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Final Presentation

"Deep Learning Approach for localizing and distinguishing white Blood Cells and its precursors in Microscopic Images"

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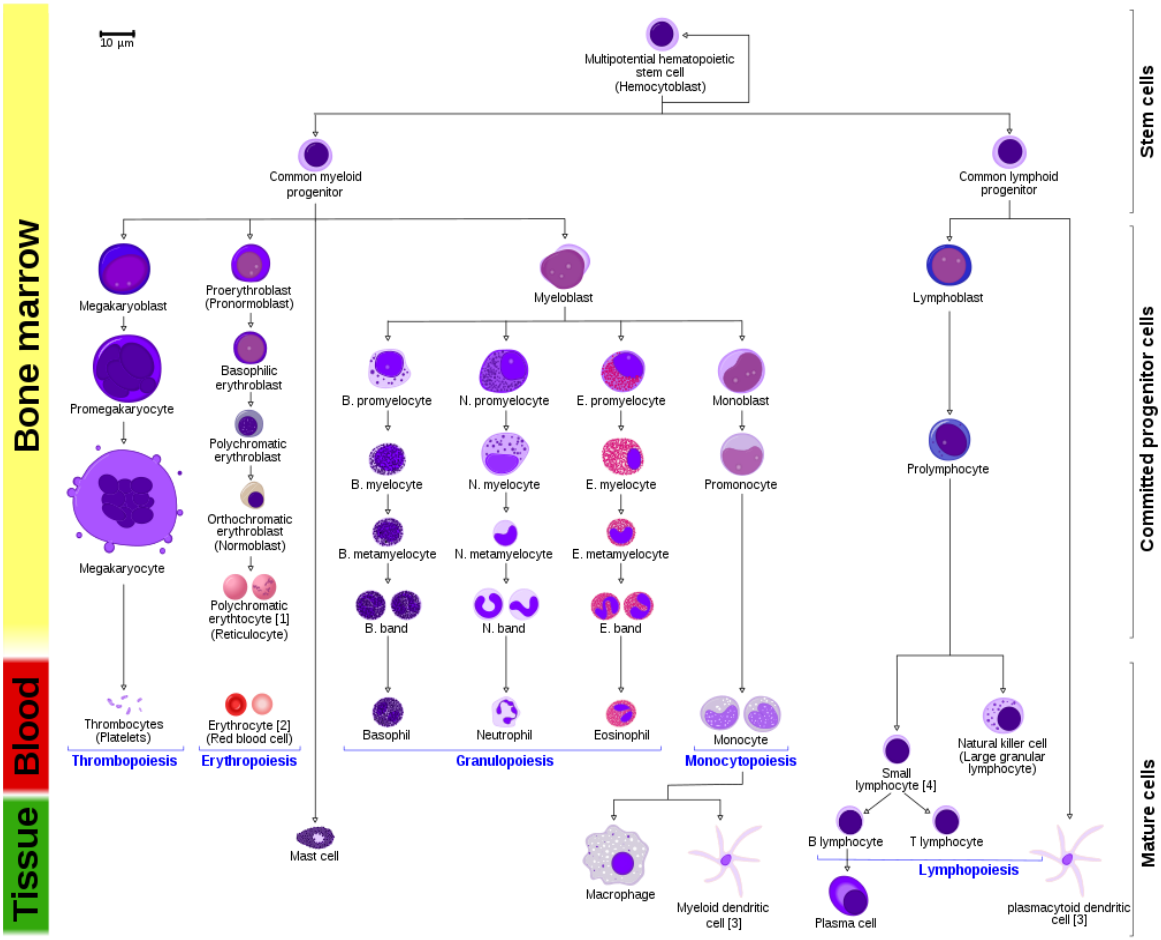
Introduction
Background

Fig: Peripheral white blood cells with its precursors and Blast cells, “Hematopoiesis”



Introduction
White Blood Cell morphology

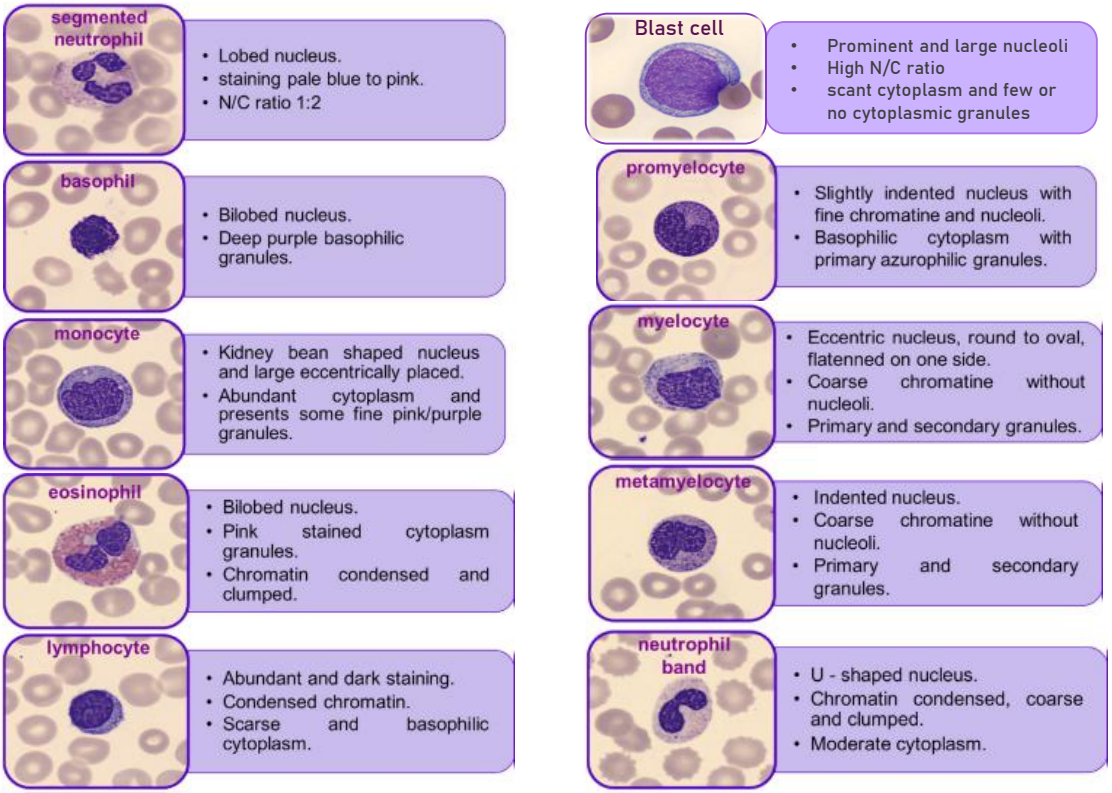


Fig: Different cell types images depicting their distinct morphological characteristics

