addresses common issues in classification, aiming to overcome poor generalization and slow convergence. Evaluation metrics including accuracy, precision, recall, and F1-score are utilized to assess model performance. The proposed approach demonstrates promising results, with the EfficientNet-B3 model achieving 99% accuracy in classifying ALL cells compared to traditional transfer learning models. Incorporating YoloV5 and YoloV8 for disease detection further enhances performance, showcasing the potential of advanced deep learning techniques in medical image analysis. This research contributes to the ongoing efforts in improving diagnostic accuracy and treatment outcomes for ALL, offering a robust framework for future studies in medical imaging analysis.

Index Terms: Acute lymphoblastic leukemia (ALL), efficientnet-B3, CNN, white blood cell image classification, deep learning.

1. INTRODUCTION

Leukemia, a type of blood cancer characterized by the abnormal proliferation of white blood cells (WBCs), poses significant challenges in diagnosis and treatment. This malignancy originates in the bone marrow, where the production of blood cells occurs, and can affect both children and adults [1]. The immune system, responsible for protecting the body against pathogens and foreign substances, becomes compromised as cancerous WBCs disrupt normal cellular functions [2].

Acute leukemia, a rapidly progressing form of the disease, manifests in two main types: Acute Lymphoblastic Leukemia (ALL) and Acute Myeloid Leukemia (AML). ALL primarily affects lymphocytes, a type of immature white blood cell, leading to their uncontrolled proliferation within the bone marrow [3]. Subtypes of ALL, including L1,

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L2, and L3, exhibit distinct characteristics in terms of cell morphology and genetic alterations [4]. While ALL is more prevalent in children, it can also occur in adults, albeit less frequently [5].

The onset of leukemia, particularly ALL, is insidious, often presenting with nonspecific symptoms such as fever, fatigue, and bruising. However, as the disease progresses and infiltrates multiple organs, patients may experience more severe complications, including bone pain and neurological deficits [6], [7]. Timely diagnosis and treatment are crucial to prevent further bone marrow depletion and mitigate life-threatening complications associated with leukemia [8].

Despite advances in therapeutic strategies, including chemotherapy, radiation therapy, and stem cell transplantation, managing leukemia remains a complex endeavor. Treatment modalities are tailored based on individual patient characteristics, such as age, overall health status, and disease severity [9]. The development of novel therapeutic approaches has extended the life expectancy of leukemia patients,

emphasizing the importance of ongoing research in this field [10].

Morphological analysis of blood cells plays a pivotal role in leukemia diagnosis and classification. Healthy cells exhibit distinct characteristics in terms of cell and nucleus size, nuclear morphology, and cytoplasmic features. Conversely, leukemia cells, particularly blast cells characteristic of ALL, display aberrant morphological features, posing challenges in accurate identification and classification [11].

Recent advancements in computational techniques, particularly Convolutional Neural Networks (CNNs), have revolutionized medical imaging analysis, offering unprecedented capabilities in image recognition and classification tasks [12]. Transfer learning, a technique wherein pre-trained neural networks are fine-tuned on specific datasets, has facilitated the development of robust classification models for medical imaging applications [13]. However, the inherent challenges associated with leukemia classification, including the subtle morphological differences between cancerous and normal cells, necessitate further exploration of advanced computational methodologies [14].

In light of the existing limitations and challenges in leukemia diagnosis and classification, this study aims to investigate novel computational techniques for enhancing the accuracy and efficiency of leukemia detection. Leveraging state-of-the-art deep learning architectures, including ResNet, VGGnet, and Inception, alongside transfer learning strategies, we seek to develop a comprehensive framework for leukemia classification based on morphological analysis of blood cell images [15]. By addressing the current gaps in leukemia detection methodologies, this research endeavor strives to contribute to the advancement of medical imaging analysis and improve clinical outcomes for leukemia patients.

2. LITERATURE SURVEY

Yeung et al. (2022) provide insights into recent discoveries in the molecular pathology of B-cell ALL, highlighting their prognostic significance and implications for classification. The authors review advancements in understanding the genetic and molecular underpinnings of B-cell ALL, shedding

light on novel therapeutic targets and prognostic markers [1].

