**School of Computer Engineering and Technology**
**MIT World Peace University, Kothrud,**
**Pune 411 038, Maharashtra - India**
**2022-2023**

**Project Report**

on

# Hematology report data extraction and inference generation

Submitted by

**Group B17**

**Project Members**

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**SCHOOL OF COMPUTER ENGINEERING AND TECHNOLOGY**

# CERTIFICATE

This is to certify that,

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of BTech.( Computer Science & Engineering) have completed their project titled "*Haematology report data extraction and inference generation*" and have submitted this Capstone Project Report towards fulfillment of the requirement for the Degree-Bachelor of Computer Science & Engineering (BTech-CSE) for the academic year 2022-2023.

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# Acknowledgement

The successful completion of this research paper would not have been possible without the invaluable support, guidance, and encouragement from numerous individuals. We would like to express our heartfelt gratitude to our project mentor Dr. Vrushali Y. Kulkarni, project coordinator Prof. Madhura Phatak, all the field specialists and doctors that we consulted, for their contributions and mentorship throughout this research endeavor.

We extend our deepest appreciation to Dr.Vrushali Y. Kulkarni for her unwavering commitment, expertise, and patience. Her guidance and insightful feedback have been instrumental in shaping the direction and quality of this research. We are grateful for the precious time she dedicated to providing us with direction and support.

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Our heartfelt appreciation goes to our parents for their unwavering support and encouragement throughout this research journey. Their love, belief in our abilities, and constant motivation have been the driving force behind our achievements. We are forever grateful for their sacrifices and for instilling in us the values of hard work and perseverance.

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Preetika Sastry

Pranav Nirmal

Ayush Shrivastav

Aniket Sharma

# Abstract

Haematology is a critical branch of medicine that deals with the study, diagnosis, and treatment of blood disorders. This field involves the analysis of various blood components such as red blood cells, white blood cells, and platelets, as well as their function and interaction. Haematology reports provide essential information about a patient's blood count, differential, and other factors that aid in the diagnosis and monitoring of blood-related conditions. With the help of Deep learning algorithms and Optical Character Recognition (OCR) technology, haematology reports can be efficiently processed and analysed, allowing for structured and more accurate diagnoses. Haematologists work closely with other medical specialists to provide comprehensive care to patients, making haematology a crucial component of modern medicine.

# List of Figures


| | | |
|---|---|---|
| 5.1 | High Level System Block Diagram | 8 |
| 5.2 | System Class Diagram | 9 |
| 5.3 | Use Case Diagram | 10 |
| 7.1 | YOLOv8 Architecture……... | 15 |
| 7.2 | EasyOCR Framework……... | 18 |
| 7.3 | Tesseract OCR Architecture…….. | 19 |
| 7.4 | GUI directory | 22 |
| 7.5 | Homepage | 23 |
| 7.6 | Result page | 23 |
| 7.7 | Downloaded report | 24 |
| 8.1 | RoboFlow model performance…….. | 28 |
| 9.1 | YOLOv8 result…….. | 38 |
| 9.2 | RoboFlow 2.0 Object Detection (Fast) result……... | 38 |

# List of Tables


| | | |
|---|---|---|
| 1.1 | Information …… | 1 |
| 2.1 | Literature Survey…… | 4 |
| 9.1 | Object detection model comparison…… | 38 |
| 9.2 | OCR Comparison……... | 40 |

# Contents

Abstract . . . . . I
List of Figures . . . . . .II
List of Tables . . . . . .III

| | | | |
|---|---|---|---|
| 1 | Introduction | | 1 |
| | 1.1 | Problem definition | 1 |
| | 1.2 | Scope | 2 |
| 2 | Objective | | 3 |
| 3 | Literature Survey | | 4 |
| 4 | Technologies used | | 7 |
| 5 | System Design | | 8 |
| 6 | System requirements | | 11 |
| | 6.1 | Software requirements | 11 |
| | 6.2 | Hardware requirements | 11 |
| 7 | Techniques used | | 12 |
| | 7.1 | Libraries used | 12 |
| | 7.2 | Dataset Description and Data Pre-processing | 12 |
| | 7.3 | Module 1: Object Detection | 14 |
| | 7.4 | Module 2: Image Processing | 17 |
| | 7.5 | Module 3: OCR Text Extraction | 18 |
| | 7.6 | Module 4: Report Generation | 20 |
| | 7.7 | Module 5: GUI | 22 |
| 8 | Coding | | 25 |
| | 8.1 | Data augmentation | 25 |
| | 8.2 | Annotation | 27 |
| | 8.3 | Model Training | 27 |
| | 8.4 | Image processing and text/ value extraction | 30 |
| | 8.5 | Report generation | 32 |
| | 8.6 | GUI | 35 |
| 9 | Testing | | 38 |

| | | |
|---|---|---|
| 10 | Conclusion | 43 |
| 11 | Future prospects of the project | 44 |
| 12 | References | 45 |
| | A. Base Paper(s) | 47 |
| | B. Plagiarism Report from any open source | |

# Chapter 1
# Introduction

In the field of medical diagnostics, accurate and efficient extraction of key data from hematology reports is of paramount importance. These reports contain vital information such as hemoglobin levels, white blood cell (WBC) count, platelet count, red blood cell (RBC) count, neutrophil and lymphophil percentages, as well as patient-specific details like age, name, and sex. Extracting this data accurately and quickly is crucial for timely diagnosis and effective patient care.

Traditionally, the process of data extraction from hematology reports has relied on manual entry, which is not only time-consuming but also prone to human errors. Furthermore, these reports are often in unstructured formats, making it challenging to efficiently extract and utilize the data contained within. Therefore, there is a pressing need for automated methods that can extract and structure the information from hematology reports accurately and reliably

## 1.1 Problem definition

The traditional manual entry of data from hematology reports is time-consuming and error-prone. Additionally, the unstructured nature of these reports poses a challenge in extracting and utilizing the data effectively. This necessitates the development of automated methods that can accurately and reliably extract key parameters from hematology reports, such as hemoglobin levels, WBC count, platelet count, RBC count, neutrophil and lymphophil percentages, as well as patient-specific details like age, name, and sex.

To address this problem, we propose a novel approach that combines object detection and optical character recognition (OCR) techniques. By utilizing object detection, specific regions of interest in hematology report images, such as tables or sections containing key data elements, can be identified and isolated. Subsequently, OCR techniques are applied to convert the textual content in the identified regions into machine-readable text, enabling the extraction of specific data points.

The extracted data can then be utilized to generate a structured diagnosis report, providing healthcare professionals with an easily interpretable summary of the patient's condition. This automation not only saves time but also reduces the potential for errors that may occur during

manual data entry, leading to more accurate and consistent diagnoses.

In summary, the problem at hand is the manual and error-prone process of data extraction from unstructured hematology reports. The proposed approach aims to overcome this challenge by combining object detection and OCR techniques, facilitating the automated extraction and structuring of vital parameters. This research seeks to contribute to the advancement of medical document processing and improve the efficiency and accuracy of diagnostic procedures, ultimately enhancing patient care.

## 1.2 Scope

This research project aims to develop an automated system for extracting key data from hematology reports and generating structured diagnosis reports. The focus will be on utilizing object detection and optical character recognition (OCR) techniques to extract parameters such as hemoglobin levels, WBC count, platelet count, RBC count, neutrophil and lymphophil percentages, as well as patient-specific details (age, name, and sex).

The project does not cover the analysis or interpretation of the extracted data for medical diagnosis. It will focus on the extraction process using object detection and OCR. The limitations of the proposed approach will be identified and discussed.

Overall, this project aims to automate data extraction and improve the efficiency of generating structured diagnosis reports in hematology. The system developed will streamline the diagnostic process, leading to enhanced patient care.

# Chapter 2
# Objective

The objective of this research project is to develop an automated system for efficient extraction of key data from hematology reports and generation of structured diagnosis reports. The project aims to achieve the following objectives:

The project will involve:

- Data Collection and Preparation: Gathering a diverse dataset of hematology reports, augmenting and annotating it with ground truth labels.
- Object Detection Model Development: Training a deep learning-based model to identify and localize relevant regions in hematology report images, such as data sections like name, age, sex, etc.
- OCR Integration and Data Extraction: Implementing OCR techniques to convert textual content within the identified regions into machine-readable text and extracting specific data points.
- Diagnosis Report Generation: Utilizing the extracted data to generate structured diagnosis reports summarizing the patient's condition.
- Evaluation and Performance Metrics: Assessing the system's performance using evaluation metrics like accuracy, precision, recall, and F1 scores.

By achieving these objectives, this research project aims to contribute to the advancement of automated data extraction and diagnosis report generation in the field of hematology. The ultimate goal is to improve the efficiency, accuracy, and quality of patient care by streamlining the diagnostic process and providing healthcare professionals with structured and reliable information extracted from hematology reports.

# Chapter 3
# Literature Survey

| Title | Authors | Year | Aim/Objective | Methodology | Architecture |
|---|---|---|---|---|---|
| Text Detection and Recognition for Images of Medical Laboratory Reports With a Deep Learning Approach | WEN YUAN XUE 1, QING YONG LI 1, (Member, IEEE), QIYUAN XUE2 | 2019 | Using deep learning, medical laboratory report photos can now be read for text. | There are various phases in the technique employed in the study. The supplied image is first preprocessed to improve contrast and lower noise. Followed by object detection model, Then, Following that, the text portions that were recognised are cropped, scaled, and input into the OCR model for text recognition. | Text detection: Faster R-CNN model is employed to find the areas in the picture that contain text.<br>Text recognition: CRNN with the final layer connected to BLSTM. |
| Text Mining the History of Medicine | Paul Thompson, John McNaught and Sophia Ananiadou | 2020 | By minimising mistakes in OCR-generated text, this OCR correction technique is tailored for historical medical records and increases the effectiveness of search engines. The approach combines a medically-tuned spell checking strategy that is directed by subject-specific language usage with rule-based correction of common mistakes. | To fix OCR problems, use rule-based and spell-checking techniques. They compare the effectiveness of four spellcheckers and choose to base their error-correction method on Hunspell. | Hunspell, rule-based spell checker, is a default dictionary used for OCR correction, and it provides spelling suggestions that are ranked by frequency. It is also mentioned that a medically-enhanced version of Hunspell is used, which includes specialized medical terminology.<br>The proposed method of incorporating corpus-based information and augmenting Hunspell's dictionary with specialized vocabulary helps to refine its suggestions and avoid over-correction of valid words. |

| | | | | | |
|---|---|---|---|---|---|
| Deep Learning for Automated Extraction of Primary Sites from Cancer Pathology Reports | John X. Qiu, Hong-Jun Yoon, Paul A. Fearn, and Georgia D. Tourassi | 2016 | Highlights how OCR systems based on AI can automate medical transcription and extract information from handwritten clinical notes, leading to a better understanding of entire processes. The project aims to develop an OCR application using deep learning for offline character recognition in the medical sector, addressing challenges posed by large and dispersed datasets. | In the article, word embedding techniques and vector space models (VSMs) are discussed in relation to natural language processing (NLP). In contrast to word embedding methods, which are learnt representations of words taught using deep learning techniques, VSMs are used to encode documents inside a corpus with a feature vector based on word counts. The usage of the word2vec skip-gram approach for training word vectors is also covered in the paper. The learned word vectors may be used to create a document matrix and are used to represent a word's location within a corpus. | Making an OCR model using CNN and RNN. According to the results, random embeddings perform better for the information extraction problem with well-populated classes. Pre-trained embeddings performed better, nevertheless, when the classification challenge comprised classes with low prevalence. |
| Diagnosis of Diseases from Medical Check-up Test Reports Using OCR Technology with BoW and AdaBoost algorithms | Wisam A. Qader, Musa M. Ameen | 2020 | a method to diagnose illness using test results from health checkups. The suggested method uses optical character recognition (OCR) technology to transform hard copy test reports into text data that may be edited. | OCR Library Used: Tesseract<br>Feature Selection: BoW<br>Classification Algorithm: Naive Bayes<br>Improved Accuracy via AdaBoost Algorithm | OCR Technology for Disease Diagnosis from Medical Check-up Test Reports Using BoW and AdaBoost Algorithms |

| | | | | | |
|---|---|---|---|---|---|
| AUTOMATED DATA EXTRACTION FROM LAB REPORTS | Vivek Vijayan | 2021 | The goal is to automate data extraction from laboratory results to increase accuracy and efficiency while lowering manual labour and mistakes. | The process entails extracting the text from the lab results using optical character recognition (OCR). The relevant data is then identified and retrieved from the extracted text using natural language processing (NLP) techniques. Finally, a structured format is used to store the extracted data. | Preprocessing modules for OpenCV Tesseract: a free and open-source OCR engine developed by Google labelImg: a tool for labelling images Faster R-CNN: to assess the object detection models using Mean Average Precision (mAP) |

# Chapter 4
# Technologies Used

**LabelImg**: LabelImg is a popular open-source graphical image annotation tool used for creating bounding box annotations on images. It allows researchers to manually label and annotate regions of interest, such as tables and data sections, in hematology report images. LabelImg provides an intuitive user interface that simplifies the annotation process and generates annotations in widely used formats such as XML or CSV.

**Computer Vision (OpenCV)**: A popular open-source computer vision library called OpenCV (Open Source Computer Vision Library) offers a wide range of algorithms and methods for processing images and videos. OpenCV was used in this research study for a variety of tasks, including picture preparation, image augmentation, and image modification. It provides a variety of potent tools for improving image quality, lowering noise, and carrying out actions like image thresholding, cropping, and resizing.

**Roboflow AutoML Model and YOLOv8** for Object Detection: An automated machine learning framework called Roboflow AutoML makes it easier to develop and use object identification models. Without considerable machine learning knowledge, it enables researchers to train unique models on their annotated dataset. In this project, an object detection model was trained using Roboflow AutoML using the annotated dataset. A real-time object identification system known as YOLOv8 (You Only Look Once) architecture is renowned for its speed and accuracy in recognising several items inside an image. For the best level of accuracy, the YOLOv8x model was trained using our unique annotated dataset.

**Optical Character Recognition (OCR)** - Google created Tesseract, an open-source OCR engine that has been widely used to extract text from photos. It is customizable for certain use cases and supports a variety of languages. Simple optical character recognition (OCR) libraries like EasyOCR make it easier to extract text from photos. It has a user-friendly interface and supports a variety of languages, making it adaptable for use in a variety of applications. EasyOCR will be used in this project to conduct OCR on the selected regions of interest in the haematology report pictures, turning the text into machine-readable format. EasyOCR uses deep learning models to reliably recognise and extract text from photos.