Introduction
Motivation of the project

The main driving force for undertaking the project is to :

- Leverage **deep learning algorithms to elevate diagnostic capabilities** in the domain of Hematology.
- By accurately categorizing WBCs based on their types and anomalies, the project aims to **support clinicians in discerning and overseeing** various infections, autoimmune diseases, and hematologic malignancies.
- This classification can bring about **early detection of critical health issues, initiate prompt treatment decisions, and improved disease management, ultimately boosting overall healthcare outcomes and lifestyle standards for patients.**

Introduction
Problem statement

The main challenge lies in developing an automated system for WBC and its precursors classification integrated with Artificial Intelligence that can effectively overcome several setbacks currently faced such **as compatibility issues, variance in lighting conditions, different staining techniques, complex cell morphology, and lack of standardized datasets etc.**

Thus, it is of utmost importance to devise an efficient system that can address these limitations while be able to seamlessly integrate into the healthcare workflow.

Introduction
Objectives

1. To conduct comprehensive research to evaluate and compare different methodologies such as machine learning and deep learning for precise detection and classification of the white blood cells and its precursors which includes Blast cells, immature granulocytes (Promyelocytes, Myelocytes, Metamyelocytes, Band forms), Neutrophil, Eosinophil, Basophil, Lymphocyte and Monocytes.

2. Develop a robust algorithm which is scalable, GPU/CPU compatible, agnostic to staining techniques, independent of image input size. Furthermore, the algorithm should optimize time and memory and should be integrated into the current clinical workflow to detect different cell types and predict its differential distribution percentage.

Literature Review

Author & year	Dataset	Classes detected	Methodology	Accuracy
Acevedo et al., 2019 [3]	Hospital-Acquired Datasets	8 classes: 5 mature WBC, immature granulocytes, erythroblasts and platelets	CNN, SVM	96.2%
Siddique et.al, 2020 [4]	BCCD	4 classes: Lymphocyte, monocyte eosinophil and neutrophil	SqueezeNet	93.8%
Ferhat Ucar, 2020 [5]	PBC	8 classes: 5 mature WBC, erythroblast, IG and platelets	ShuffleNet	97.94%
El-Seoud et al., 2020 [6]	Kaggle dataset	4 classes: eosinophil, lymphocyte, monocyte and neutrophil.	custom CNN architecture	96.78%
Das and Meher, 2021 [7]	ALLIDB1 and ALLIDB2	5 classes: 5 mature WBC	hybrid transfer-learning-based CNN technique with MobileNetV2 and ResNet18 integrated	97.18%
Girdhar et al., 2022 [8]	BCCD	4 classes: neutrophil, lymphocyte, monocyte and eosinophil	custom CNN model	98.55%

Literature Review

Author & year	Dataset	Classes detected	Methodology	Accuracy
Tamang et al., 2022 [9]	BCCD	5 classes: 5 mature WBC	Best performing model DenseNet 161 with added methods Normalization, Mixup Augmentation and Label Smoothing	~ 0.99%.
Li et al., 2023 [10]	BCCD	4 classes: neutrophil, lymphocyte, monocyte and eosinophil	mask generation and ensemble integration of ResNet50, ResNet101 and other tiny CNN models	Train accuracy 99% and test accuracy 88%
Ali et al., 2023 [11]	PBC and BCCD	4 classes: neutrophil, lymphocyte, monocyte and eosinophil	transfer learning based framework with Google ViT and ImageNet CNN	PBC: Google ViT got 100% validation accuracy BCCD: Google ViT got 88.36% validation accuracy outperformed ImageNet models in all cases
Khan et al., 2024 [12]	PBC, LISC, and Raabin-WBC	5 classes: 5 mature WBC	CNN integrated with a dual-attention network as core framework (CNN models includes Faster R–CNN and MobileNetV2)	PBC: 99.83%, LISC: 99.60%, and Raabin-WBC: 99.35
Tarimo et al., 2024 [13]	Hospital-Acquired Datasets	16 classes: Artefact, Large Granular Lymphocyte, Promyelocyte, Immature Cell, 5 mature WBCs , nRBC, Lymphocyte Variant, Smudge Cell, Band Neutrophil, Myelocyte, Giant Platelet	2-way 2-stage framework with integrated Yolov5 and pre-trained ViT	96.449%

Methodology
Data Collection

- For our study, we have obtained in total **25 slides (slides of disease such as Leukaemia, Chronic Myeloid Leukaemia and Eosinophilia) stained with Leishman stain** for capturing WBC cell images and its precursors

- We have acquired **around 901 images**. Whole image's key metrics include 24 bits color depth, 96 dpi and image definition of **1280 x 1024** pixels. The images post digitization are saved in PNG format.

- We have segmented all the images from database for cell labelling and annotated by the company's in-house consultant pathologist. Ground truth labels of the dataset are stored in a comma-separated values (csv) file.