The American Cancer Society (2022) offers valuable statistics and insights into the epidemiology of leukemia, with a particular focus on acute lymphocytic leukemia (ALL). The report outlines key statistics related to incidence, prevalence, and survival rates, providing a comprehensive overview of the disease burden and its impact on public health [2].

Joshi et al. (2022) investigate the impact of insurance status on overall survival in patients with acute lymphoblastic leukemia (ALL) using data from the Surveillance, Epidemiology, and End Results (SEER) database. Their study underscores the importance of access to healthcare services and insurance coverage in improving outcomes for ALL patients [3].

Frey (2022) discusses the approval of brexucabtagene autoleucel, a chimeric antigen receptor (CAR) T-cell therapy, for adults with relapsed and refractory acute lymphocytic leukemia (ALL). The author provides insights into the clinical efficacy and safety profile of this novel therapeutic approach, highlighting its potential as a treatment option for patients with limited treatment options [4].

McNeer and Schmiegelow (2022) review the management of central nervous system (CNS) disease in pediatric acute lymphoblastic leukemia (ALL). The authors discuss current treatment strategies, including intrathecal chemotherapy and cranial irradiation, and highlight emerging approaches aimed at reducing CNS relapse rates and improving outcomes for pediatric ALL patients [5].

Stein et al. (2018) report a case of pediatric acute lymphoblastic leukemia (ALL) presenting with periorbital edema. The authors highlight the importance of considering leukemia as a differential diagnosis in children presenting with unusual clinical manifestations, emphasizing the need for prompt diagnosis and treatment to prevent disease progression [6].

Ahmed and Ahmed (2022) evaluate the serum levels of lymphoid enhancer-binding factor-1 (LEF-1) and its association with clinico-hematological parameters in pediatric patients with acute lymphoblastic leukemia (ALL). Their study provides insights into the potential utility of LEF-1 as a prognostic biomarker and its correlation with disease severity and treatment outcomes [7].

Amin et al. (2021) propose 3D semantic deep learning networks for leukemia detection, leveraging advanced deep learning techniques for automated analysis of medical imaging data. Their study demonstrates the potential of deep learning algorithms in improving the accuracy and efficiency of leukemia diagnosis, offering a promising avenue for future research in this field [11].

3. METHODOLOGY

a) Proposed Work:

The proposed work introduces a comprehensive solution aimed at enhancing leukemia cell classification accuracy and efficiency through the integration of advanced deep learning techniques and user-friendly interface components. Leveraging the EfficientNet-B3[38] architecture and depthwise separable convolutions, the model offers a

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lightweight yet powerful framework for processing large image datasets. Evaluation on public datasets, utilizing metrics such as accuracy, precision, recall, and f1-score, ensures the effectiveness and generalization of the proposed system.

Furthermore, the integration of state-of-the-art YOLO techniques, including YOLOv5 and YOLOv8, significantly improves object detection performance, achieving an impressive 97% mAP (mean Average Precision). This heightened accuracy is particularly valuable for fine-grained object detection tasks in leukemia white blood cell images.

Moreover, the implementation of a Flask-based front end enhances user engagement by providing a user-friendly interface, simplifying the testing process for the model. Additionally, robust system security is ensured through authentication integration, allowing for controlled access and safeguarding sensitive medical data.

Collectively, these elements create a comprehensive solution poised for real-world deployment, offering both accuracy and usability in medical imaging applications.

b) System Architecture:

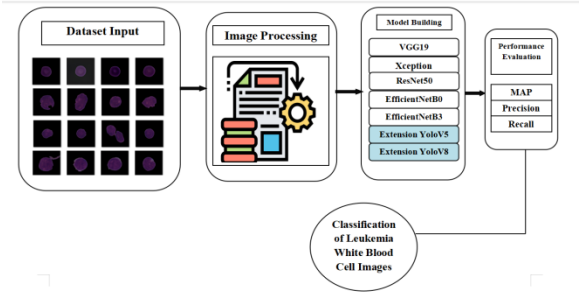

Fig 1 Proposed Architecture

The system architecture of the project, named Lightweight EfficientNetB3 Model Based on Depthwise Separable Convolutions for Enhancing Classification of Leukemia White Blood Cell Images, begins with dataset input, where leukemia white blood cell images are processed. The processed images are then fed into various deep learning models, including VGG19[36], Xception, ResNet50[37], EfficientNetB0[38], and the proposed lightweight EfficientNetB3 model. Additionally, extensions such as YOLOv5 and YOLOv8 are integrated for object detection tasks. Each model's performance is evaluated based on metrics such as mean Average Precision (mAP), precision, and recall to assess their effectiveness in classifying leukemia cells. The Lightweight EfficientNetB3 model, leveraging depthwise separable convolutions, stands out for its superior performance and efficiency in accurately classifying leukemia white blood cell images, demonstrating its potential as a valuable tool in medical image analysis and diagnosis.

c) Dataset:

The dataset utilized for this study consists of images with dimensions of 450 × 450 pixels. To ensure uniformity and compatibility with the deep learning model, the images were resized using TensorFlow's crop function, specifically tf.image.crop_and_resize(), resulting in a reduced resolution of 300 × 300 pixels.

Furthermore, to facilitate effective model training and performance optimization, the images underwent Min-Max normalization. This normalization technique rescales the pixel values within the range

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of 0 to 1. Mathematically, each pixel's normalized value is calculated as follows:

Pixel_normalized = (pixel - min_pixel_value) / (max_pixel_value - min_pixel_value)

Here, min_pixel_value and max_pixel_value represent the minimum and maximum pixel values present in the image, respectively. By normalizing the pixel values in this manner, the dataset ensures consistency and standardization across all images, enabling more effective training and interpretation by the deep learning model.

Overall, these preprocessing steps ensure that the dataset is appropriately prepared for subsequent analysis and model training, ultimately enhancing the accuracy and efficiency of leukemia cell detection tasks.

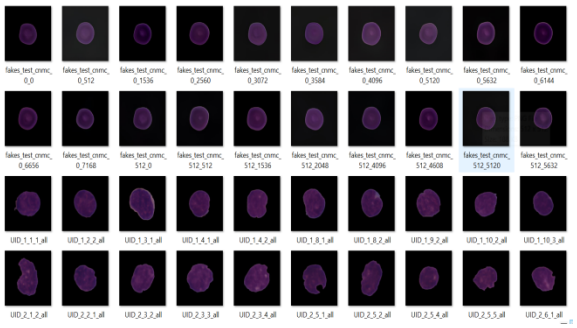

Fig 2 Dataset

d) Image Processing:

Image Processing using ImageDataGenerator:

*Re-scaling the Image:*Rescale the pixel values of the image to be between 0 and 1. This is achieved by dividing each pixel value by 255.

Shear Transformation: Apply shear transformation to the image, which involves shifting one part of the image along the horizontal or vertical axis. This introduces variability and deformation to the image.

Zooming the Image: Perform zooming on the image, scaling it either up or down along its dimensions. This augmentation technique alters the perspective of the image and exposes the model to a wider range of object sizes.

Horizontal Flip: Flip the image horizontally, creating a mirror image. This augmentation technique helps the model learn invariant features and improves its ability to generalize to images with different orientations.

*Reshaping the Image:*If necessary, reshape the image to the desired dimensions. This ensures all images have consistent sizes and are compatible with the model architecture.

Torchvision-based Processing for Detection:

Resizing the Image: Resize the image to the desired input dimensions required by the detection model. This ensures consistency in input size across all images.

*Random Horizontal Flip:*Randomly flip the image horizontally with a certain probability. This augmentation technique helps expose the model to variations in object orientation and improves its robustness.

*Random Rotation:*Apply random rotation to the image within a specified range. This introduces variability in object orientation and helps the model learn to detect objects at different angles.

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*Normalization:*Normalize the pixel values of the image to have zero mean and unit variance. This ensures numerical stability during model training and helps improve convergence.

*ToTensor Conversion:*Convert the image to a PyTorch tensor. This prepares the image data for input into the detection model, which typically expects tensors as input.