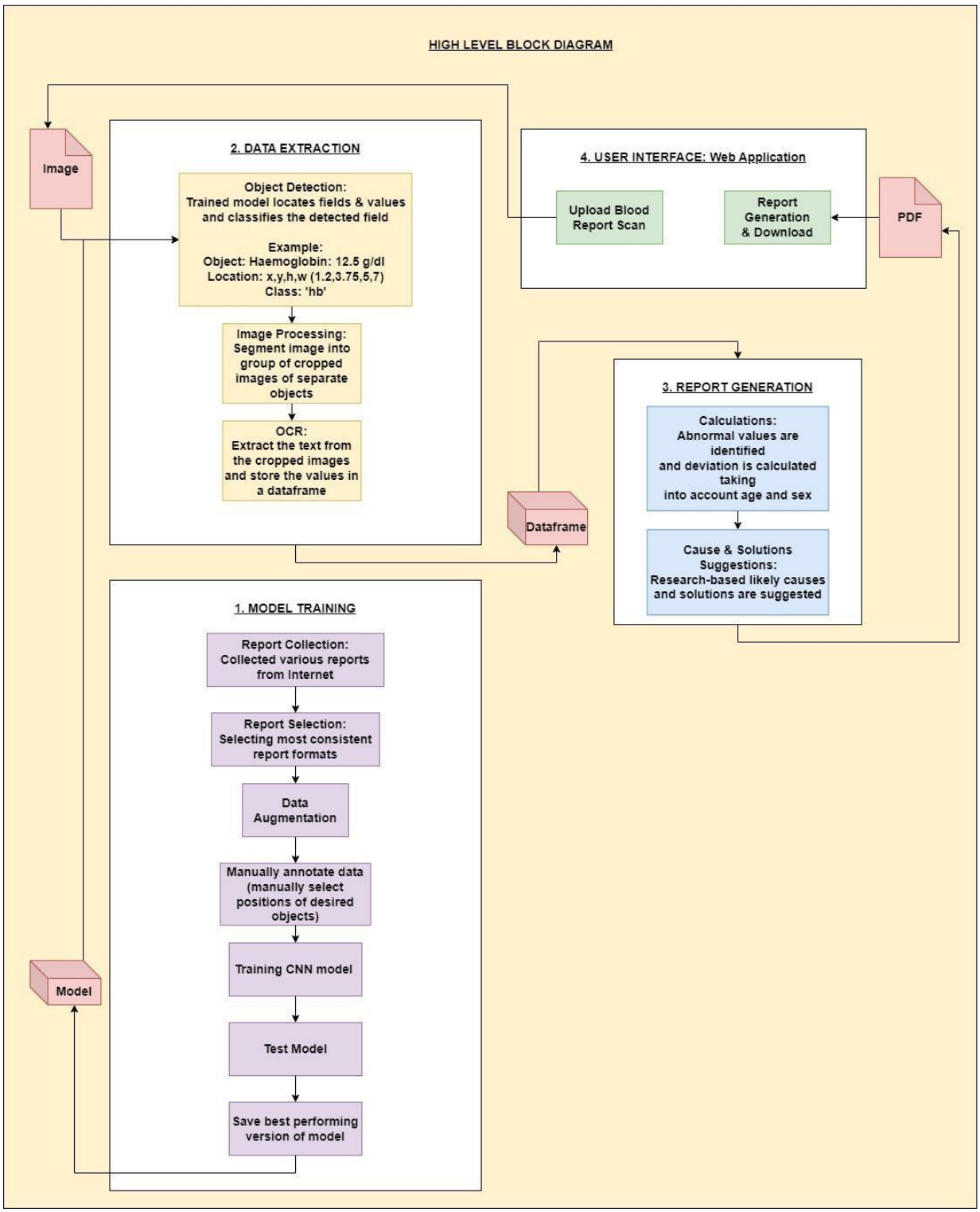
**Google Colab**: a cloud-based platform that allows group coding and offers free access to computer resources. Python code may be executed on Google Colab, and data processing activities can be carried out along with model training. The YOLOv8x model for this project was trained utilising the Google Colab interface and the Nvidia T4 server grade tensor GPU.

**Pandas**: a robust Python data analysis and manipulation module. Pandas is useful for processing and organising extracted data from haematology reports because it provides effective data structures and capabilities for managing structured data.

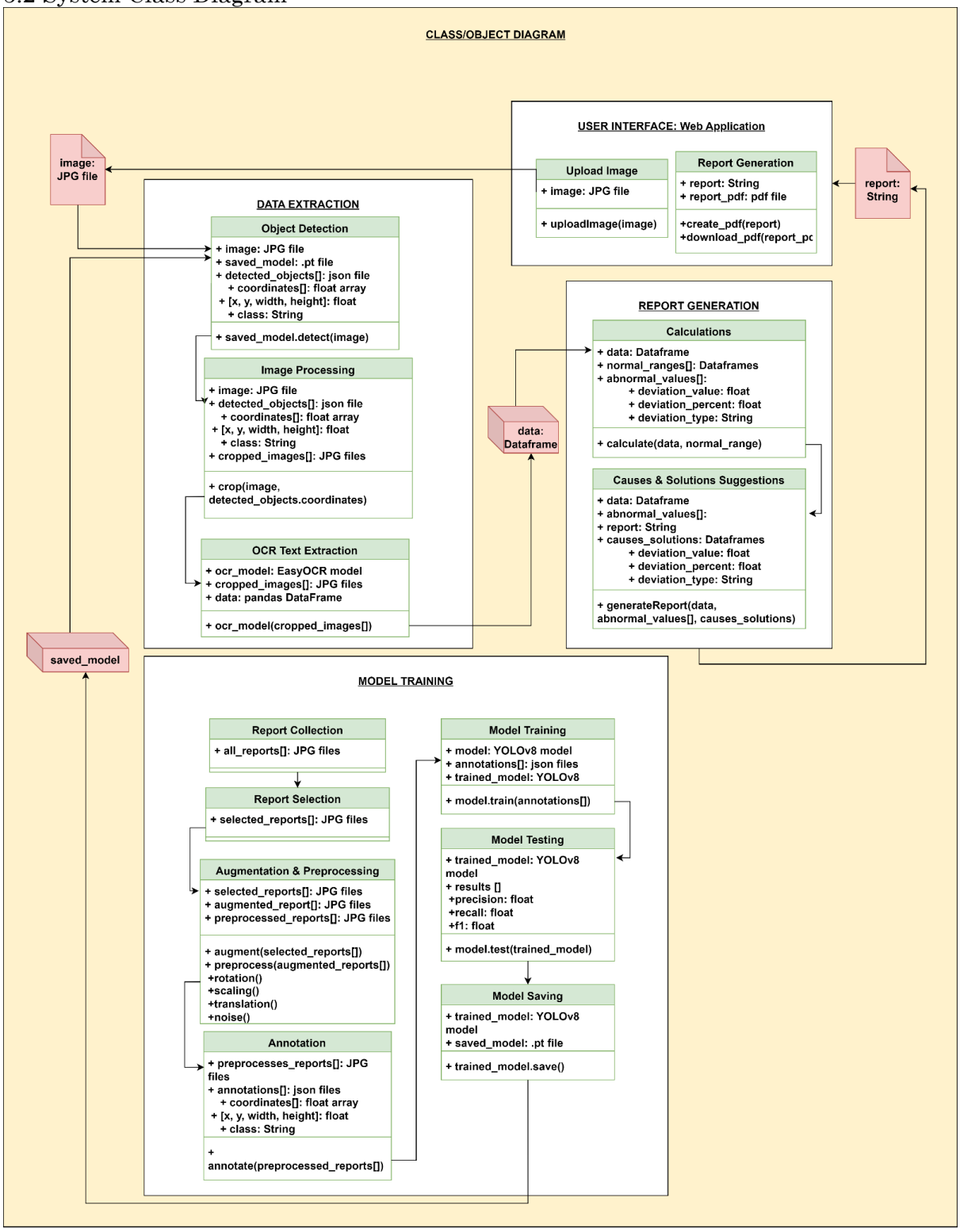
These technologies collectively enable the automation of data extraction from hematology reports through image annotation, computer vision techniques, object detection model training, optical character recognition, and data manipulation tasks.

# Chapter 5
# System Design

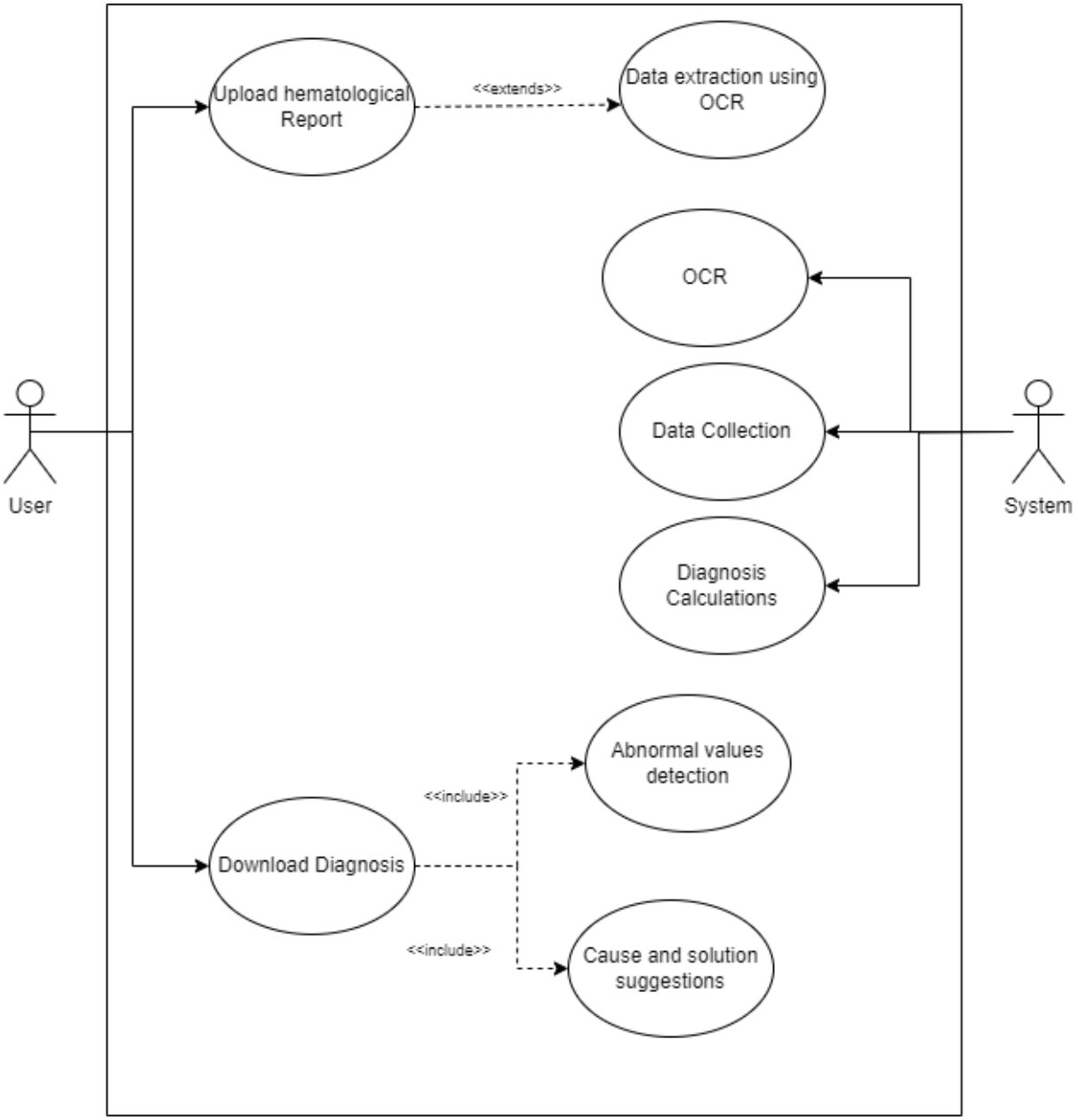
## 5.1 High Level System Block Diagram



## 5.2 System Class Diagram



5.3 Use Case Diagram



# Chapter 6
# System Requirements

## 6.1 Software Requirements

- Jupyter NB
- Python
- Anaconda
- Text editor
- Web browser (internet connection)

## 6.2 Hardware Requirements

- Processor: Intel core i5, 8th gen and above
- RAM: 8GB and above
- Storage: 80GB and above
- Display: CRT/ LCD/ LED
- Camera: pixel resolution of at least 5 MP
- Mouse: Compatible mouse
- Keyboard: normal or multimedia

# Chapter 7
# Techniques Used

## 7.1 Libraries Used:

- pytesseract
- PIL
- re
- os
- openCV2
- pandas
- numpy
- scipy
- random
- roboflow
- easyocr
- flask

## 7.2 Dataset Description and Data Pre-processing

The dataset used in this study consists of blood report images collected from the internet. The images were obtained from various laboratories and hospitals, resulting in a diverse range of formats and layouts. The reports were preprocessed using normalisation, binarization, and noise reduction techniques to improve performance. We ran the different formats of reports through our OCR models to determine which formats performed the best. Some reports were found to perform poorly in the OCR models. The future scope of this project could include such reports as well, but due to the limited project scope, we remove these before performing data augmentation.

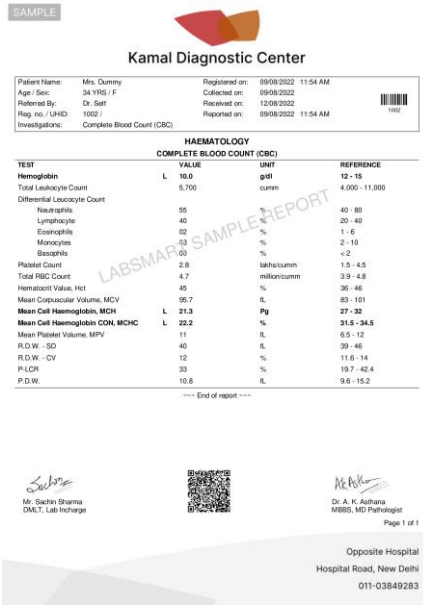
To perform data augmentation, we used OpenCV's inbuilt methods. These included the following:

- Rotation: This involves rotating an image by a given angle. In OpenCV, the getRotationMatrix2D() and warpAffine() functions can be used for rotation.
- Scaling: This involves resizing an image to a new size. In OpenCV, the resize() function can be used to resize an image.
- Translation: This involves shifting an image horizontally or vertically. In OpenCV, the warpAffine() function can be used to translate an image.
- Noise: Generating random noise and scaling it based on the input image and clipping the image within its valid range.
- Blur: Applying gaussian blur to the input image.
- Grayscale: Converting images to grayscale using OpenCV's cvtColor, simplifying the input data by removing the colour information.
- Colour hue: Converting the image to HSV colour space and then adding the hue value to the hue channel, converting the image back to BGR colour space.
- Skew: Skewing the image at a given angle to simulate the distortion or misalignments caused during the scanning of the image.

The above functions were applied in a random variation to each one of the 4 report formats selected so as to increase the size of the dataset for the model training.

Since the model is to be trained for object detection for a similarly structured dataset, augmentation on the same images didn't have any adverse effect on the accuracy.