Methodology
Data Collection

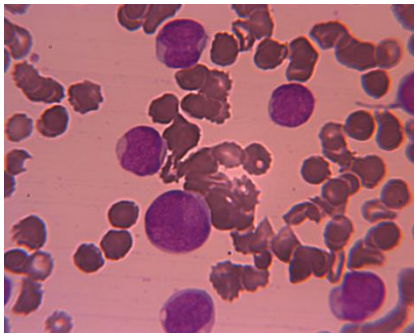


Fig: Blast cells

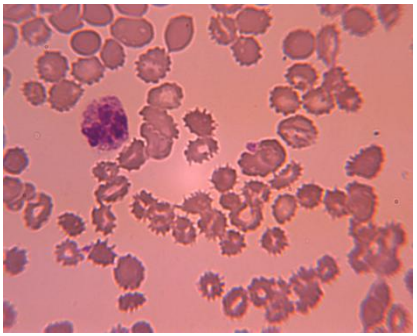


Fig: Neutrophil

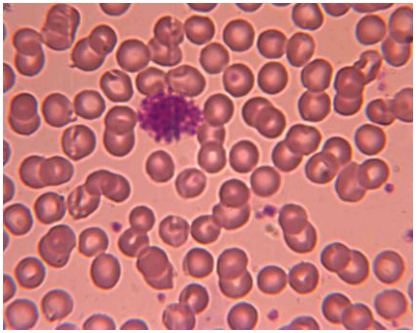


Fig: Basophil

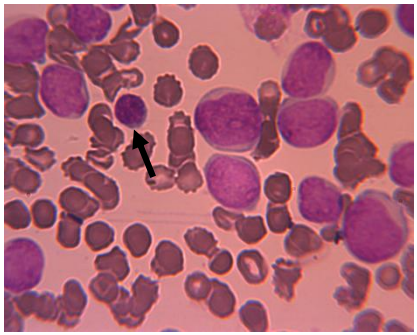


Fig: Lymphocyte

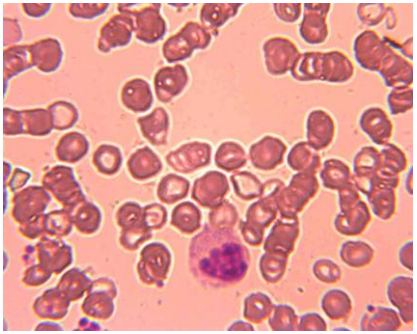


Fig: monocyte

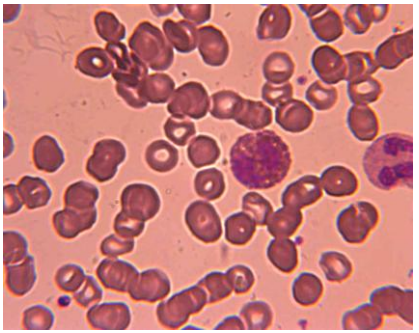
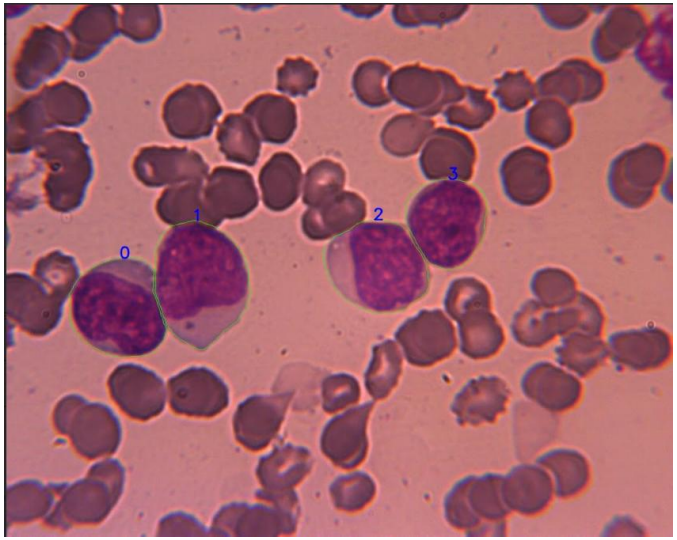


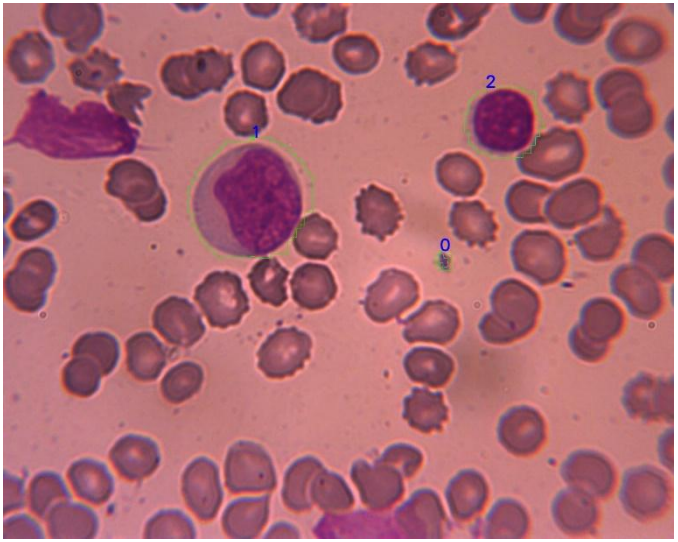
Fig: Eosinophils

*Image source: Bosch -Engineering healthcare

Methodology
Data Collection



a



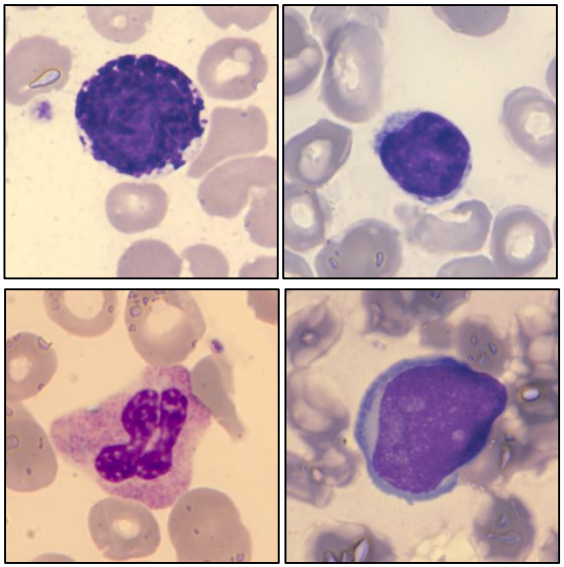
b

Fig: Sample images from our WBC dataset with:

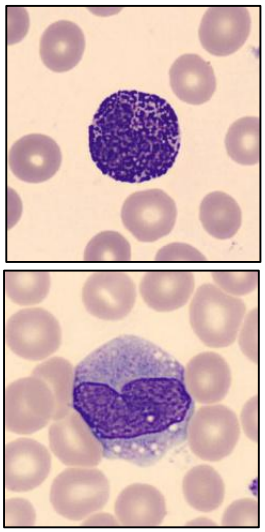
a) Sample image containing annotated blast cells- 0,1,2,3
b) Annotated cells 0 - platelet, 1- Blast, 2- Lymphocyte
* Image source: Bosch -Engineering healthcare

Methodology
Data Collection

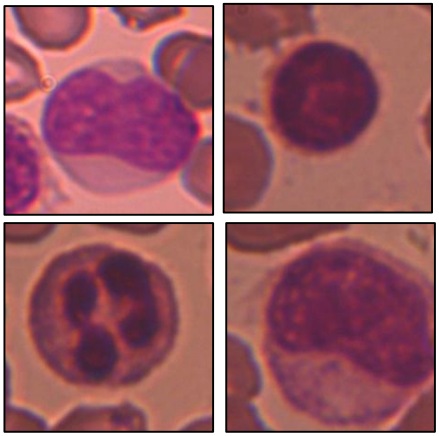
1200 x 1200 x 3



363 x 360 x 3



224 x 224 x 3



External dataset

Digitized slide image (cropped)