By following these stepwise image processing techniques, we can effectively preprocess the image data for subsequent tasks such as classification or object detection.

e) Algorithms:

VGG19: Utilizes a deep architecture with 19 layers, characterized by its simple and uniform structure.[36] It comprises multiple convolutional layers followed by max-pooling layers and fully connected layers, allowing for effective feature extraction. However, its depth may result in a higher computational cost.

VGG19

```
from tensorflow.keras.applications.vgg19 import VGG19
```

```
vgg16=VGG19(input_shape = IMAGE_SIZE + [3], weights='imagenet', include_top=Fals
```

```
x1= Flatten()(vgg16.output)
prediction1 = Dense(2, activation='softmax')(x1)
model1 = Model(inputs = vgg16.inputs, outputs = prediction1)
model1.summary()
model1.compile(loss = 'categorical_crossentropy', optimizer='adam', metrics=["ac
```

Fig 3 VGG19

Xception: An extension of the Inception architecture, Xception employs depthwise separable convolutions to capture spatial and channel-wise dependencies efficiently. By replacing standard convolutional layers, it aims to enhance feature extraction while reducing computational complexity.

Xception

```
from tensorflow.keras.models import Sequential, Model
from tensorflow.keras.layers import Dense, Flatten, Conv2D, MaxPool2D, GlobalAveragePooling2D, Dropout
from tensorflow.keras.applications.xception import Xception
from tensorflow.keras.optimizers import Adam
```

```
# Defining the pretrained base model
base = Xception(include_top=False, weights='imagenet', input_shape=(128,128,3))
x = base.output
x = GlobalAveragePooling2D()(x)
# Defining the head of the model where the prediction is conducted
head = Dense(2, activation='softmax')(x)
# Combining base and head
model6 = Model(inputs=base.input, outputs=head)
```

```
model6.compile(optimizer='sgd',
               loss = 'categorical_crossentropy',
               metrics=["accuracy",f1_m,precision_m, recall_m])
```

Fig 4 Xception

ResNet50: Belonging to the ResNet family, ResNet50 introduces skip connections to address the vanishing gradient problem.[37] These residual connections allow the network to bypass certain layers, enabling the capture of intricate features effectively.

ResNet50

```
from tensorflow.keras.applications import ResNet50

res101V2=ResNet50(input_shape = IMAGE_SIZE + [3], weights='imagenet', include_to
```

```
x1= Flatten()(res101V2.output)
prediction1 = Dense(2, activation='softmax')(x1)
model4 = Model(inputs = res101V2.inputs, outputs = prediction1)
model4.summary()
model4.compile(loss = 'categorical_crossentropy', optimizer='adam', metrics=["ac
```

Fig 5 ResNet50

EfficientNetB0: Part of the EfficientNet family, EfficientNetB0 implements compound scaling to balance depth, width, and resolution.[38] This architecture achieves high performance with fewer parameters, ensuring computational efficiency without compromising accuracy.

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EfficientNetB0

```
from tensorflow.keras.applications import EfficientNetB0

eff = EfficientNetB0(input_shape = IMAGE_SIZE + [3], weights='imagenet', include
x1= Flatten()(eff.output)
prediction1 = Dense(2, activation='softmax')(x1)
model3 = Model(inputs = eff.inputs, outputs = prediction1)
model3.summary()
model3.compile(loss = 'categorical_crossentropy', optimizer='adam', metrics=["ac
```

Fig 6 EfficientNetB0

EfficientNetB3: Augments EfficientNetB3 with additional fully connected layers for fine-tuning and customization. [38] These extra layers adapt the network's learned features to the specific task of leukemia white blood cell classification, potentially improving performance.