The selected report formats:



SAMPLE

Kamal Diagnostic Center

| | | | |
|---|---|---|---|
| Patient Name: | Mrs. Dummy | Registered on: | 09/08/2022 11:54 AM |
| Age / Sex: | 34 YRS / F | Collected on: | 09/08/2022 |
| Referred By: | Dr. Self | Received on: | 12/08/2022 |
| Reg. no. / UHID: | 1002 / | Reported on: | 09/08/2022 11:54 AM |
| Investigations: | Complete Blood Count (CBC) | | |

HAEMATOLOGY

COMPLETE BLOOD COUNT (CBC)

| TEST | | VALUE | UNIT | REFERENCE |
|---|---|---|---|---|
| **Hemoglobin** | L | **10.0** | **g/dl** | **12 - 15** |
| Total Leukocyte Count | | 5,700 | cumm | 4,000 - 11,000 |
| Differential Leucocyte Count | | | | |
| Neutrophils | | 55 | % | 40 - 80 |
| Lymphocyte | | 40 | % | 20 - 40 |
| Eosinophils | | 02 | % | 1 - 6 |
| Monocytes | | 03 | % | 2 - 10 |
| Basophils | | 03 | % | < 2 |
| Platelet Count | | 2.8 | lakhs/cumm | 1.5 - 4.5 |
| Total RBC Count | | 4.7 | million/cumm | 3.9 - 4.8 |
| Hematocrit Value, Hct | | 45 | % | 36 - 46 |
| Mean Corpuscular Volume, MCV | | 95.7 | fL | 83 - 101 |
| **Mean Cell Haemoglobin, MCH** | L | **21.3** | **Pg** | **27 - 32** |
| **Mean Cell Haemoglobin CON, MCHC** | L | **22.2** | **%** | **31.5 - 34.5** |
| Mean Platelet Volume, MPV | | 11 | fL | 6.5 - 12 |
| R.D.W. - SD | | 40 | fL | 39 - 46 |
| R.D.W. - CV | | 12 | % | 11.6 - 14 |
| P-LCR | | 33 | % | 19.7 - 42.4 |
| P.D.W. | | 10.8 | fL | 9.6 - 15.2 |

~~~ End of report ~~~

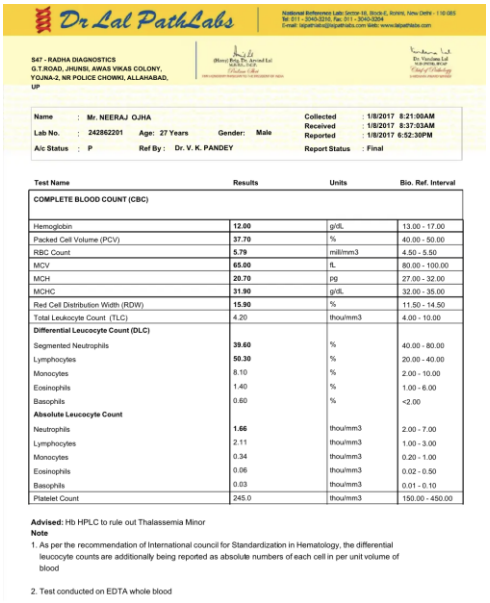
LABSMART SAMPLE REPORT

Mr. Sachin Sharma
DMLT, Lab Incharge

Dr. A. K. Asthana
MBBS, MD Pathologist

Page 1 of 1

Opposite Hospital
Hospital Road, New Delhi
011-03849283



Dr Lal PathLabs

547 - RADHA DIAGNOSTICS
G.T.ROAD, JHUNSI, AWAS VIKAS COLONY, YOJNA-2, NR POLICE CHOWKI, ALLAHABAD, UP

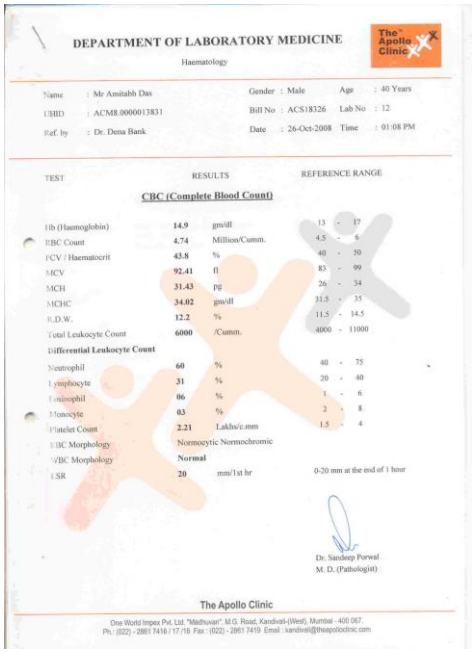
| | | | |
|---|---|---|---|
| Name | : Mr. NEERAJ OJHA | Collected | : 1/8/2017 8:21:00AM |
| Lab No. | : 242862201 Age: 27 Years Gender: Male | Received | : 1/8/2017 8:37:03AM |
| | | Reported | : 1/8/2017 6:52:30PM |
| A/c Status | : P Ref By : Dr. V. K. PANDEY | Report Status | : Final |

| Test Name | Results | Units | Bio. Ref. Interval |
|---|---|---|---|
| COMPLETE BLOOD COUNT (CBC) | | | |
| Hemoglobin | **12.00** | g/dL | 13.00 - 17.00 |
| Packed Cell Volume (PCV) | **37.70** | % | 40.00 - 50.00 |
| RBC Count | **5.79** | mill/mm3 | 4.50 - 5.50 |
| MCV | **65.00** | fL | 80.00 - 100.00 |
| MCH | **20.70** | pg | 27.00 - 32.00 |
| MCHC | **31.90** | g/dL | 32.00 - 35.00 |
| Red Cell Distribution Width (RDW) | **15.90** | % | 11.50 - 14.50 |
| Total Leukocyte Count (TLC) | 4.20 | thou/mm3 | 4.00 - 10.00 |
| **Differential Leucocyte Count (DLC)** | | | |
| Segmented Neutrophils | **39.60** | % | 40.00 - 80.00 |
| Lymphocytes | **50.30** | % | 20.00 - 40.00 |
| Monocytes | 8.10 | % | 2.00 - 10.00 |
| Eosinophils | 1.40 | % | 1.00 - 6.00 |
| Basophils | 0.60 | % | <2.00 |
| **Absolute Leucocyte Count** | | | |
| Neutrophils | **1.66** | thou/mm3 | 2.00 - 7.00 |
| Lymphocytes | 2.11 | thou/mm3 | 1.00 - 3.00 |
| Monocytes | 0.34 | thou/mm3 | 0.20 - 1.00 |
| Eosinophils | 0.06 | thou/mm3 | 0.02 - 0.50 |
| Basophils | 0.03 | thou/mm3 | 0.01 - 0.10 |
| Platelet Count | 245.0 | thou/mm3 | 150.00 - 450.00 |

**Advised:** Hb HPLC to rule out Thalassemia Minor

**Note**

1. As per the recommendation of International council for Standardization in Hematology, the differential leucocyte counts are additionally being reported as absolute numbers of each cell in per unit volume of blood
2. Test conducted on EDTA whole blood



DEPARTMENT OF LABORATORY MEDICINE

Haematology

The Apollo Clinic

| | | | |
|---|---|---|---|
| Name | : Mr Amitabh Das | Gender : Male | Age : 40 Years |
| UHID | : ACM8.0000013831 | Bill No : ACS18326 | Lab No : 12 |
| Ref. by | : Dr. Dena Bank | Date : 26-Oct-2008 | Time : 01:08 PM |

CBC (Complete Blood Count)

| TEST | RESULTS | | REFERENCE RANGE |
|---|---|---|---|
| Hb (Haemoglobin) | 14.9 | gm/dl | 13 - 17 |
| RBC Count | 4.74 | Million/Cumm. | 4.5 - 5 |
| PCV / Haematocrit | 43.8 | % | 40 - 50 |
| MCV | 92.41 | fl | 83 - 99 |
| MCH | 31.43 | pg | 26 - 34 |
| MCHC | 34.02 | gm/dl | 31.5 - 35 |
| R.D.W. | 12.2 | % | 11.5 - 14.5 |
| Total Leukocyte Count | 6000 | /Cumm. | 4000 - 11000 |
| **Differential Leukocyte Count** | | | |
| Neutrophil | 60 | % | 40 - 75 |
| Lymphocyte | 31 | % | 20 - 40 |
| Eosinophil | 06 | % | 1 - 6 |
| Monocyte | 03 | % | 2 - 8 |
| Platelet Count | 2.21 | Lakhs/c.mm | 1.5 - 4 |
| RBC Morphology | Normocytic Normochromic | | |
| WBC Morphology | Normal | | |
| ESR | 20 | mm/1st hr | 0-20 mm at the end of 1 hour |

Dr. Sandeep Porwal
M. D. (Pathologist)

The Apollo Clinic

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9123456789 / 8912345678
smartpatholab@gmail.com

105 -108, SMART VISION COMPLEX, HEALTHCARE ROAD, OPPOSITE HEALTHCARE COMPLEX, MUMBAI - 689578

**Yash M. Patel**
Age : 21 Years
Sex : Male
PID : 555

**Sample Collected At:**
125, Shivam Bungalow, S G Road, Mumbai
**Ref. By: Dr. Hiren Shah**

**Registered on:** 02:31 PM 02 Dec, 22
**Collected on:** 03:11 PM 02 Dec, 22
**Reported on:** 04:35 PM 02 Dec, 22

Complete Blood Count (CBC)

| Investigation | Result | | Reference Value | Unit |
|---|---|---|---|---|
| Primary Sample Type : | Blood | | | |
| **HEMOGLOBIN** | | | | |
| Hemoglobin (Hb) | **12.5** | Low | 13.0 - 17.0 | g/dL |
| **RBC COUNT** | | | | |
| Total RBC count | 5.2 | | 4.5 - 5.5 | mill/cumm |
| **BLOOD INDICES** | | | | |
| Packed Cell Volume (PCV) | **57.5** | High | 40 - 50 | % |
| Mean Corpuscular Volume (MCV) | 87.75 | | 83 - 101 | fL |
| MCH (Calculated) | 27.2 | | 27 - 32 | pg |
| MCHC (Calculated) | 32.8 | | 32.5 - 34.5 | g/dL |
| RDW | 13.6 | | 11.6 - 14.0 | % |
| **WBC COUNT** | | | | |
| Total WBC count | 9000 | | 4000-11000 | cumm |
| **DIFFERENTIAL WBC COUNT** | | | | |
| Neutrophils | 60 | | 50 - 62 | % |
| Lymphocytes | 31 | | 20 - 40 | % |
| Eosinophils | 1 | | 00 - 06 | % |
| Monocytes | 7 | | 00 - 10 | % |
| Basophils | 1 | | 00 - 02 | % |
| **PLATELET COUNT** | | | | |
| Platelet Count | 320000 | | 150000 - 410000 | cumm |

**Instruments:** Fully automated cell counter - Mindray 300

**Interpretation:** Further confirm for Anemia

Thanks for Reference

\*\*\*\*End of Report\*\*\*\*

Smart Pathology Laboratory
Drlogy Lab

**Medical Lab Technician**
(DMLT, BMLT)

**Dr. Payal Shah**
(MD, Pathologist)

**Dr. Vimal Shah**
(MD, Pathologist)

Generated on : 02 Dec, 2022 05:00 PM

Page 1 of 1

Sample Collection 9123456789
~~~

## 7.3 Module 1: Object Detection

Object detection models are used while working with our scanned blood reports to find important objects inside the document. In our case these objects include a set of the label and the value (Eg: Haemoglobin: 13). The patterns, forms, and traits associated with the items of interest, such as certain values or data points in the blood report, are taught to these models during training. The model can precisely extract the desired information by learning the locations of these items. In order to train object detection models for scanned blood reports, our manually annotated data is given to the models. Images of blood reports that have had the relevant objects, such as values or data points, noted or highlighted are known as annotated data. The model then learns to connect the visual characteristics of these tagged items with the labels or categories that belong to them.

**Roboflow AutoML:** We leveraged Roboflow's AutoML product to streamline the process of using our annotated data to train an object detection model. AutoML optimizes the model's performance against the provided data and provides detailed metrics and visualizations for model evaluation. We chose Roboflow as it allows users to upload their labeled image datasets in various annotation formats and provides tools for data augmentation, data cleaning, and preprocessing.

**YOLOv8:** The YOLOv8 object detection model is what we chose to employ. A family of real-time object identification models for computer vision known as YOLO (You Only Look Once) work through full pictures or videos in a single pass, thus the name. In order for YOLO to work, each picture must first be divided into a grid, after which bounding boxes and class probabilities must be predicted for each grid cell. This technique enables YOLO to swiftly and precisely detect objects, including those that are partially hidden. The most recent version, YOLOv8, was published in 2021 and is the one we're using.

The 'backbone' and 'head' of the fully convolutional neural network used by YOLOv8 may be considered its two fundamental components. YOLOv8 is built on a modified version of the CSPDarknet53 architecture. This design, which consists of 53 convolutional layers, makes advantage of cross-stage partial connections to improve information flow across the network's various tiers. The YOLOv8 algorithm's head consists of a number of convolutional layers and a series of fully linked layers. Forecasting the object detection bounding boxes, objectness ratings, and class probabilities fall within the purview of these layers. One of YOLOv8's distinctive features is the use of a self-attention mechanism in the network's brain.

With the aid of this mechanism, the model is able to change its attention to various aspects of the image according on their relevance to the task at hand. The capability of YOLOv8 to carry out multi-scale object detection is another crucial feature. The model makes use of a feature pyramid network to find items in an image that are different sizes and scales. The numerous layers of this feature pyramid network recognise items at various scales, enabling the model to recognise both large and small things in an image.