* Image source: Bosch -Engineering healthcare

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Methodology
Data Collection

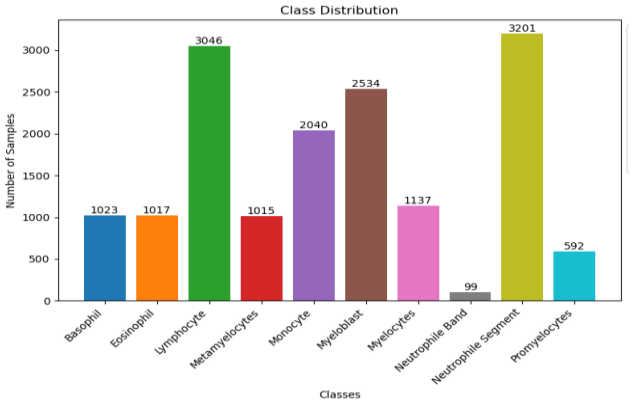
External dataset

Precursors = PBC dataset

WBC + Blast = External + Few from PBC dataset

Total Samples: 15,704

10 Classes: Myeloblast, Promyelocytes, Myelocytes, Metamyelocytes, Band forms, Neutrophil, Eosinophil, Basophil, Lymphocyte, Monocytes



Current dataset

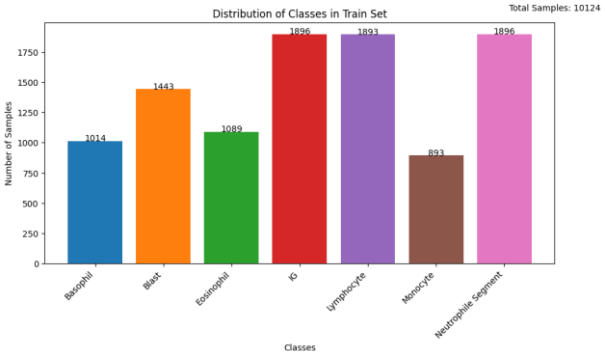
Precursors =PBC dataset

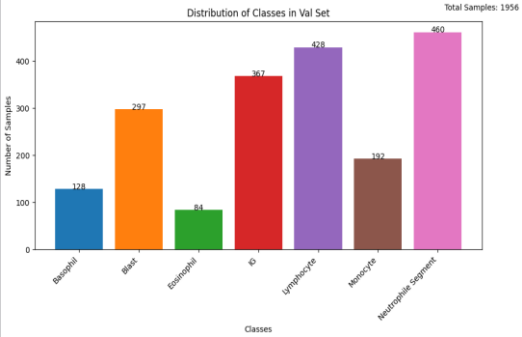
WBC + Blast = External + Few from PBC dataset

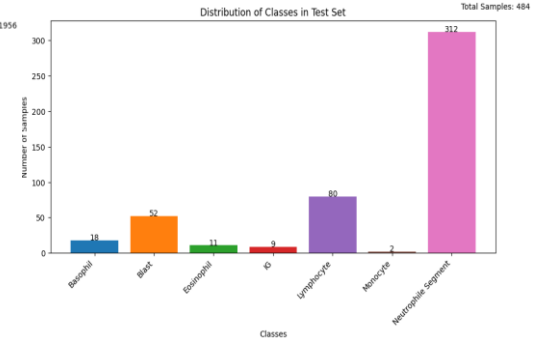
Train: External+PBC+ Captured images

Test = Captured images

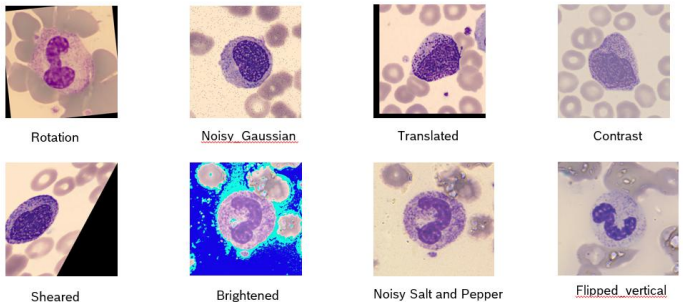
Valid = External +PBC



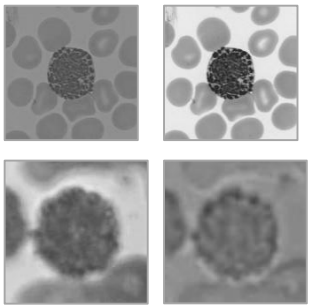




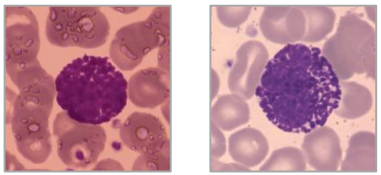
Methodology
Initial Augmentations and trials tested



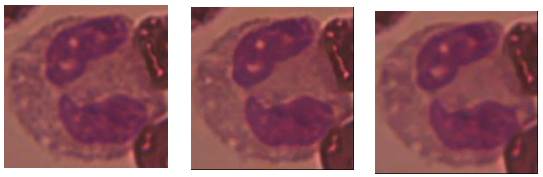
Data Augmentation on external sets



Grayscale + B channel of LAB



Stain conversion on external dataset (May-Grünwald Stain + Leishman Stain)