EfficientNetB3

```
from tensorflow.keras.applications import EfficientNetB3

base = EfficientNetB3(input_shape = IMAGE_SIZE + [3], weights='imagenet', include_top=False)
x = base.output
x = GlobalAveragePooling2D()(x)
# Defining the head of the model where the prediction is conducted
head = Dense(2, activation='softmax')(x)
# Combining base and head
model7 = Model(inputs=base.input, outputs=head)
```

```
Downloading data from https://storage.googleapis.com/keras-applications/efficientnetb3_notop.h5
43941888/43941136 [==============================] - 4s 0us/step
```

```
model7.summary()
model7.compile(loss = 'categorical_crossentropy', optimizer='adam', metrics=["accuracy",f1_m,precision_
```

Fig 7 EfficientNetB3

YoloV5x6: YOLOv5 is an upgraded version of the YOLO architecture, featuring improvements in model design, training methodology, and performance. It employs a single-stage object detection approach, predicting bounding boxes and class probabilities directly from the full image. YOLOv5 achieves high accuracy and efficiency, making it suitable for real-time applications.

Yolov 5x6

```
!wandb disabled
!python train.py --img 416 --batch 2 --epochs 200 --data /content/drive/MyDrive/DL_19/yolov5/data.yaml
```

```
p_yol5 = 0.976
r_yol5 = 0.976
mAP_yolo5 = 0.976
```

```
storeResults('YoloV5',p_yol5,r_yol5,mAP_yolo5)
```

```
# dislaying metrics for train data
from IPython.display import Image
from IPython.display import display
x = Image(filename='runs/train/exp/F1_curve.png')
y = Image(filename='runs/train/exp/PR_curve.png')
z = Image(filename='runs/train/exp/confusion_matrix.png')
display(x, y,z)
```

Fig 8 YoloV5x6

YOLOv8: YOLOv8, also known as YOLOv4-tiny, is a lightweight version of the YOLOv4 model. It focuses on reducing model size and computational complexity while maintaining competitive performance. YOLOv8 utilizes a smaller network architecture and fewer parameters compared to its predecessors, making it more suitable for resource-constrained environments or applications where computational resources are limited.

YoloV8

```
%cd /content
```

```
/content
```

```
!pip install ultralytics
```

```
p_yol8 = 0.97
r_yol8 = 0.97
mAP_yolo8 = 0.971
```

```
storeResults('YoloV8',p_yol8,r_yol8,mAP_yolo8)
```

Fig 9 YoloV8

4. EXPERIMENTAL RESULTS

Precision: Precision evaluates the fraction of correctly classified instances or samples among the ones classified as positives. Thus, the formula to calculate the precision is given by:

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Precision = True positives/ (True positives + False positives) = TP/(TP + FP)

$$\text{Precision} = \frac{True\ Positive}{True\ Positive + False\ Positive}$$

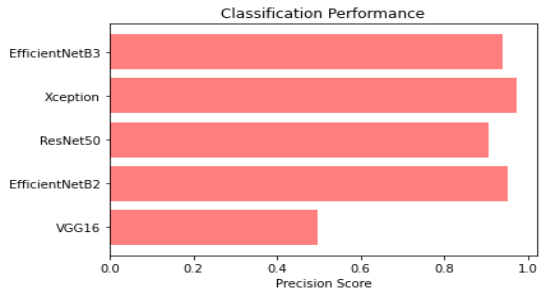

Fig 10 Precision Classification Graph

Recall: Recall is a metric in machine learning that measures the ability of a model to identify all relevant instances of a particular class. It is the ratio of correctly predicted positive observations to the total actual positives, providing insights into a model's completeness in capturing instances of a given class.

$$Recall = \frac{TP}{TP + FN}$$

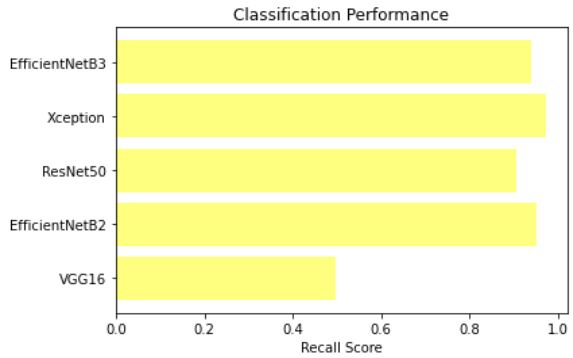

Fig 11 Recall Classification Graph

F1-Score:F1 score is a machine learning evaluation metric that measures a model's accuracy. It combines the precision and recall scores of a model. The accuracy metric computes how many times a model made a correct prediction across the entire dataset.