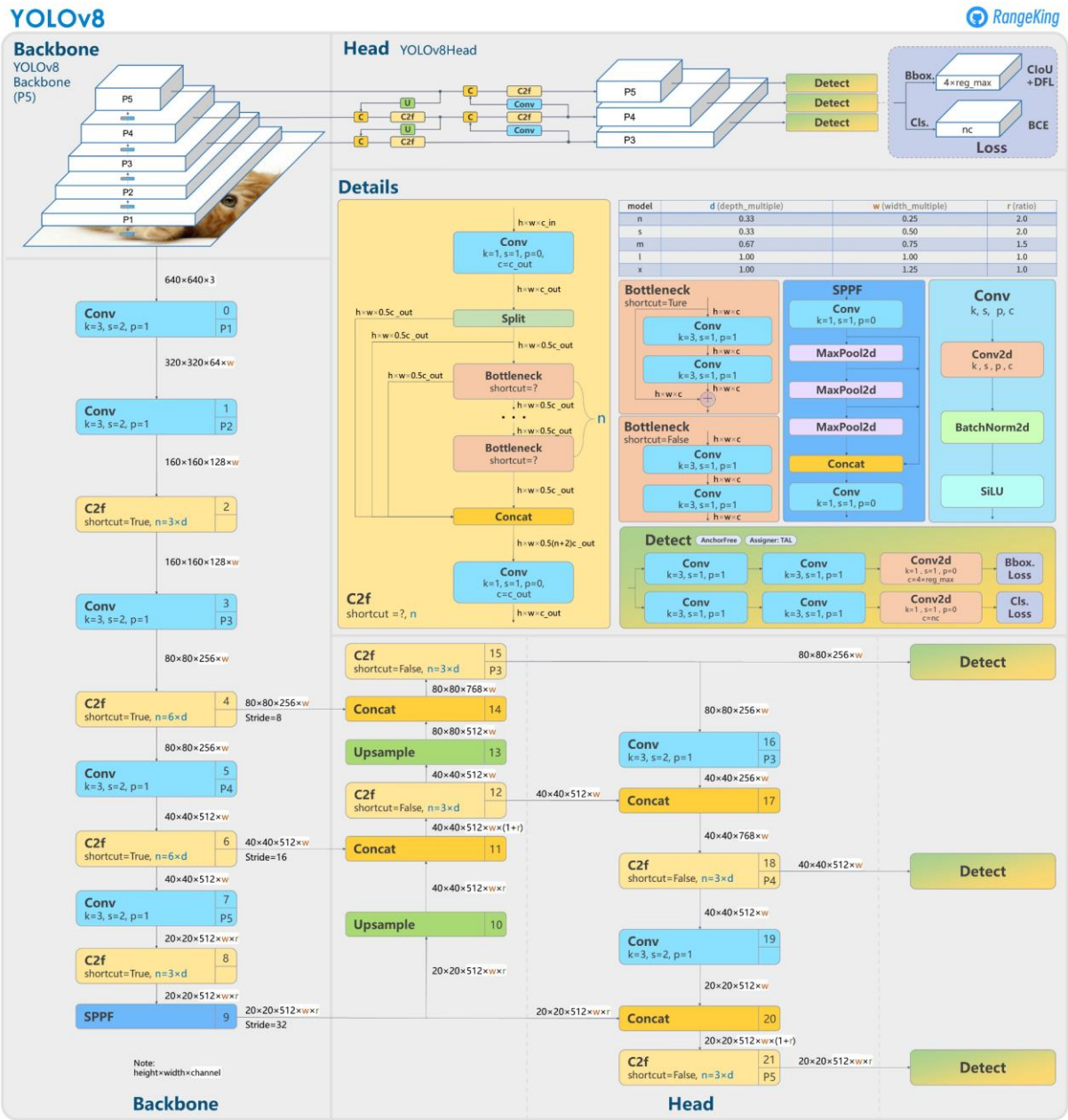
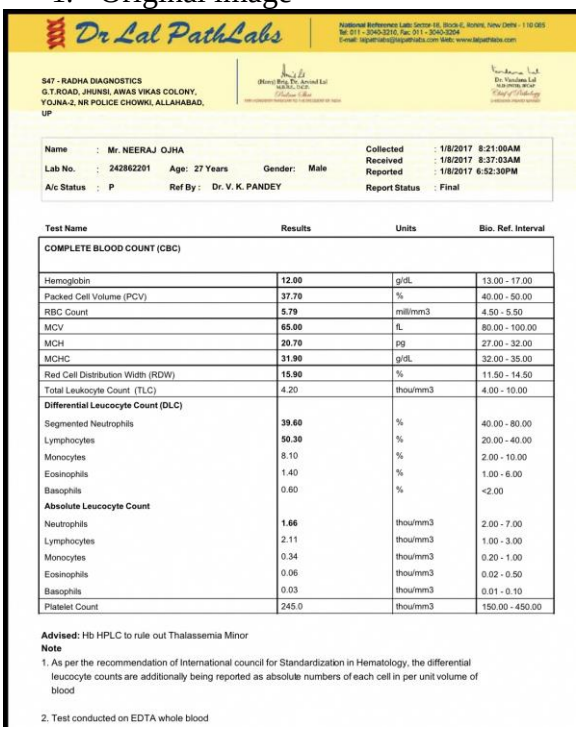
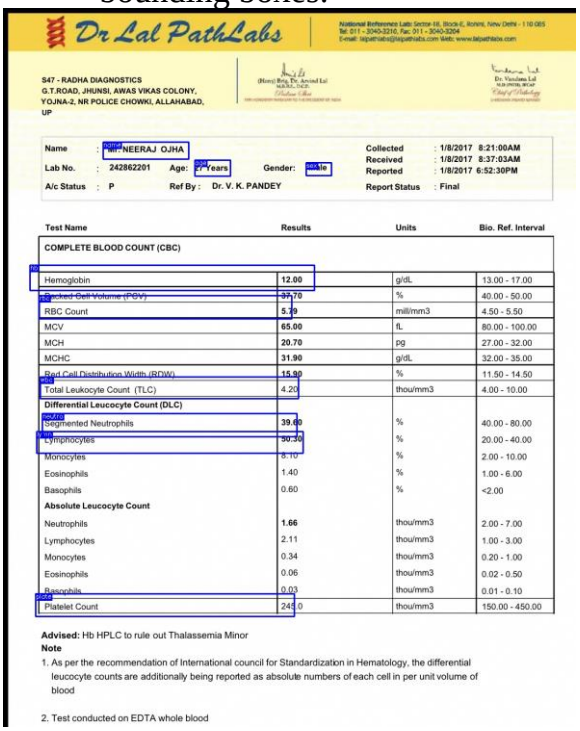



Fig 7.1. YOLOv8 Architecture

| Input for module 1 | Output from module 1 |
|---|---|
| 1. Original image  | 1. Original image with predicted bounding boxes:  2. (json): coordinates (x,y,w,h) and confidence of the classes detected by the model. |

Dr Lal PathLabs

S47 - RADHA DIAGNOSTICS
G.T.ROAD, JHUNSI, AWAS VIKAS COLONY, YOJNA-2, NR POLICE CHOWKI, ALLAHABAD, UP

Name : Mr. NEERAJ OJHA
Lab No. : 242862201 Age: 27 Years Gender: Male
A/c Status : P Ref By : Dr. V. K. PANDEY

Collected : 1/8/2017 8:21:00AM
Received : 1/8/2017 8:37:03AM
Reported : 1/8/2017 6:52:30PM
Report Status : Final

| Test Name | Results | Units | Bio. Ref. Interval |
|---|---|---|---|
| **COMPLETE BLOOD COUNT (CBC)** | | | |
| Hemoglobin | **12.00** | g/dL | 13.00 - 17.00 |
| Packed Cell Volume (PCV) | **37.70** | % | 40.00 - 50.00 |
| RBC Count | **5.79** | mill/mm3 | 4.50 - 5.50 |
| MCV | **65.00** | fL | 80.00 - 100.00 |
| MCH | **20.70** | pg | 27.00 - 32.00 |
| MCHC | **31.90** | g/dL | 32.00 - 35.00 |
| Red Cell Distribution Width (RDW) | **15.90** | % | 11.50 - 14.50 |
| Total Leukocyte Count (TLC) | 4.20 | thou/mm3 | 4.00 - 10.00 |
| **Differential Leucocyte Count (DLC)** | | | |
| Segmented Neutrophils | **39.60** | % | 40.00 - 80.00 |
| Lymphocytes | **50.30** | % | 20.00 - 40.00 |
| Monocytes | 8.10 | % | 2.00 - 10.00 |
| Eosinophils | 1.40 | % | 1.00 - 6.00 |
| Basophils | 0.60 | % | <2.00 |
| **Absolute Leucocyte Count** | | | |
| Neutrophils | **1.66** | thou/mm3 | 2.00 - 7.00 |
| Lymphocytes | 2.11 | thou/mm3 | 1.00 - 3.00 |
| Monocytes | 0.34 | thou/mm3 | 0.20 - 1.00 |
| Eosinophils | 0.06 | thou/mm3 | 0.02 - 0.50 |
| Basophils | 0.03 | thou/mm3 | 0.01 - 0.10 |
| Platelet Count | 245.0 | thou/mm3 | 150.00 - 450.00 |

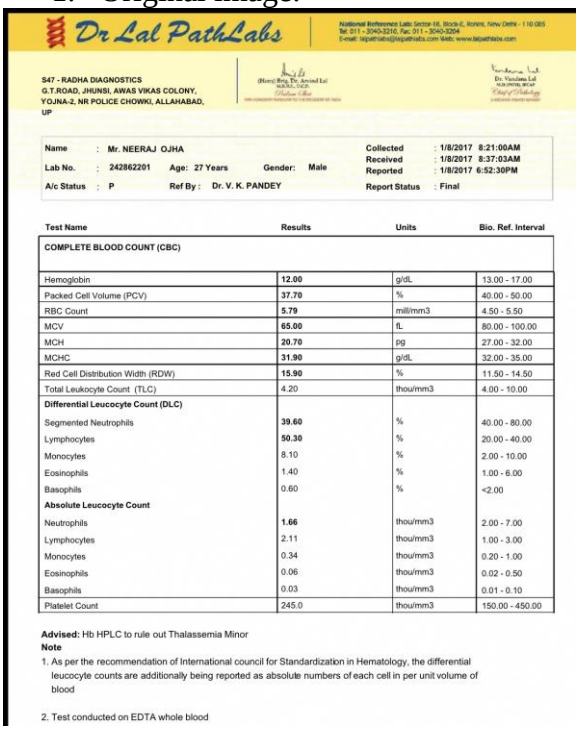
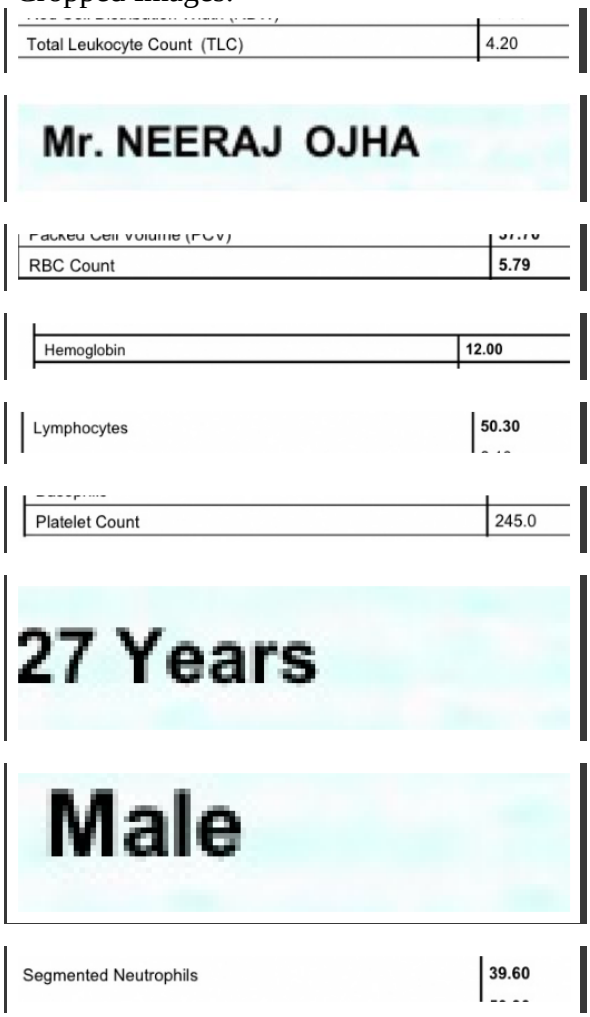
**Advised:** Hb HPLC to rule out Thalassemia Minor
**Note**
1. As per the recommendation of International council for Standardization in Hematology, the differential leucocyte counts are additionally being reported as absolute numbers of each cell in per unit volume of blood

2. Test conducted on EDTA whole blood


```
{'predictions': [{'x': 322.5, 'y': 737.0, 'width': 501.0, 'height': 42.0, 'confidence': 0
.8670761585235596, 'class': 'wbc', 'image_path': '4.jpg', 'prediction_type':
'ObjectDetectionModel'}, {'x': 277.0, 'y': 276.5, 'width': 166.0, 'height': 33.0, 'confidence':
0.8346527814865112, 'class': 'name', 'image_path': '4.jpg', 'prediction_type':
'ObjectDetectionModel'}, {'x': 315.0, 'y': 580.5, 'width': 490.0, 'height': 45.0, 'confidence':
0.7787464261054993, 'class': 'rbc', 'image_path': '4.jpg', 'prediction_type':
'ObjectDetectionModel'}, {'x': 328.0, 'y': 523.5, 'width': 552.0, 'height': 49.0, 'confidence':
0.7568410634994507, 'class': 'hb', 'image_path': '4.jpg', 'prediction_type':
'ObjectDetectionModel'}, {'x': 323.5, 'y': 843.0, 'width': 517.0, 'height': 42.0, 'confidence':
0.7463908195495605, 'class': 'lymp', 'image_path': '4.jpg', 'prediction_type':
'ObjectDetectionModel'}, {'x': 314.0, 'y': 1159.0, 'width': 502.0, 'height': 44.0, 'confidence':
0.7463420629501343, 'class': 'plate', 'image_path': '4.jpg', 'prediction_type':
'ObjectDetectionModel'}, {'x': 406.5, 'y': 310.5, 'width': 69.0, 'height': 31.0, 'confidence': 0
.7365566492080688, 'class': 'age', 'image_path': '4.jpg', 'prediction_type':
'ObjectDetectionModel'}, {'x': 612.5, 'y': 312.5, 'width': 49.0, 'height': 25.0, 'confidence': 0
.693543553352356, 'class': 'sex', 'image_path': '4.jpg', 'prediction_type':
'ObjectDetectionModel'}, {'x': 323.0, 'y': 809.5, 'width': 494.0, 'height': 45.0, 'confidence':
0.5823017954826355, 'class': 'neutro', 'image_path': '4.jpg', 'prediction_type':
'ObjectDetectionModel'}], 'image': {'width': '1112', 'height': '1396'}}
```

## 7.4 Module 2: Image Processing

The main aim of our Image Processing module is to take the output of our object recognition module and use it to separate our single scanned image into multiple smaller cropped images. Cropping is a key component of many computer vision tasks, especially Optical Character Recognition (OCR) tasks. To increase the accuracy of the OCR output and lower noise, it is frequently required to crop or isolate particular regions of interest, such as the prediction regions. Once the object detection model has determined the location of the desired objects, i.e. the x, y, h(height), w(width) coordinates are stored in the output json file and used to crop the image.

| Input for module 2 | Output from module 2 |
|---|---|
| 1. Original image:  2. Coordinates for the classes detected by the module 1: {'predictions': [{'x': 322.5, 'y': 737.0, 'width': 501.0, 'height': 42.0, 'confidence': 0 .8670761585235596, 'class': 'wbc', 'image_path': '4.jpg', 'prediction_type': 'ObjectDetectionModel'}, {'x': 277.0, 'y': 276.5, 'width': 166.0, 'height': 33.0, 'confidence': 0.83465278148651 12, 'class': 'name', 'image_path': '4.jpg', 'prediction_type': 'ObjectDetectionModel'}, {'x': 315.0, 'y': 580.5, 'width': 490.0, 'height': 45.0, 'confidence': 0.7787464261054993, 'class': 'rbc', 'image_path': '4.jpg', 'prediction_type': 'ObjectDetectionModel'}, {'x': 328.0, 'y': 523.5, 'width': 552.0, 'height': 49.0, 'confidence': 0.7568410634994507, 'class': 'hb', 'image_path': '4.jpg', 'prediction_type': 'ObjectDetectionModel'}, {'x': 323.5, 'y': 843.0, 'width': 517.0, 'height': 42.0, 'confidence': 0.7463908195495605, 'class': 'lymp', 'image_path': '4.jpg', 'prediction_type': 'ObjectDetectionModel'}, {'x': 314.0, 'y': 1159.0, 'width': 502.0, 'height': 44.0, 'confidence': 0.7463420629501343, 'class': 'plate', 'image_path': '4.jpg', 'prediction_type': 'ObjectDetectionModel'}, {'x': 406.5, 'y': 310.5, 'width': 69.0, 'height': 31.0, 'confidence': 0 .7365566492080688, 'class': 'age', 'image_path': '4.jpg', 'prediction_type': 'ObjectDetectionModel'}, {'x': 612.5, 'y': 312.5, 'width': 49.0, 'height': 25.0, 'confidence': 0 .69354355352356, 'class': 'sex', 'image_path': '4.jpg', 'prediction_type': 'ObjectDetectionModel'}, {'x': 323.0, 'y': 809.5, 'width': 494.0, 'height': 45.0, 'confidence': 0.5823017954826355, 'class': 'neutro', 'image_path': '4.jpg', 'prediction_type': 'ObjectDetectionModel'}], 'image': {'width': '1112', 'height': '1396'}} | Cropped Images:   |

## 7.5 Module 3: OCR Text Extraction

After the cropping process, the next step in the process was extracting the text from the cropped images. The text extraction was done using pre-trained OCR models. We performed text extraction using both the EasyOCR and Tesseract models and compared their performance. Our model of choice was ultimately EasyOCR as it gave us better results for our problem statement.