Data Augmentation on digitized slide images – BM3D

*Image source: Bosch -Engineering healthcare

Methodology
Proposed Framework

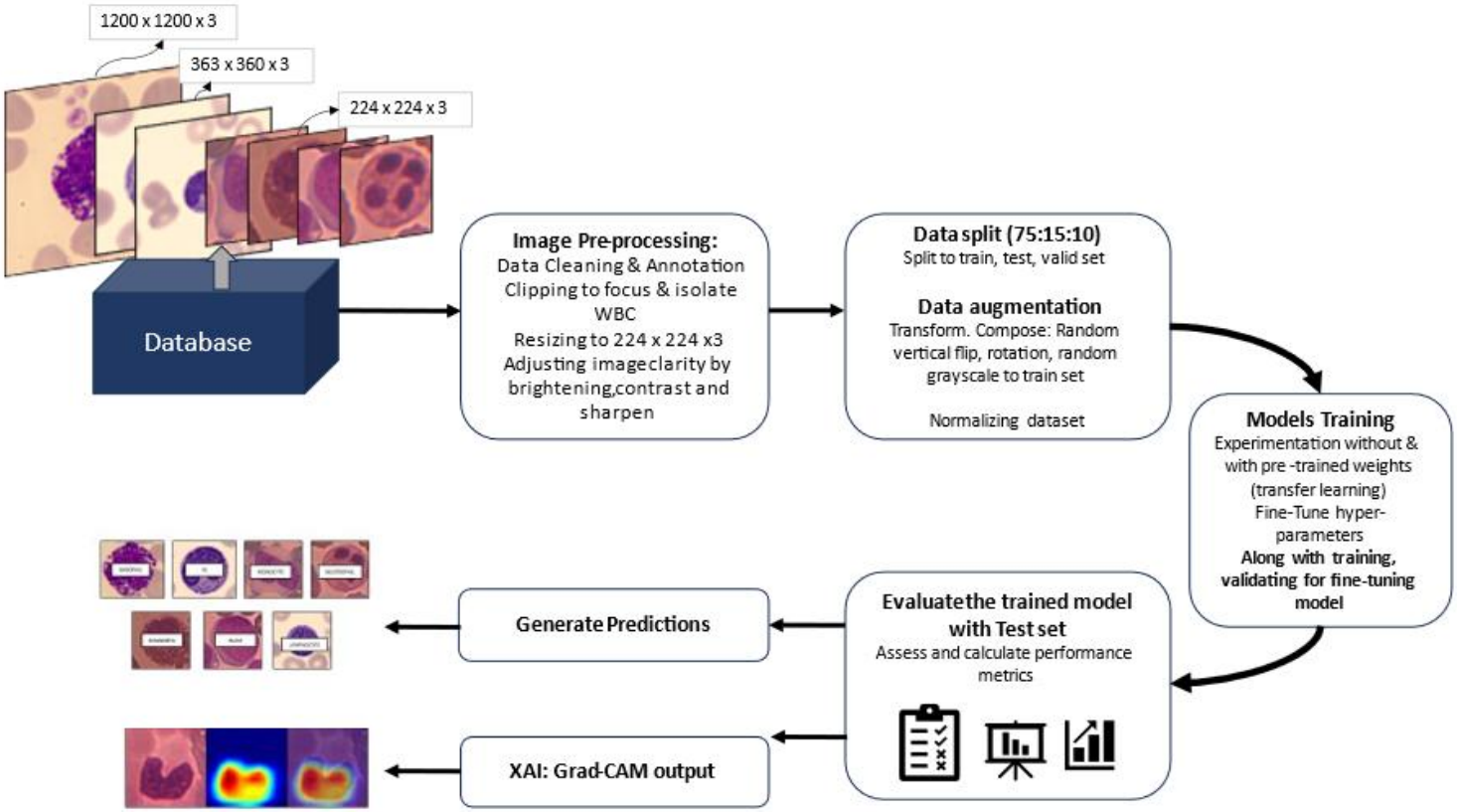


Fig: Architecture of our Proposed Approach for WBC and its precursor classification

Methodology
Pre-processing

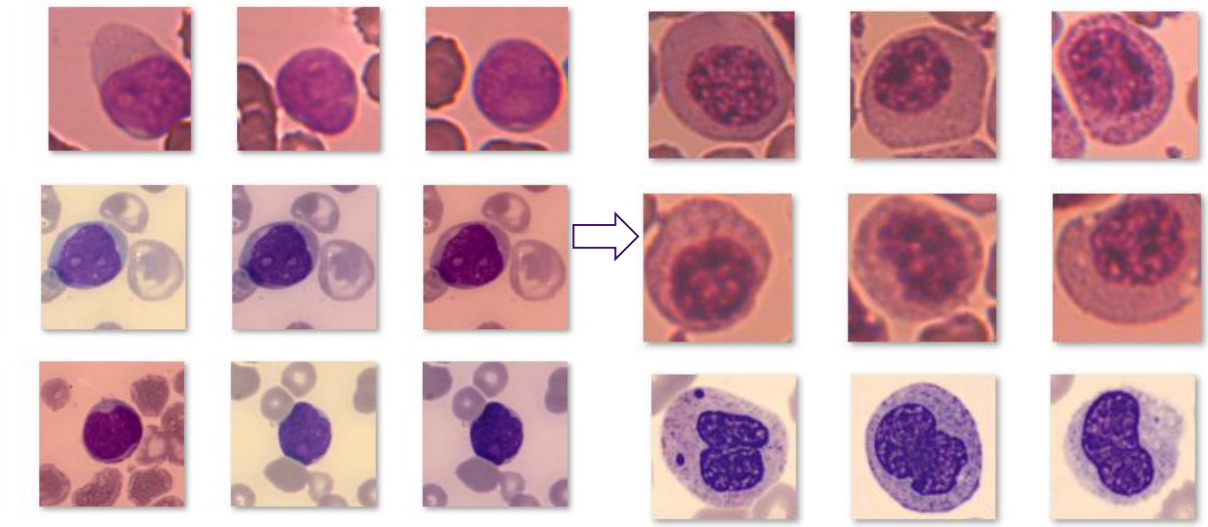


Fig: Initial Dataset with varying WBC focus

Fig: Current Dataset with focus on WBC

*Image source: Bosch -Engineering healthcare

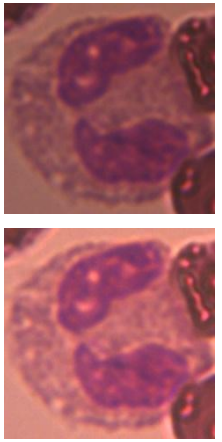


Fig: Final Data Augmentation on Captured sets – Brighten & Contrast + Sharpening

Methodology
Pre-processing

Data augmentation using function Compose transform:

resizing :224x224x3

random vertical flip, random rotation to degree of 15

random transform of 30% if the dataset to grayscale*

*except YOLOv8s

Table: Distribution of the compiled image database and dataset after test_train split

	Collected set	Train, Test and valid Split		
Class	**Database**	**Train**	**Val**	**Test**
Basophil	1160	1014	128	18
Blast	1792	1443	297	52
Eosinophil	1184	1089	84	11
IG	2272	1896	367	9
Lymphocyte	2401	1893	428	80
Monocyte	1087	893	192	2
Neutrophil	2668	1896	460	312