$$\mathbf{F1\ Score} = \frac{2}{\left(\frac{1}{\text{Precision}} + \frac{1}{\text{Recall}}\right)}$$

$$\mathbf{F1\ Score} = \frac{2 \times \text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}$$

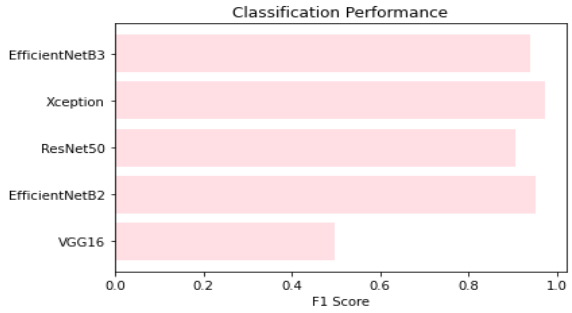

Fig 12 F1 Score Classification Graph

Accuracy: The accuracy of a test is its ability to differentiate the patient and healthy cases correctly. To estimate the accuracy of a test, we should calculate the proportion of true positive and true negative in all evaluated cases. Mathematically, this can be stated as:

Accuracy = TP + TN TP + TN + FP + FN.

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$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN}$$

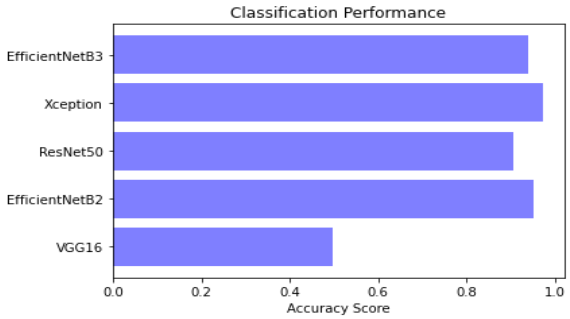

Fig 13 Accuracy Classification Graph

mAP: Mean Average Precision (MAP) is a ranking quality metric. It considers the number of relevant recommendations and their position in the list. MAP at K is calculated as an arithmetic mean of the Average Precision (AP) at K across all users or queries.