**Easy OCR**

Combining deep learning methods, EasyOCR uses LSTM for sequence labelling, ResNet for feature extraction, and the Connectionist Temporal Classification (CTC) algorithm for decoding.

**Feature Extraction:** ResNet is utilised in EasyOCR for feature extraction. In order to learn hierarchical representations of visual features, it is first pretrained on large-scale image classification tasks, such as the ImageNet dataset.

**Sequence Labelling:** EasyOCR uses Long Short-Term Memory (LSTM) networks for sequence labelling. LSTMs are used in the context of OCR to identify and label each distinct character or symbol among the retrieved characteristics. The input properties of the annotated data used to train the LSTM networks are connected to the corresponding character labels. The networks learn to capture the dependencies and context within the sequence of extracted characteristics by utilising the memory cells and gates within the LSTM architecture, enabling precise character recognition.

**Decoding (CTC):** After the LSTM networks have independently tagged each character, EasyOCR decodes the sequence using the Connectionist Temporal Classification (CTC) method. The OCR output is vary in length, and the CTC algorithm manages sequences with repeated or missing characters. It provides a probability distribution for each possible letter sequence while also taking into consideration the labelling produced by the LSTM networks. EasyOCR can convert the series of character labels into the final recognised text using the CTC decoding technique.

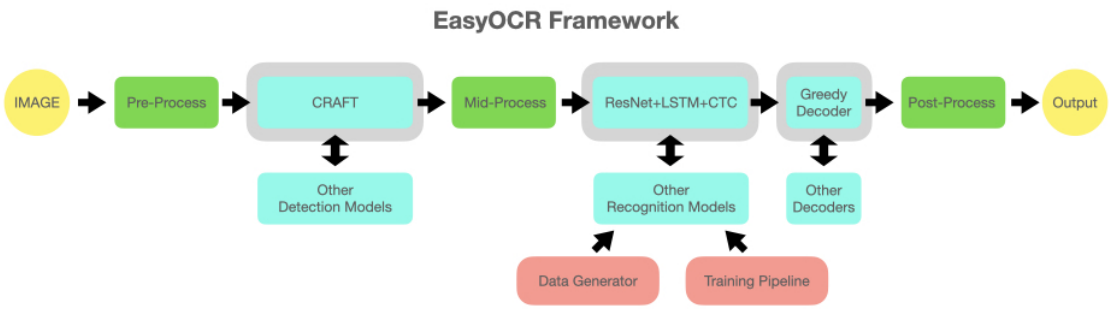



Fig 7.2. EasyOCR Framework

**Tesseract**

A new neural network subsystem configured as a text line recognizer is part of Tesseract 4.00. It is based on the Python-based LSTM implementation from OCRopus and was adapted for Tesseract in C++. CNNs are frequently used to identify images with a single character. To overcome these issues, RNNs—of which LSTM is a well-liked variant—should be utilised in many situations, including ours, where the character sequences make up text of any length. For this reason, we chose LSTM-based models. Preprocessing on the input picture comprises scaling, deskewing, binarization, and noise reduction. After that, character segmentation is done to isolate certain characters. Then, Tesseract uses its deep learning model to extract information from each character. These networks are trained using character images that have been labelled, then backpropagation is used to alter internal parameters to increase recognition accuracy. The trained model receives the extracted features during classification and assigns probability to each character class. The recognised output is determined by the character with the highest likelihood.

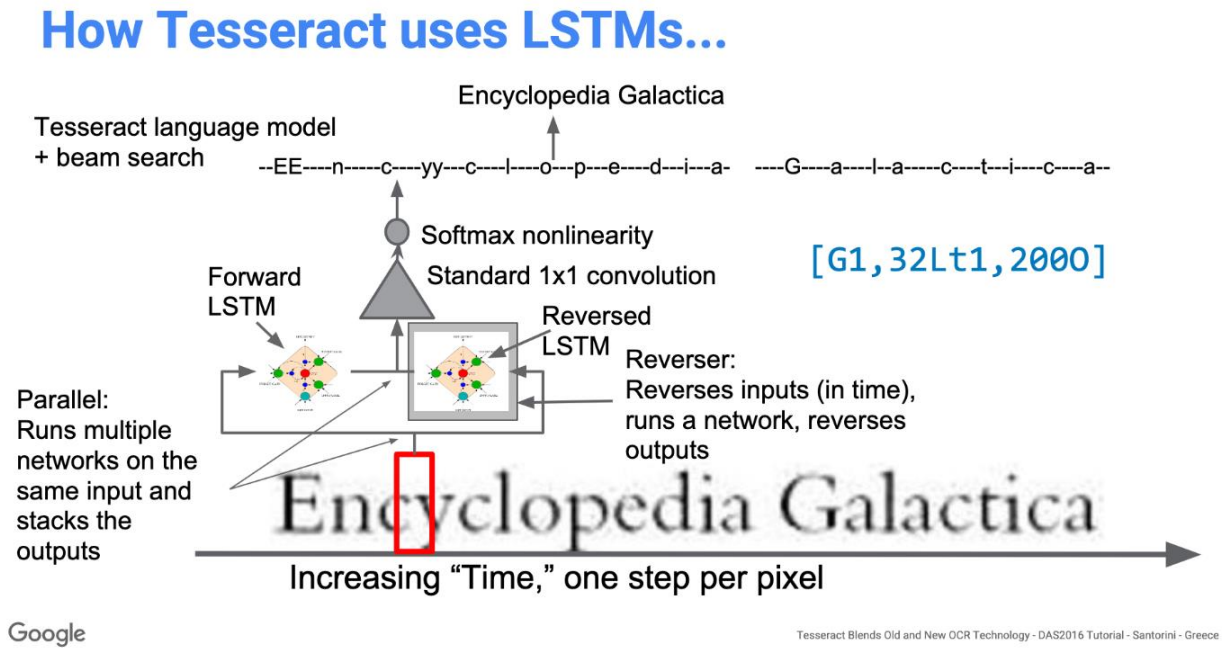
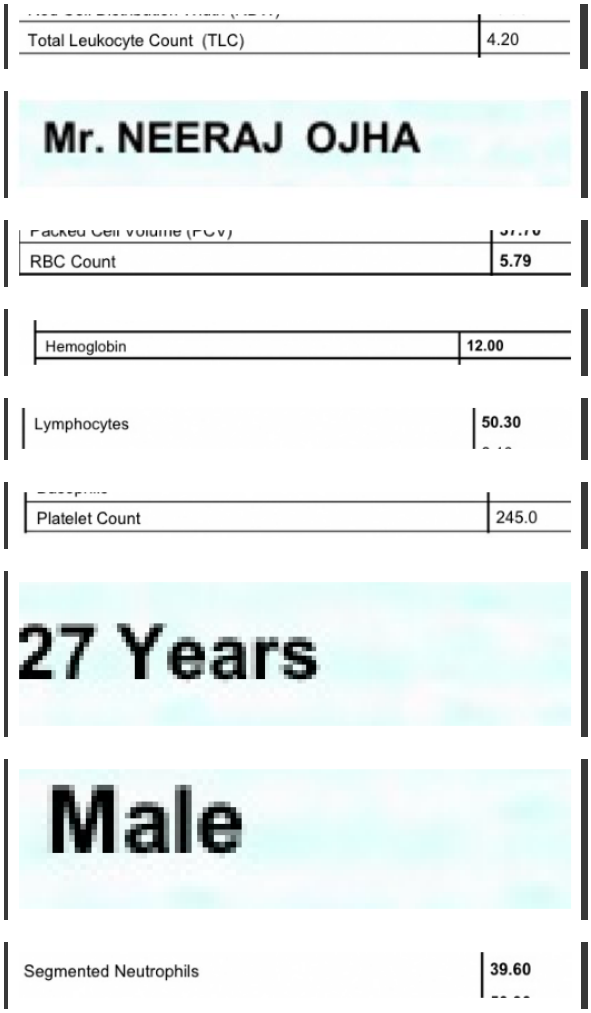



Fig 7.3. Tesseract OCR Architecture

<table>
<tr><th>Input for module 3</th><th>Output from module 3</th></tr>
<tr><td>Cropped Images (from module 2)<br> 
</td>
<td>1. Easy OCR output<br>['Total Leukocyte Count (TLC)', '4.20']<br>['Mr. NEERAJ OJHA']<br>['Tacneu', 'VUiunt', 'RBC Count', '5.79']<br>['Hemoglobin', '12.00']<br>['Lymphocytes', '50.30']<br>['Platelet Count', '245.0']<br>['27 Years']<br>['Male']<br>['Segmented Neutrophils', '39.60']<br>2. Key values extraction from the OCR result:<br>
<table>
<tr><th></th><th>name</th><th>text</th></tr>
<tr><td>0</td><td>wbc</td><td>4.20</td></tr>
<tr><td>1</td><td>name</td><td>Mr. NEERAJ OJHA</td></tr>
<tr><td>2</td><td>rbc</td><td>5.79</td></tr>
<tr><td>3</td><td>hb</td><td>12.00</td></tr>
<tr><td>4</td><td>lymp</td><td>50.30</td></tr>
<tr><td>5</td><td>plate</td><td>245.0</td></tr>
<tr><td>6</td><td>age</td><td>27</td></tr>
<tr><td>7</td><td>sex</td><td>Male</td></tr>
<tr><td>8</td><td>neutro</td><td>39.60</td></tr>
</table></td></tr>
</table>

## 7.6 Module 4: Report Generation

The last stage of our problem statement was to generate a report based on the extracted values. We collected information about the normal ranges of values, potential causes and suggested treatments based on age and sex. The medical information was collected from research papers, Indian lab reports and other reputed sources.

General Values & Likely Causes: [5], [6], [7], [8]
For Age and Gender based Normal Values: [1], [2], [3]
WBC Counts for Elderly : [4]

RBC Counts for Adults: [9]
RBC Counts for Adolescents: [10]
Normal Ranges for Children: [11], [12]

Values from the OCR model were passed to a newly structured Dataframe. The values were then processed by age-group as different age groups had different normal ranges and different likely causes. (Eg: Smoking is an unlikely cause in children). For some values ('RBC Count' and 'Haemoglobin'), the patient's sex was also taken into account as the differences between the normal ranges for each gender was significant. We maintained 4 normal-range tables, one for each age group. The age groups were divided as follows:

Children: 0-10 years
Adolescent: 10-18 years
Adult: 18-50 years
Elderly: 50+ years

Each item's values were calculated as either HIGH, LOW or Normal based on the normal-range table. The difference in normal ranges between Children and Adults can be seen below:

| A | B | C | D | E | F | G | H | I | J |
|---|---|---|---|---|---|---|---|---|---|
| value | sex | age | wbc | rbc | lymp | neutro | plate | hb | Column1 |
| high | | | 30.00 | 5.90 | 70.00 | 65.00 | 450.00 | 20.00 | Age Group: 0-10yrs |
| low | | | 5.00 | 2.70 | 20.00 | 20.00 | 150.00 | 9.00 | |
| Causes_high | | | Bacterial/Parasitic Infection, Leukemia, Inflammation | Dehydration, Lung or Heart issues, Kidney diseases, Blood | Viral/bacterial, parasitic/fungal infections, Inherited | Acute Bacterial Infection, Some Viral Infections, Inflammation, | Recent Blood Loss, Mild to moderate iron | Smoking, Living at higher altitudes, Dehydration, | |
| Causes_low | | | Viral Infection, Blood/Bone Disorder, Autoimmune Condition, Chemo/Radiation | Anemia, Vitamin B-12 or folate deficiency, | Viral Infections (such as HIV/AIDS/Influenza/COVID), | Infection (Generally Bacterial, commonly - | Bacterial Infection, Autoimmune Condition, Viral | Anemia, Iron or Vitamin B-12 or folate deficiency, | |
| solutions_high | | | High counts caused by recent infections will generally resolve naturally. | Professional Assistance Required: Follow up with | High counts caused by recent infections can | High counts caused by recent infections can | For Treating High Platelet Counts related to Iron | For Mild Cases: Increase water intake, Avoid supplements | |
| solutions_low | | | Low counts caused by recent infections will generally resolve naturally. | For Treating Mild Anaemia - B-12 Deficiency: | Acute cases will resolve naturally. | Acute cases will resolve naturally. | Professional Assistance Required: Follow up with | For Treating Mild Anaemia - B-12 Deficiency: | |
| | | | | | | | | | |
| value | sex | age | wbc | rbc | lymp | neutro | plate | hb | Column1 |
| high | | | 10.50 | 5.00 | 40.00 | 75.00 | 450.00 | 17.00 | Age Group: 18-50yrs |
| low | | | 4.50 | 4.50 | 20.00 | 40.00 | 150.00 | 13.00 | |
| Causes_high | | | Bacterial/Parasitic Infection, Leukemia, Steroid Use, Pregnancy,Inflammation | Dehydration, Lung or Heart issues, Kidney diseases, Blood | Recent infection (most commonly viral), | Acute Bacterial Infection, Some Viral Infections, Inflammation, | Recent Blood Loss, Mild to moderate iron | Living at higher altitudes, Dehydration, Heart/Lung | |
| Causes_low | | | Viral Infection, Blood/Bone Disorder, Autoimmune Condition, Chemo/Radiation | Anemia, Vitamin B-12 or folate deficiency, | Blood diseases like Hodgkin's disease, Autoimmune | Infection (Generally Bacterial, commonly - | Viruses such as mononucleosis/ HIV/AIDS, | Anemia, Iron or Vitamin B-12 or folate deficiency, | |
| solutions_high | | | High counts caused by recent infections will generally resolve naturally. | For mild cases: Exercise can help improve heart and lung | High counts caused by recent infections can | Acute cases will resolve naturally. | For Treating High Platelet Counts related to Iron | For Mild Cases: Increase water intake, Avoid supplements, | |
| solutions_low | | | Low counts caused by recent infections will generally resolve naturally. | For Treating Mild Anaemia - B-12 Deficiency: | Low counts caused by recent infections will | Acute cases will resolve naturally. | Professional Assistance Required: Follow up with | For Treating Mild Anaemia - B-12 Deficiency: | |

For any abnormal (HIGH/LOW) values, a more detailed report was generated. This included the percentage deviation from the normal value, the most likely causes for the deviation and the suggested advice. Deviations were considered 'MILD' if deviation was lower than 10%, otherwise it was categorised as 'Significant'.

## 7.7 Module 5: GUI

To connect all the modules together, provide a simple user interface which will allow the user to upload a blood report image and get the structured pdf inference based off of it. We decided to go with flask which is a web application framework developed in python.

The complete directory of the application looks like the figure mentioned below:

```
D:.
ª   app.py
ª   best.pt
+---env1
ª   +---Scripts
ª   +---share
ª       +---doc
ª       +---man
+---report_generation
ª       normal_1.xlsx
ª       normal_2.xlsx
ª       normal_3.xlsx
ª       normal_4.xlsx
+---static
ª   ª   logo.png
ª   ª   prediction.jpg
ª   +---predict
ª   ª       uploaded_image.jpg
+---templates
ª       index.html
ª       result.html
+---tmp
ª       report.pdf
ª       temp_html_file.html
ª       uploaded_image.jpg
+---__pycache__
        app.cpython-39.pyc
        hello.cpython-39.pyc
```

Fig 7.4. GUI directory

Where the app.py consists of the program for all the modules (backend), best.pt is the YOLOv8x model file, env1 is the virtual environment, report_generation folder consists of the dataset for the module 4 (Report generation), static folder consists of the images to be displayed on the web page (prediction.jpg- output from Roboflow model, predict-output from YOLOv8x), templates consists of the frontend html pages, tmp consists of the temporary data that gets generated during the runtime.