Methodology
Pre-processing

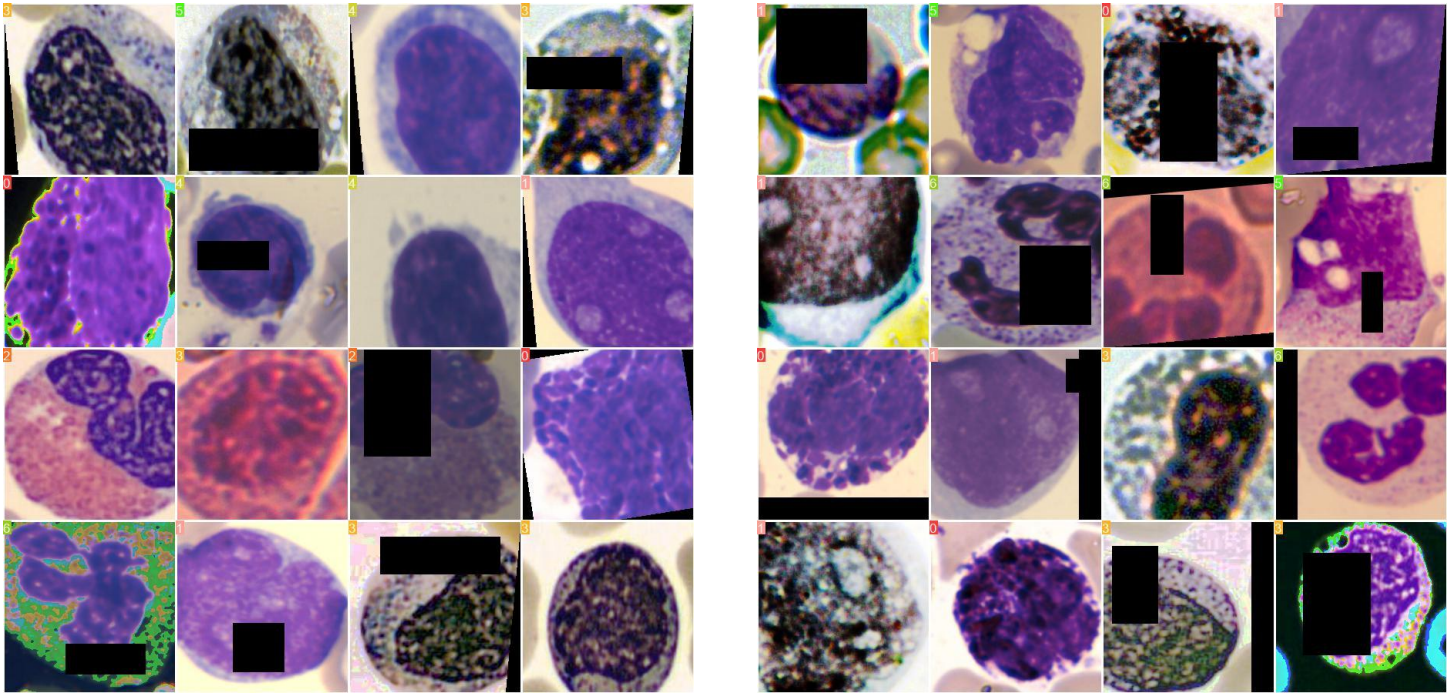


Table: Distribution of the compiled image database and dataset after test_train split

Methodology
Deep learning Approach

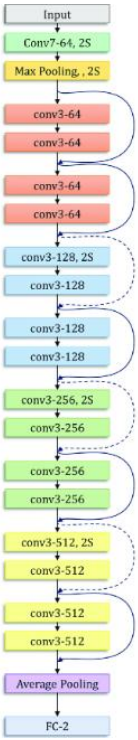


Fig: Architecture of ResNet-18

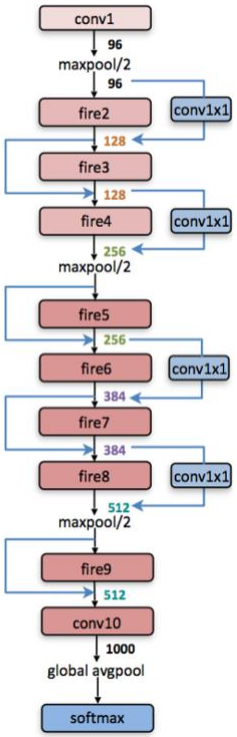


Fig: Architecture of SqueezeNet1_1

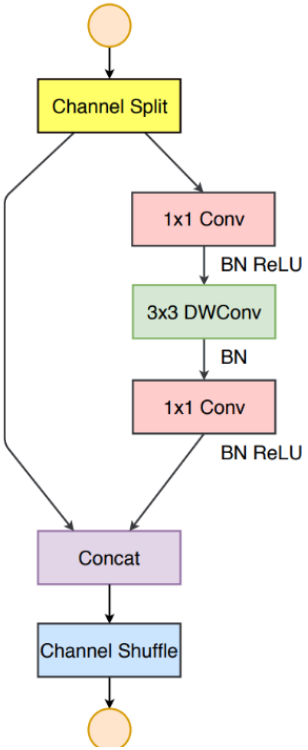


Fig: Architecture of ShuffleNet V2 x1.0

Methodology
Deep learning Approach

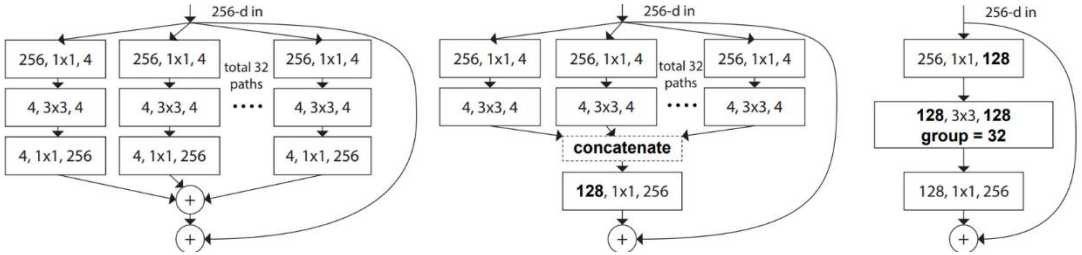


Fig: Architecture of ResNeXt50 (32x4d)

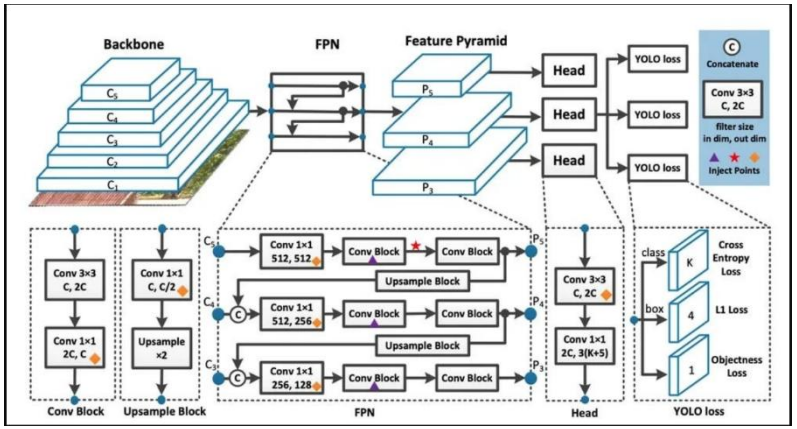


Fig: Architecture of YOLOv8s.