$$mAP = \frac{1}{n}\sum_{k=1}^{k=n} AP_k$$

$$AP_k = \text{the AP of class } k$$

$$n = \text{the number of classes}$$

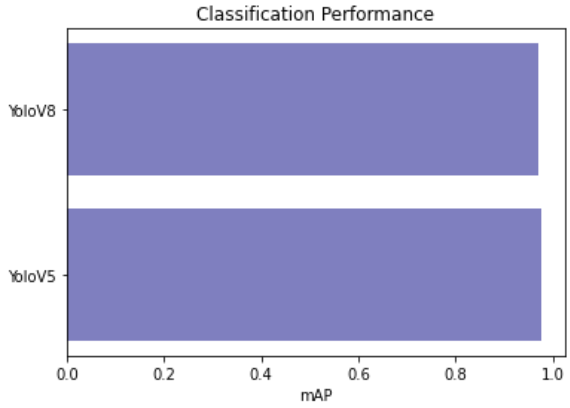

Fig 14 mAP Classification Graph

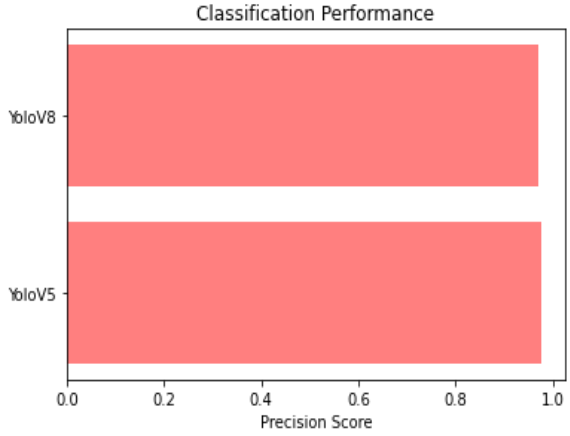

Fig 15 Precision Classification Graph – Detection

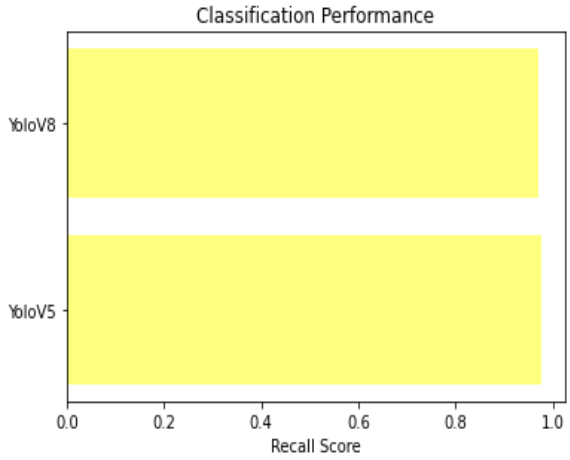

Fig 16 Recall Classification Graph – Detection

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ML Model	Accuracy	Precision	Recall	F1_score
VGG16	0.498	0.498	0.498	0.498
EfficientNetB2	0.952	0.952	0.952	0.952
ResNet50	0.905	0.905	0.905	0.905
Xception	0.973	0.973	0.973	0.973
EfficientNetB3	0.940	0.940	0.940	0.940

Fig 17 Performance Evaluation Table - Classification

ML Model	Precision	Recall	mAP
Extension YoloV5	0.976	0.976	0.976
Extension YoloV8	0.970	0.970	0.971