**Homepage:**

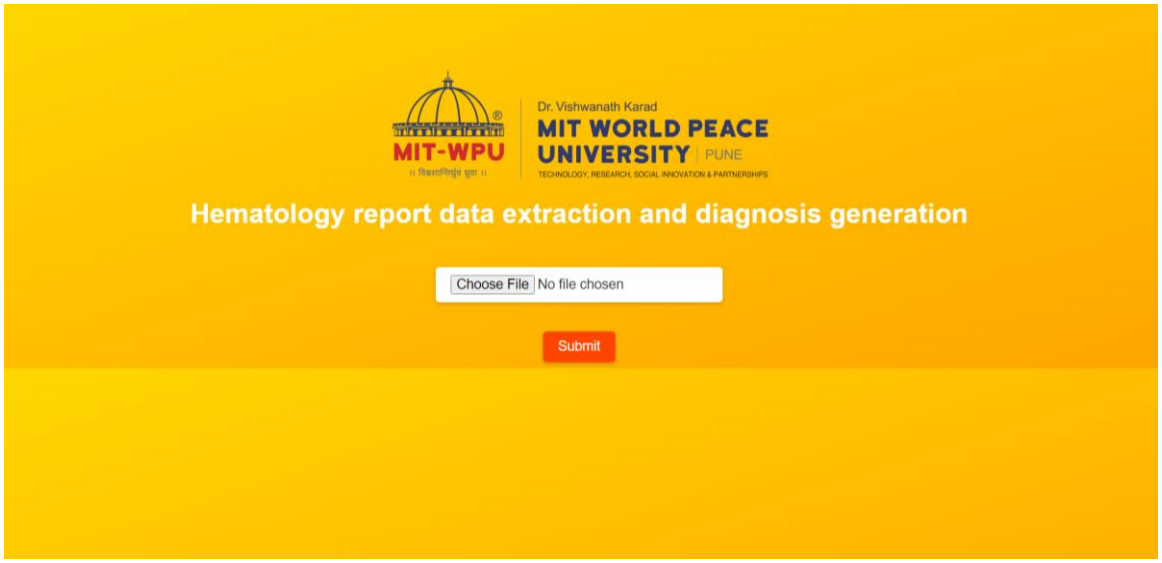



Fig 7.5. Homepage

**Result:**

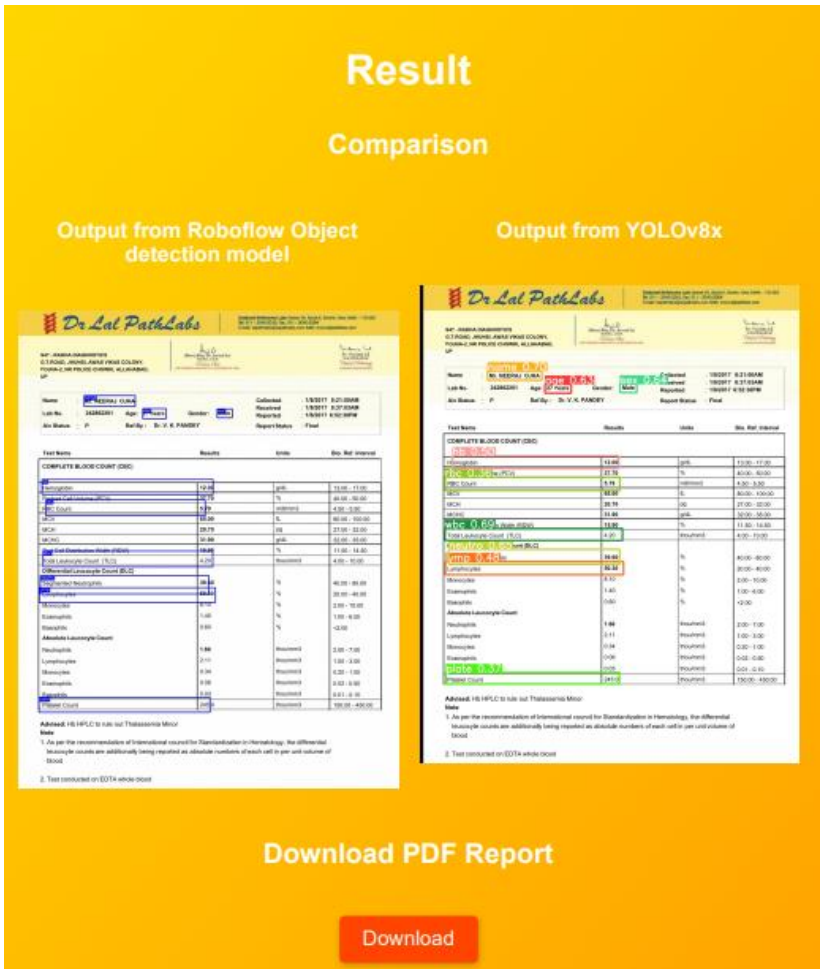



Fig 7.6. Result page

**Downloaded report:**

1 / 1 | − 100% +

```
-----------------------------------------------------------------------Generated Report-----------------------------------------------------------------------

-----------------------------------------------------------------------------------------------------------------------------------------------------------------
GENERAL INFORMATION
-----------------------------------------------------------------------------------------------------------------------------------------------------------------

Name: Mr. NEERAJ OJHA
Sex: Male
Age: 27
Age Group: Adult (18-50 years old)

-----------------------------------------------------------------------------------------------------------------------------------------------------------------
ALL RESULTS
-----------------------------------------------------------------------------------------------------------------------------------------------------------------

WBC Level: LOW
RBC Level: Normal
LYMPHOCYTE Level: HIGH
NEUTROPHIL Level: LOW
PLATELET Level: Normal
HAEMOGLOBIN Level: LOW

-----------------------------------------------------------------------------------------------------------------------------------------------------------------
DETAILED REPORT OF ABNORMAL RESULTS
-----------------------------------------------------------------------------------------------------------------------------------------------------------------

1.
WBC Level:
 - 6.67 % LOWER than normal
 - MILD deviation from normal range

Potential Causes: (Common causes are listed first)
Viral Infection, Blood/Bone Disorder, Autoimmune Condition,  Chemo/Radiation Therapy, Medication Side Effect


2.
LYMPHOCYTE Level:
 - 25.75 % HIGHER than normal
 - !! Significant deviation from normal range

Potential Causes: (Common causes are listed first)
Recent infection (most commonly viral),
Long-term inflammation (such as rheumatoid arthritis),
Medication Side Effect, Trauma,
Spleen Removal, Certain types of cancer (like leukemia or lymphoma)


Suggestions:
High counts caused by recent infections can resolve naturally.

For more severe symptoms contact a medical professional.
-----------------------------------------------------------------------------------------------------------------------------------------------------------------

3.
NEUTROPHIL Level:
 - 1.0 % LOWER than normal
 - MILD deviation from normal range

Potential Causes: (Common causes are listed first)
Infection (Generally Bacterial, commonly -  Tuberculosis, Dengue, HIV), Inflammation, Chemotherapy, Blood Cancer (rare), Leukemia (rare)


4.
HAEMOGLOBIN Level:
 - 14.29 % LOWER than normal
 - !! Significant deviation from normal range
```

Fig 7.7. Download report

# Chapter 8
# Coding

## 8.1 Data augmentation

As explained above (6.2) about the data preprocessing and data generation procedure, OpenCV library was extensively used to augment the 4 report formats selected to populate the dataset.

```python
import cv2
import numpy as np
import random
import os

# Rotation
def rotate(image, angle):
    # Calculate image center
    center = tuple(np.array(image.shape[1::-1]) / 2)
    # Build the rotation matrix
    matrix = cv2.getRotationMatrix2D(center, angle, 1.0)
    # Perform the actual rotation and return the result
    return cv2.warpAffine(image, matrix, image.shape[1::-1], flags=cv2.INTER_LINEAR)

def add_noise(image, scale=0.1):
    """
    Add random noise to the input image.
    """
    # Generate random noise and scale it based on the input image
    noise = np.random.normal(scale=scale, size=image.shape)
    # Add the noise to the image
    noisy_image = image + noise
    # Clip the pixel values to be within the valid range [0, 255]
    noisy_image = np.clip(noisy_image, 0, 255).astype(np.uint8)
    return noisy_image

def blur(image, kernel_size=3):
    """
    Apply Gaussian blur to the input image.
    """
    # Apply Gaussian blur to the image using the specified kernel size
    blurred_image = cv2.GaussianBlur(image, (kernel_size, kernel_size), 0)
    return blurred_image

def grayscale(image):
    if image.shape[-1] > 1:
        result = cv2.cvtColor(image, cv2.COLOR_BGR2GRAY)
    else:
        result = image
    return result

def color_hue(image, hue):
    if image.shape[-1] >= 3:
        # Convert the image to HSV color space
        hsv = cv2.cvtColor(image, cv2.COLOR_BGR2HSV)
        # Add the hue value to the Hue channel
        hsv[:, :, 0] = (hsv[:, :, 0] + hue) % 180
        # Convert the image back to BGR color space
        result = cv2.cvtColor(hsv, cv2.COLOR_HSV2BGR)
    else:
        result = image
    return result
```

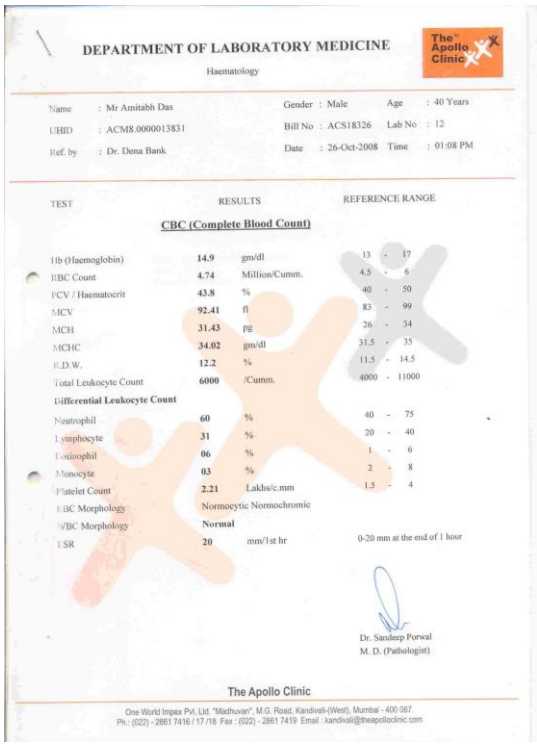
```python
def skew(image, angle=1, scale=1.0):
    """
    Skew the input image by a given angle.
    """
    # Define the transformation matrix
    matrix = np.float32([[1, 0, 0], [0, 1, 0]])
    angle_radians = angle * np.pi / 180.0
    matrix[0, 1] = np.tan(angle_radians)
    matrix[1, 0] = np.tan(angle_radians)
    # Apply the transformation to the image
    skewed_image = cv2.warpAffine(image, matrix, (image.shape[1], image.shape[0]))
    return skewed_image

def translate_x(image, shift=10):
    """
    Translate the input image on the x-axis by a given number of pixels.
    """
    # Define the transformation matrix
    matrix = np.float32([[1, 0, shift], [0, 1, 0]])
    # Apply the transformation to the image
    translated_image = cv2.warpAffine(image, matrix, (image.shape[1], image.shape[0]))
    return translated_image

def translate_y(image, shift=10):
    """
    Translate the input image on the y-axis by a given number of pixels.
    """
    # Define the transformation matrix
    matrix = np.float32([[1, 0, 0], [0, 1, shift]])
    # Apply the transformation to the image
    translated_image = cv2.warpAffine(image, matrix, (image.shape[1], image.shape[0]))
    return translated_image

# Apply one or more image variations to an input image and save the result
def apply_image_variations(img, output_path, variations):
    # Load the input image
    input_image = img

    # Apply each specified variation to the image
    for variation in variations:
        if variation == 'rotate_left':
            input_image = rotate(input_image, random_float())
        elif variation == 'rotate_right':
            input_image = rotate(input_image, -1 * random_float())
        elif variation == 'add_noise':
            input_image = add_noise(input_image)
        elif variation == 'blur':
            input_image = blur(input_image)
        elif variation == 'grayscale':
            input_image = grayscale(input_image)
        elif variation == 'color_hue':
            input_image = color_hue(input_image, 30)
        elif variation == 'translate_x':
            input_image = translate_x(input_image)
        elif variation == 'translate_y':
            input_image = translate_y(input_image)
        elif variation == 'skew':
            input_image = skew(input_image, random_float())

    # Save the resulting image to the specified output path
    cv2.imwrite(output_path, input_image)
```

```python
def get_random_elements():
    input_list = ['add_noise', 'color_hue', 'skew', 'translate_y', 'translate_x']
    num_elements = random.randint(1, len(input_list))
    random.shuffle(input_list)
    return input_list[:num_elements]

def random_float():
    return random.uniform(-3, 3)

def load_images_from_folder(folder):
    images = []
    for filename in os.listdir(folder):
        img = cv2.imread(os.path.join(folder,filename))
        if img is not None:
            images.append([filename,img])
    return images

def main():
    FOLDER_NAME = 'Pathology Reports'
    for [filename, image] in load_images_from_folder(FOLDER_NAME):
        for i in range(20):
            variations = get_random_elements()
            output_filename = f"Edited/edited-{filename}_{'-'.join(variations)}.jpg"
            print(f"[Output]: {output_filename}")
            apply_image_variations(image, output_filename, variations)
```

```python
main()
```

```
[Output]: Edited/edited-1.jpg_color_hue-translate_x-add_noise.jpg
[Output]: Edited/edited-1.jpg_skew-color_hue-translate_y-translate_x.jpg
[Output]: Edited/edited-1.jpg_translate_x-add_noise-skew-color_hue.jpg
[Output]: Edited/edited-1.jpg_color_hue-add_noise.jpg
[Output]: Edited/edited-1.jpg_translate_x-add_noise-translate_y-color_hue-skew.jpg
[Output]: Edited/edited-1.jpg_color_hue-add_noise-translate_x-skew.jpg
[Output]: Edited/edited-1.jpg_skew-color_hue.jpg
[Output]: Edited/edited-1.jpg_color_hue-translate_x-skew-add_noise.jpg
[Output]: Edited/edited-1.jpg_skew-color_hue-translate_x-translate_y-add_noise.jpg
[Output]: Edited/edited-1.jpg_skew-translate_x.jpg
[Output]: Edited/edited-1.jpg_translate_y-color_hue-translate_x-skew.jpg
[Output]: Edited/edited-1.jpg_add_noise-translate_x-color_hue-skew-translate_y.jpg
[Output]: Edited/edited-1.jpg_translate_y.jpg
[Output]: Edited/edited-1.jpg_add_noise-skew-color_hue-translate_x-translate_y.jpg
[Output]: Edited/edited-1.jpg_skew-color_hue-translate_y-add_noise.jpg
[Output]: Edited/edited-1.jpg_skew-translate_x.jpg
[Output]: Edited/edited-1.jpg_skew-translate_y.jpg
[Output]: Edited/edited-1.jpg_translate_y-skew-color_hue-add_noise-translate_x.jpg
[Output]: Edited/edited-1.jpg_color_hue-translate_x-skew.jpg
[Output]: Edited/edited-1.jpg_translate_y-translate_x.jpg
[Output]: Edited/edited-10.png_skew-color_hue-translate_x.jpg
[Output]: Edited/edited-10.png_translate_x-translate_y-add_noise-skew-color_hue.jpg
[Output]: Edited/edited-10.png_add_noise-translate_y.jpg
[Output]: Edited/edited-10.png_translate_x-translate_y-add_noise-skew.jpg
[Output]: Edited/edited-10.png_translate_y-translate_x-add_noise.jpg
[Output]: Edited/edited-10.png_color_hue-add_noise.jpg
[Output]: Edited/edited-10.png_translate_y-skew.jpg
[Output]: Edited/edited-10.png_translate_x.jpg
[Output]: Edited/edited-10.png_translate_x.jpg
[Output]: Edited/edited-10.png_skew-add_noise.jpg
[Output]: Edited/edited-10.png_color_hue-translate_x-skew-translate_y.jpg
[Output]: Edited/edited-10.png_translate_x-color_hue-skew-add_noise-translate_y.jpg
[Output]: Edited/edited-10.png_skew-color_hue-add_noise-translate_x.jpg
[Output]: Edited/edited-10.png_translate_x-add_noise-skew-translate_y-color_hue.jpg
[Output]: Edited/edited-10.png_add_noise.jpg
```