Experimental Setup
Setup specifications

Hardware specification:

- **Experimental setup**: Laptop Intel core i7 10850H and 32 GB memory
- **GPU**: Quadro RTX 3000 with 6144MiB (6GB) of memory capacity
- **Image Capturing:** Fair quality peripheral blood smear images using 100x magnification (oil immersion) objective lens are obtained using a digital microscope, and imaging parameters are optimized to capture clear and detailed representations of blood cells.

Software specifications:

- **Image Annotation**: open-source graphics editor (GIMP) was used for emphasizing regions of interest to be annotated.
- **Machine learning framework**: Pytorch framework based on Torch library.
- Several **image processing libraries** such as scikit-learn, matplotlib, NumPy, pillow.
- **CUDA Toolkit (NVIDIA):** For the intent of training and validating the model, we accessed the GPU-accelerated computing toolkit.
- **Visual Studio Code:** source-code editor for running the deep learning scripts.

Experimental Setup

Hyper parameters across all the experiments

Table : Best Hyper parameters used across all the experiments*

Parameter	Values
Number of epochs	70
Batch size	32
Learning rate	0.0001
activation function	Softmax
Loss function	CrossEntropyLoss
Optimizer	Adam

* Except YOLOv8s

Parameter	Value
Number of epochs	10
Batch Size	16
Image Size	224
Optimizer	AdamW (auto-selected)
Learning Rate (lr0)	Automatically determined (starting at 0.000714)
Momentum	0.9
Weight Decay	0.0005
Pretrained Weights	Yes
AMP (Automatic Mixed Precision)	Enabled

RESULTS AND DISCUSSION
Training and Validation Results

Table: Training and Validation findings for all 5 models

Model	Pre - trained weights	Train Accuracy	Train Loss	Validation Accuracy	Validation Loss	Test Accuracy	Test Loss
ShuffleNet v2x1.0	No	0.9477	0.1467	0.9708	0.0903	0.4922	1.819
SqueezeNet1_1	No	0.9118	0.2788	0.9239	0.2194	0.6172	1.189
ResNeXt 50 32x4d	Yes	0.9415	0.1737	0.9642	0.0998	0.6777	1.159
ResNet-18	Yes	0.9903	0.0289	0.9955	0.0221	0.748	0.738
YOLOv8s	**Yes**	**0.99131**	**0.03673**	**0.803**	**0.1749**	**0.76**	**0.712**

RESULTS AND DISCUSSION
Comparative classification report analysis

Table: Classification report analysis of all 5 best performing models

Models	Precision	Accuracy	Recall	F1 Score	Misclassifications	Support
ShuffleNet v2x1.0	0.786	0.49	0.491	0.569	246	484
SqueezeNet1_1	0.813	0.62	0.621	0.69	182	484
ResNeXt 50 32x4d	0.801	0.67	0.674	0.715	158	484
ResNet-18	0.836	0.43	0.435	0.504	129	484
YOLOv8s	**0.825**	**0.76**	**0.761**	**0.777**	**116**	484

RESULTS AND DISCUSSION

Accuracy and loss curve:YOLOv8s model

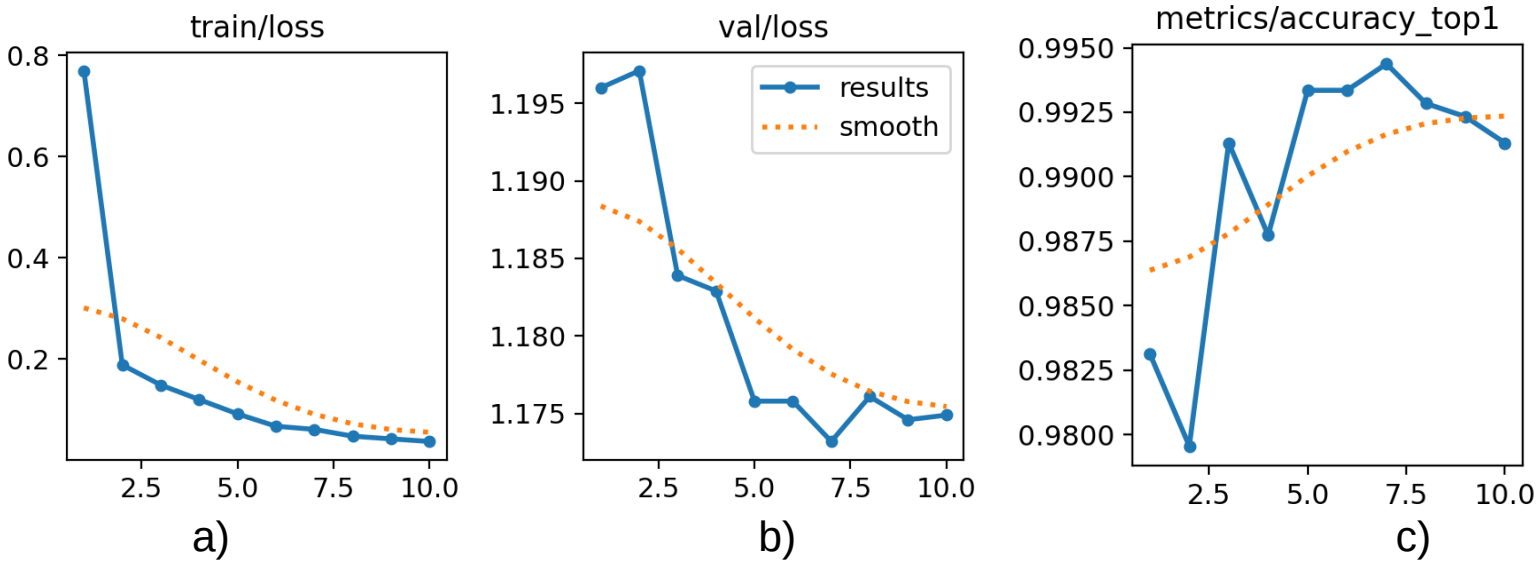
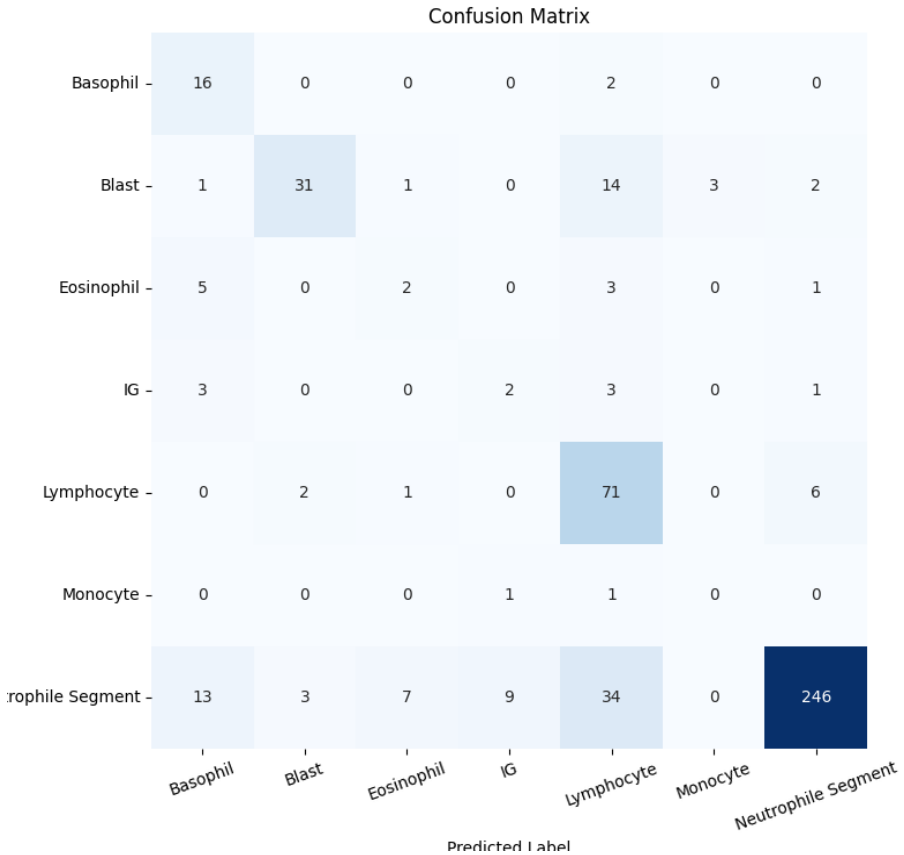