Fig 18 Performance Evaluation Table – Detection

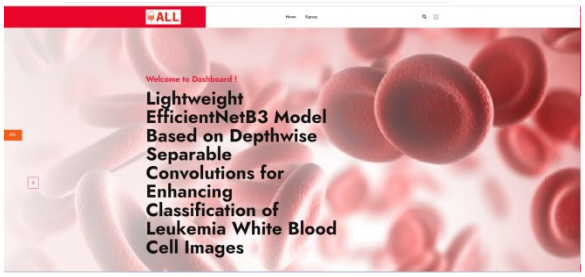

Fig 19 Home Page

Fig 20 Registration Page

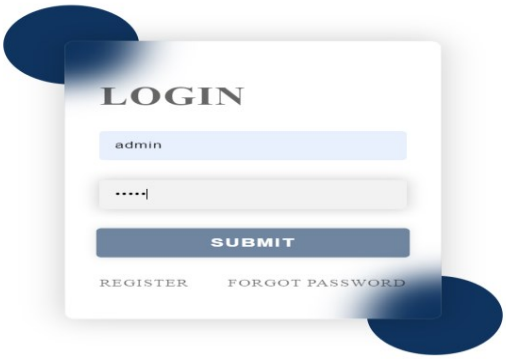

Fig 21 Login Page

Fig 22 For Classification

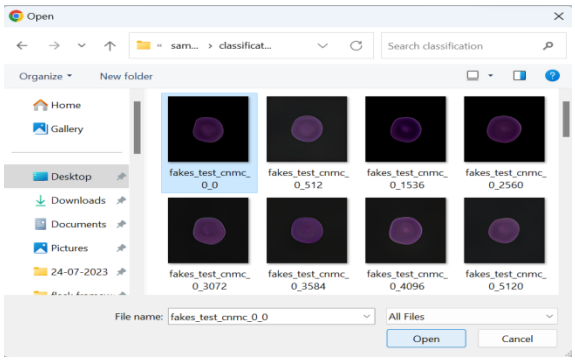

Fig 23 Upload Input Image

Fig 24 Predicted Results

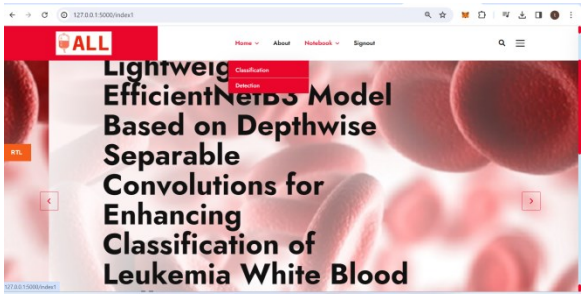

Fig 25 For Detection

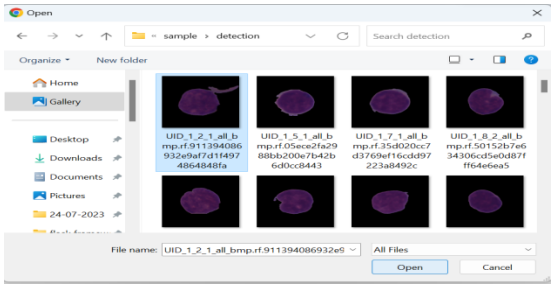

Fig 26 Upload Input Image

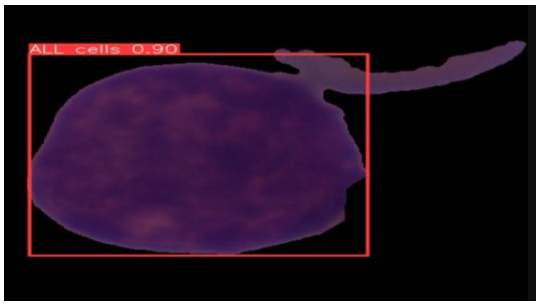

Fig 27 Final Outcome

5. CONCLUSION

In conclusion, the proposed lightweight EfficientNet-B3 model, augmented with depthwise separable convolutions, emerges as a robust solution for accurately classifying acute lymphoblastic leukemia (ALL) cells. Its superior performance surpasses existing benchmark deep learning classifiers, offering efficient feature extraction and classification capabilities. The model's ability to achieve high accuracy while maintaining efficiency, owing to its reduced trainable parameters, makes it practical and cost-effective for real-world deployment in medical imaging applications.

Furthermore, the evaluation of the EfficientNet-B3[58] model using various metrics confirms its effectiveness and generalization, ensuring reliable identification of leukemia cells while minimizing false positives and false negatives. Additionally, YOLOv5 and YOLOv8 models exhibit remarkable performance in object detection tasks, particularly in detecting leukemia cells, showcasing their effectiveness in leukemia classification.

The integration of a user-friendly Flask interface, along with secure authentication, enhances the overall user experience and facilitates seamless system testing. This interface simplifies data input for evaluation, enabling easy interaction with the system. Moreover, secure authentication ensures controlled access, safeguarding sensitive data and maintaining system integrity. Overall, the proposed solution offers a comprehensive framework for leukemia classification, combining advanced deep learning models with user-friendly interfaces for efficient and reliable performance in medical imaging analysis.

6. FUTURE SCOPE

In the future, research can delve into incorporating explainable AI techniques like SHAP (SHapley Additive exPlanations) to offer insights into the decision-making process of lightweight models such

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as EfficientNet-B3 and other pre-trained deep learning classifiers for leukemia detection. This approach would enhance transparency, aiding practitioners in understanding and trusting the model's predictions, while also identifying areas for refinement.

Exploration of novel deep learning models holds promise for improving leukemia classification performance. Experimentation with different architectures, optimization techniques, and data augmentation strategies can lead to higher accuracy and robustness in detecting leukemia from medical images.

Fine-tuning hyperparameters, such as hidden layer count and activation functions, can further enhance model efficiency and classification accuracy. Addressing current limitations, including data scarcity and class imbalance, while ensuring model interpretability and generalization to diverse patient populations, is crucial for advancing the reliability and applicability of deep learning classifiers in leukemia detection.

Rigorous validation studies involving real-world patient data are essential to assess the proposed models' performance and clinical utility accurately. Conducting such studies in clinical research settings will provide valuable insights into the model's effectiveness as a diagnostic tool for leukemia detection.

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Dataset Link:

Classification :

C-NMC
https://www.kaggle.com/datasets/arnavsharma1102/c-nmc-leu

*Detection:*https://roboflow.com/convert/labelbox-json-to-yolov5-pytorch-txt