Original image



DEPARTMENT OF LABORATORY MEDICINE

Haematology

The Apollo Clinic

Name : Mr Amitabh Das
UHID : ACM8.0000013831
Ref. by : Dr. Dena Bank

Gender : Male Age : 40 Years
Bill No : ACS18326 Lab No : 12
Date : 26-Oct-2008 Time : 01:08 PM

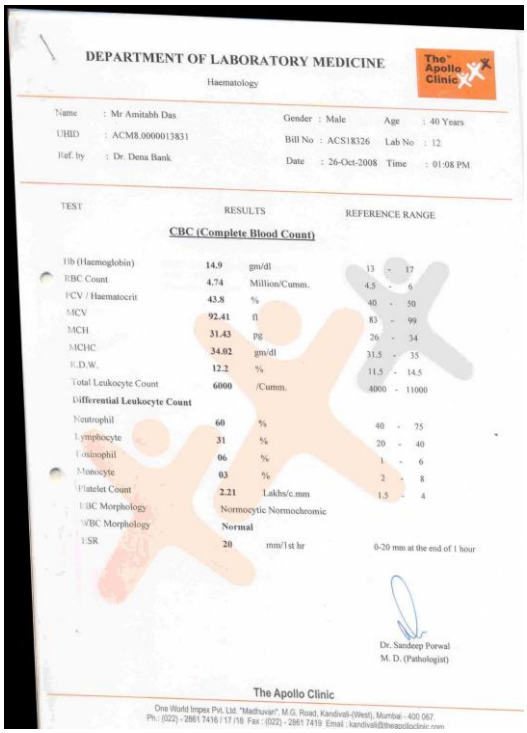
| TEST | RESULTS | | REFERENCE RANGE |
|---|---|---|---|
| **CBC (Complete Blood Count)** | | | |
| Hb (Haemoglobin) | 14.9 | gm/dl | 13 - 17 |
| RBC Count | 4.74 | Million/Cumm. | 4.5 - 6 |
| PCV / Haematocrit | 43.8 | % | 40 - 50 |
| MCV | 92.41 | fl | 83 - 99 |
| MCH | 31.43 | pg | 26 - 34 |
| MCHC | 34.02 | gm/dl | 31.5 - 35 |
| R.D.W. | 12.2 | % | 11.5 - 14.5 |
| Total Leukocyte Count | 6000 | /Cumm. | 4000 - 11000 |
| **Differential Leukocyte Count** | | | |
| Neutrophil | 60 | % | 40 - 75 |
| Lymphocyte | 31 | % | 20 - 40 |
| Eosinophil | 06 | % | 1 - 6 |
| Monocyte | 03 | % | 2 - 8 |
| Platelet Count | 2.21 | Lakhs/c.mm | 1.5 - 4 |
| RBC Morphology | Normocytic Normochromic | | |
| WBC Morphology | Normal | | |
| ESR | 20 | mm/1st hr | 0-20 mm at the end of 1 hour |

Dr. Sandeep Porwal
M. D. (Pathologist)

The Apollo Clinic

One World Impex Pvt. Ltd. "Madhuvan", M.G. Road, Kandivali-(West), Mumbai - 400 067.
Ph.: (022) - 2861 7416 / 17 /18 Fax : (022) - 2861 7419 Email : kandivali@theapolloclinic.com

Edited image after augmentation



DEPARTMENT OF LABORATORY MEDICINE

Haematology

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| MCH | 31.43 | pg | 26 - 34 |
| MCHC | 34.02 | gm/dl | 31.5 - 35 |
| R.D.W. | 12.2 | % | 11.5 - 14.5 |
| Total Leukocyte Count | 6000 | /Cumm. | 4000 - 11000 |
| **Differential Leukocyte Count** | | | |
| Neutrophil | 60 | % | 40 - 75 |
| Lymphocyte | 31 | % | 20 - 40 |
| Eosinophil | 06 | % | 1 - 6 |
| Monocyte | 03 | % | 2 - 8 |
| Platelet Count | 2.21 | Lakhs/c.mm | 1.5 - 4 |
| RBC Morphology | Normocytic Normochromic | | |
| WBC Morphology | Normal | | |
| ESR | 20 | mm/1st hr | 0-20 mm at the end of 1 hour |

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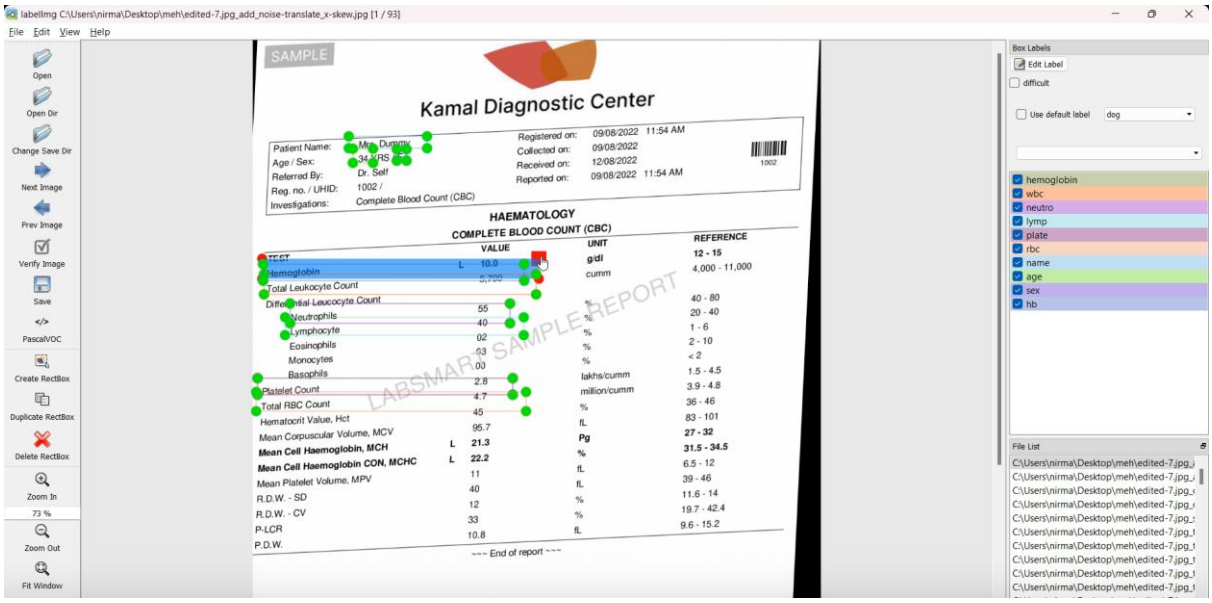
## 8.2 Annotation

For annotation of the newly generated data, we used LabelImg tool, an open source tool that allows us to annotate images by drawing bounding boxes for the desired classes and export the annotations in xml, json or txt formats supported by various popular dataset norms/ object detection models like PASCAL VOC, yolo, coco, etc.




## 8.3 Model training

For model training we went with a 70-20-10 training, validation and testing split.

Initial train-test-val split code:

```
In [1]: import random
        import os


        def split_dataset(image_files, train_ratio=0.7, val_ratio=0.2, test_ratio=0.1):
            # shuffle the image files
            random.shuffle(image_files)

            # calculate the number of images for each set
            num_train = int(len(image_files) * train_ratio)
            num_val = int(len(image_files) * val_ratio)
            num_test = int(len(image_files) * test_ratio)

            # split the image files into the sets
            train_files = image_files[:num_train]
            val_files = image_files[num_train:num_train+num_val]
            test_files = image_files[num_train+num_val:]

            return train_files, val_files, test_files
```

```
In [3]: # Set folder path
        folder_path = 'meh'

        # Get list of image files in folder
        image_files = [os.path.join(folder_path, file) for file in os.listdir(folder_path) if file.endswith('.jpg')]

        # Shuffle image files
        random.shuffle(image_files)

        # Split image files into train and test sets
        train_split = 0.7
        num_train = int(len(image_files) * train_split)
        train_files = image_files[:num_train]
        test_files = image_files[num_train:]

        # Print number of files in train and test sets
        print('Number of training files:', len(train_files))
        print('Number of testing files:', len(test_files))

        Number of training files: 51
        Number of testing files: 22
```

ROBOFLOW 2.0 OBJECT DETECTION (FAST)

Roboflow facilitates the deployment of computer vision models to various platforms and frameworks, including cloud environments, edge devices, and web applications. It provides model export in formats compatible with popular frameworks, making it easy to integrate trained models into production pipelines. Roboflow also offers APIs and SDKs for seamless integration with existing software systems and workflows. Using APIs for model training.

```
from roboflow import Roboflow
import os
from PIL import Image
rf = Roboflow(api_key="DWr88H9uUstVlVubbYIQ")
project = rf.workspace().project("medi-9sqs7")
model = project.version(1).model

pred_json=model.predict('4.jpg', confidence=40, overlap=30).json()
# infer on a local image
print(pred_json)


# visualize your prediction
model.predict('4.jpg', confidence=40, overlap=30).save("prediction.jpg")

# infer on an image hosted elsewhere
# print(model.predict("URL_OF_YOUR_IMAGE", hosted=True, confidence=40, overlap=30).json())
```

```
loading Roboflow workspace...
loading Roboflow project...
{'predictions': [{'x': 424.0, 'y': 330.5, 'width': 228.0, 'height': 61.0, 'confidence': 0.8537383079528809
```

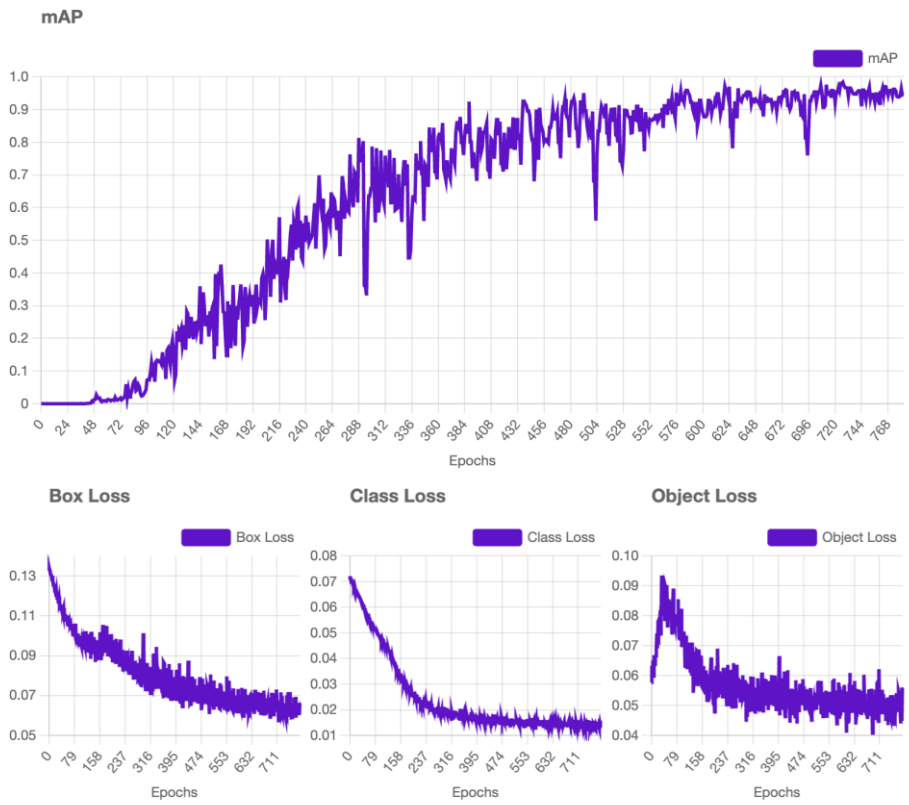



Fig 8.1. RoboFlow model performance

YOLOv8

Setting up data loaders to deliver batches of pictures and related annotations during training and loading the dataset and annotations. The model uses an input picture to generate bounding box predictions and class probabilities for the text sections during training rounds. Create a loss function that takes both categorization and localization aspects into account. Combining classification loss (such as cross-entropy loss) with bounding box regression loss (such as smooth L1 loss) is a popular choice. To minimise the specified loss function, train the YOLOv8 model using gradient descent-based optimisation techniques like Adam or SGD.