Figure: Accuracy and loss curve attained for YOLOv8s model a) train/loss b) val/loss and c) accuracy top 1 metric

RESULTS AND DISCUSSION

Confusion matrix – YOLOv8s

Figure: Confusion matrix of the best performing model YOLOv8s



RESULTS AND DISCUSSION

Interpretation of Model Predictions: XAI

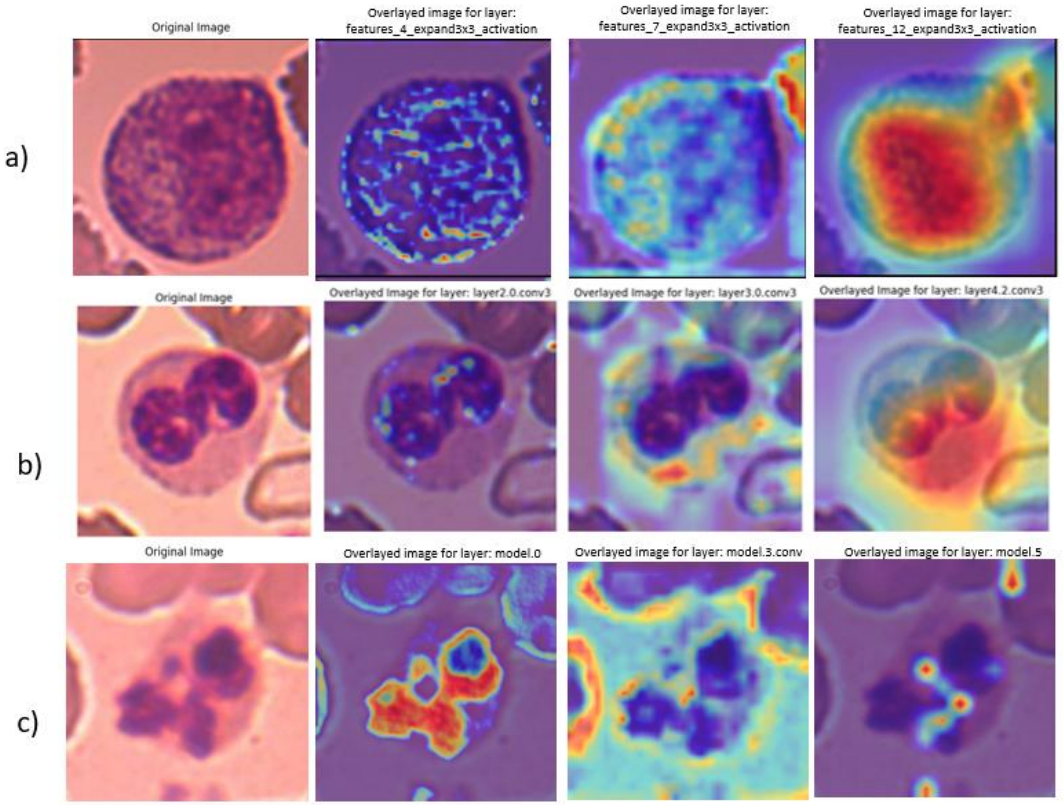


Figure: Grad-CAM Visualization on certain layers of models:

a) SqueezeNet1_1 b) ResNeXt50 (32x4d) c) YOLOv8s

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Limitations

- Despite the superior performance, our research presents some limitations pertaining to the dataset size, sample variance and class imbalance which may have a larger influence on the model's layer-wise learning and final prediction.

- Significant dependence on the quality disparity as the ratio of samples from public repository which are of higher resolution is more as compared to the digitized slide image set which are of lower resolution

Future Scope

1. Delving into implementing hybrid models that incorporate deeper networks with machine learning classifiers

1. Increase custom datasets for certain seldom found classes such as basophils, eosinophils, monocytes and immature granulocytes.

2. Incorporate more diverse samples for extensive number of classes such as myeloblasts, lymphoblasts, promyelocytes, metamyelocytes and myelocytes to encompass more variations.

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