Evaluate the trained model on the validation set after training for a sufficient number of epochs. Examine performance indicators like precision, recall, and mean average precision (mAP) to judge how well the model can properly identify text areas.

```
[ ] model = YOLO(f'/yolov8n.pt')

    Downloading https://github.com/ultralytics/assets/releases/download/v0.0.0/yolov8n.pt to /yolov8n.pt...
    100%|██████████| 6.23M/6.23M [00:00<00:00, 67.8MB/s]
```

```
!yolo task=detect mode=train model=yolov8x.pt data='/content/datasets/medi-2/data.yaml' epochs=500 imgsz=600 plots=True

Ultralytics YOLOv8.0.20 🚀 Python-3.10.11 torch-2.0.0+cu118 CUDA:0 (Tesla T4, 15102MiB)
yolo/engine/trainer: task=detect, mode=train, model=yolov8x.yaml, data=/content/datasets/medi-2/data.yaml, epochs=500, patience=50, batch
2023-05-12 05:28:00.055576: I tensorflow/core/platform/cpu_feature_guard.cc:182] This TensorFlow binary is optimized to use available CPU
To enable the following instructions: AVX2 FMA, in other operations, rebuild TensorFlow with the appropriate compiler flags.
2023-05-12 05:28:01.576057: W tensorflow/compiler/tf2tensorrt/utils/py_utils.cc:38] TF-TRT Warning: Could not find TensorRT
Overriding model.yaml nc=80 with nc=9

                   from  n    params  module                                       arguments
  0                  -1  1      2320  ultralytics.nn.modules.Conv                  [3, 80, 3, 2]
  1                  -1  1    115520  ultralytics.nn.modules.Conv                  [80, 160, 3, 2]
  2                  -1  3    436800  ultralytics.nn.modules.C2f                   [160, 160, 3, True]
  3                  -1  1    461440  ultralytics.nn.modules.Conv                  [160, 320, 3, 2]
  4                  -1  6   3281920  ultralytics.nn.modules.C2f                   [320, 320, 6, True]
  5                  -1  1   1844480  ultralytics.nn.modules.Conv                  [320, 640, 3, 2]
  6                  -1  6  13117440  ultralytics.nn.modules.C2f                   [640, 640, 6, True]
  7                  -1  1   3687680  ultralytics.nn.modules.Conv                  [640, 640, 3, 2]
  8                  -1  3   6969600  ultralytics.nn.modules.C2f                   [640, 640, 3, True]
  9                  -1  1   1025920  ultralytics.nn.modules.SPPF                  [640, 640, 5]
 10                  -1  1         0  torch.nn.modules.upsampling.Upsample         [None, 2, 'nearest']
 11             [-1, 6]  1         0  ultralytics.nn.modules.Concat                [1]
 12                  -1  3   7379200  ultralytics.nn.modules.C2f                   [1280, 640, 3]
 13                  -1  1         0  torch.nn.modules.upsampling.Upsample         [None, 2, 'nearest']
 14             [-1, 4]  1         0  ultralytics.nn.modules.Concat                [1]
 15                  -1  3   1948800  ultralytics.nn.modules.C2f                   [960, 320, 3]
 16                  -1  1    922240  ultralytics.nn.modules.Conv                  [320, 320, 3, 2]
 17            [-1, 12]  1         0  ultralytics.nn.modules.Concat                [1]
 18                  -1  3   7174400  ultralytics.nn.modules.C2f                   [960, 640, 3]
 19                  -1  1   3687680  ultralytics.nn.modules.Conv                  [640, 640, 3, 2]
 20             [-1, 9]  1         0  ultralytics.nn.modules.Concat                [1]
 21                  -1  3   7379200  ultralytics.nn.modules.C2f                   [1280, 640, 3]


                   wbc          9          9      0.747          1      0.995      0.576
Stopping training early as no improvement observed in last 50 epochs. Best results observed at epoch 219, best model saved as best.pt.
To update EarlyStopping(patience=50) pass a new patience value, i.e. `patience=300` or use `patience=0` to disable EarlyStopping.

269 epochs completed in 1.202 hours.
Optimizer stripped from runs/detect/train18/weights/last.pt, 136.7MB
Optimizer stripped from runs/detect/train18/weights/best.pt, 136.7MB

Validating runs/detect/train18/weights/best.pt...
Ultralytics YOLOv8.0.20 🚀 Python-3.10.11 torch-2.0.0+cu118 CUDA:0 (Tesla T4, 15102MiB)
Model summary (fused): 268 layers, 68132235 parameters, 0 gradients, 257.4 GFLOPs
                 Class     Images  Instances      Box(P          R      mAP50  mAP50-95): 100% 1/1 [00:00<00:00,  1.22it/s]
                   all          9         81      0.921      0.887      0.965      0.594
                   age          9          9          1      0.856      0.995       0.51
                    hb          9          9      0.894          1      0.995      0.662
                  lymp          9          9      0.847          1      0.984      0.596
                  name          9          9      0.946          1      0.995       0.59
                neutro          9          9       0.98          1      0.995      0.659
                 plate          9          9      0.833      0.554      0.806      0.572
                   rbc          9          9      0.943      0.889      0.984      0.643
                   sex          9          9          1      0.679      0.984      0.487
                   wbc          9          9      0.848          1      0.951      0.629
Speed: 0.2ms pre-process, 22.8ms inference, 0.0ms loss, 1.1ms post-process per image
Results saved to runs/detect/train18
```

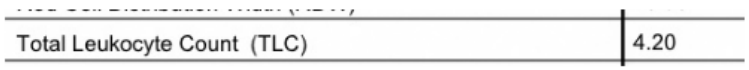
## 8.4 Image processing and text/ value extraction

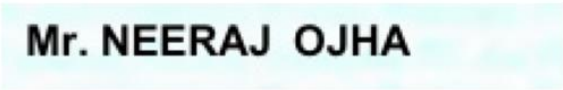
Based on the results from the object detection models, we slice the original image according to the respective detected classes and their x, y, w, h. Through thorough testing, we decided to extend the cropped images by 50 pixels which resulted in better accuracy from the OCR module.

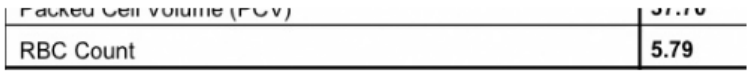
```
# load the image
img = cv2.imread('4.jpg')
im=Image.open('4.jpg')
# Initialize an empty dataframe to store the results
df = pd.DataFrame(columns=['name', 'text'])

# Process each prediction from RCNN
for pred in pred_json['predictions']:
    # Crop the image based on the object coordinates
    x, y, w, h = float(pred['x']), float(pred['y']), float(pred['width']), float(pred['height'])
    #print(x,y,w,h)
    #cropped_img = img[y:h+y, x:w+x]
#     img_res = im.crop((x, y, x+w, y+h))
#     img_res.show()
    roi_x = int(x - w / 2)
    roi_y = int(y - h / 2)
    roi_width = int(w)+50
    roi_height = int(h)
    cropped_img = img[roi_y:roi_y+roi_height, roi_x:roi_x+roi_width]
    plt.imshow(cropped_img)
    plt.axis("off")
    plt.show()
```

Example of cropped images:




Utilising an OCR model, text and value extraction from photographs or scanned documents includes automatically identifying and extracting pertinent textual information, such as words, phrases, or numeric values, to facilitate effective data retrieval and analysis.

Comparing EasyOCR and Tesseract in various scenarios, we chose to go with EasyOCR because of higher accuracy, cleaner output and faster speed.

```
[ ] import cv2
    import pytesseract
    import pandas as pd
    from PIL import Image
    import re
    from matplotlib import pyplot as plt


    # function to extract numeric information from a string
    def extract_numeric_info(text):
        return re.sub(r'[^\d.]+', '', text)

    # Function to check if a string is numeric
    def is_numeric(value):
        try:
            float(value)
            return True
        except ValueError:
            return False

    # initialize tesseract OCR with 'digits' as the allowed characters
    pytesseract.pytesseract.tesseract_cmd = r'/usr/bin/tesseract'
    tess_config = r'--psm 7'  # Set OCR mode to treat the image as a single line of text


    # load the image
    img = cv2.imread('4.jpg')
    im=Image.open('4.jpg')
    # Initialize an empty dataframe to store the results
    df = pd.DataFrame(columns=['name', 'text'])

    # Process each prediction from RCNN
    for pred in pred_json['predictions']:
        # Crop the image based on the object coordinates
```

```
#     img_res.show()
    roi_x = int(x - w / 2)
    roi_y = int(y - h / 2)
    roi_width = int(w)+50
    roi_height = int(h)
    cropped_img = img[roi_y:roi_y+roi_height, roi_x:roi_x+roi_width]


    #cv2.imshow('ImageWindow', cropped_img)
    #cv2.waitKey(0)


    # Perform OCR using Tesseract on the cropped image
    if pred['class'] in ['name', 'sex']:
        text = pytesseract.image_to_string(cropped_img, config=tess_config)
        output = reader.readtext(cropped_img,detail=0)
        text = text.replace("\n", "")
    else:
        text = pytesseract.image_to_string(cropped_img)
        output = reader.readtext(cropped_img,detail=0)
        text = text.replace("\n", "")

    # Extract numeric information for classes other than 'name' and 'sex'
    if pred['class'] not in ['name', 'sex','age']:
        #text = extract_numeric_info(text)
        numeric_values = [value for value in output if is_numeric(value)]
        text = ' '.join(numeric_values)
    if pred['class'] in ['age']:
        print(text)
        numeric_values = [extract_numeric_info(value) for value in output]
        text = ' '.join(numeric_values)
```

```
    # Add the name and extracted text to the dataframe
    df = df.append({'name': pred['class'], 'text': text}, ignore_index=True)
    print(output)


print(df)
```

After extracting the data from the OCR output, we store it in the form of a structured pandas dataframe

```
     name              text
0     wbc              4.20
1    name  Mr. NEERAJ OJHA
2     rbc              5.79
3      hb             12.00
4    lymp             50.30
5   plate             245.0
6     age                27
7     sex              Male
8  neutro             39.60
```

## 8.5 Report generation

1. The output from our OCR model was passed into a Dataframe structured as follows. This represented a single 'item' to be processed.

```
[4] item
```

| | name | sex | age | wbc | rbc | lymp | neutro | plate | hb |
|---|---|---|---|---|---|---|---|---|---|
| 0 | Mr. Neeraj Ohja | Male | 27 | 4.2 | 5.79 | 50.3 | 39.6 | 245.0 | 12 |

2. Normal range table was pulled based on the item's age group. HB and RBC values were updated by gender for adult and adolescent age groups.

```
..
sample_data
normal_1.xlsx
normal_2.xlsx
normal_3.xlsx
normal_4.xlsx
```

```
if(item['age'][0]>=0 and item['age'][0]<=10):
  n=pd.read_excel("/content/normal_1.xlsx")
  print("Age Group: Child (0-10 years old)\n")
elif(item['age'][0]>10 and item['age'][0]<=18):
  n=pd.read_excel("/content/normal_2.xlsx")
  print("Age Group: Adolescent (10-18 years old)\n")
  if(str(item["sex"][0])==str("Male")):
    n['hb'][0]=18
    n['hb'][1]=14
    n['rbc'][0]=5.9
    n['rbc'][1]=4
  if(str(item["sex"][0])==str("Female")):
    n['hb'][0]=16
    n['hb'][1]=12
    n['rbc'][0]=5.2
    n['rbc'][1]=3.8
elif(item['age'][0]>18 and item['age'][0]<=50):
  n=pd.read_excel("/content/normal_3.xlsx")
  print("Age Group: Adult (18-50 years old)\n")
```

3. The item's values were calculated as either HIGH, LOW or Normal based on the normal-range table.

   The general normal range table for 'Adults' is shown below:

```
[5] n
```

| | value | sex | age | wbc | rbc | lymp | neutro | plate | hb |
|---|---|---|---|---|---|---|---|---|---|
| 0 | high | NaN | NaN | 10.5 | 6.1 | 40 | 75 | 450 | 17 |
| 1 | low | NaN | NaN | 4.5 | 4.5 | 20 | 40 | 150 | 13 |
| 2 | Causes_high | NaN | NaN | Bacterial/Parasitic Infection, Leukemia, Ster... | Dehydration,\nLung or Heart issues, Kidney dis... | Recent infection (most commonly viral),\nLong-... | Acute Bacterial Infection, Some Viral Infectio... | Recent Blood Loss,\nMild to moderate iron defi... | Living at higher altitudes, Dehydration, Heart... |
| 3 | Causes_low | NaN | NaN | Viral Infection, Blood/Bone Disorder, Autoimmu... | Anemia, \nVitamin B-12 or folate deficiency, \... | Blood diseases like Hodgkin's disease,\nAutoim... | Infection (Generally Bacterial, commonly - Tu... | Viruses such as mononucleosis/HIV/AIDS, Autoim... | Anemia, Iron or\nVitamin B-12 or folate defici... |
| 4 | solutions_high | NaN | NaN | High counts caused by recent infections will g... | For mild cases: Exercise can help improve hear... | High counts caused by recent infections can re... | Acute cases will resolve naturally.\n\nIf chro... | For Treating High Platelet Counts related to I... | For Mild Cases: Increase water intake, Avoid s... |
| 5 | solutions_low | NaN | NaN | Low counts caused by recent infections will ge... | For Treating Mild Anaemia - \n\nB-12 Deficienc... | Low counts caused by recent infections will ge... | Acute cases will resolve naturally.\n\nIf chro... | Professional Assistance Required: Follow up w... | For Treating Mild Anaemia - \n\nB-12 Deficienc... |

```
print("-----------------------------------------------------------------------------------------------

count=0
for i in cols[3:]:
  if(item[str(i)][0]>n[str(i)][0]):
    print((str(cols_dict.get(i))).upper()+" Level: "+"\033[1m \033[4m" +"HIGH"+"\033[0m")
  elif(item[str(i)][0]<=n[str(i)][0] and item[str(i)][0]>=n[str(i)][1]):
    print((str(cols_dict.get(i))).upper()+" Level: Normal")
  elif(item[str(i)][0]<n[str(i)][1]):
    print((str(cols_dict.get(i))).upper()+" Level: "+"\033[1m \033[4m" +"LOW"+"\033[0m")


print("\n-----------------------------------------------------------------------------------------------
```

4. Code for generating the detailed report for abnormal values:

```
count=1
for i in cols[3:]:
  if(item[str(i)][0]>n[str(i)][0]):
    print(str(count)+". ",end="")
    count=count+1
    perc=str(round((   (item[str(i)][0]-n[str(i)][0])  /   n[str(i)][0]  )*100,2))
    print(str(cols_dict.get(i)).upper()+" Level:\n - "+perc+" % HIGHER than normal")
    if(float(perc)<=10):
      print(" - MILD deviation from normal range")
    elif(float(perc)>10):
      print(" - !! Significant deviation from normal range")
    print("\033[1m \033[4m" +"\nPotential Causes: (Common causes are listed first)\n"+"\033[0m\n"+n[str(i)][2]+"\n")
    print("\033[1m \033[4m" +"\nSuggestions:\n"+"\033[0m\n"+n[str(i)][4]+"\n-----------------------------------------------------------
  elif(item[str(i)][0]<n[str(i)][1]):
    print(str(count)+".",end="")
    count=count+1
    perc=str(round((   (n[str(i)][1]-item[str(i)][0])  /   n[str(i)][1]  )*100,2))
    print(str(cols_dict.get(i)).upper()+" Level:\n - "+perc+" % LOWER than normal")
    if(float(perc)<=10):
      print(" - MILD deviation from normal range")
    elif(float(perc)>10):
      print(" - !! Significant deviation from normal range")
    print("\033[1m \033[4m" +"\nPotential Causes: (Common causes are listed first)\n"+"\033[0m\n"+n[str(i)][3]+"\n")
    print("\033[1m \033[4m" +"\nSuggestions:\n"+"\033[0m\n"+n[str(i)][5]+"\n-----------------------------------------------------------
```

5. The full report is generated and looks as follows:

----------Generated Report----------

GENERAL INFORMATION

Name: Mr. Neeraj Ohja
Sex: Male
Age: 27
Age Group: Adult (18-50 years old)

ALL RESULTS

WBC Level: LOW
RBC Level: Normal
LYMPHOCYTE Level: HIGH
NEUTROPHIL Level: LOW
PLATELET Level: Normal
HAEMOGLOBIN Level: LOW

DETAILED REPORT OF ABNORMAL RESULTS

1.WBC Level:
- 6.67 % LOWER than normal
- MILD deviation from normal range

Potential Causes: (Common causes are listed first)

Viral Infection, Blood/Bone Disorder, Autoimmune Condition, Chemo/Radiation Therapy, Medication Side Effect

Suggestions:

Low counts caused by recent infections will generally resolve naturally.

Otherwise professional assistance may be required: Follow up with your healthcare provider for prescriptions/further testing

2. LYMPHOCYTE Level:
- 25.75 % HIGHER than normal
- !! Significant deviation from normal range

Potential Causes: (Common causes are listed first)

Recent infection (most commonly viral),
Long-term inflammation (such as rheumatoid arthritis),
Medication Side Effect, Trauma,

Suggestions:

High counts caused by recent infections can resolve naturally.

For more severe symptoms contact a medical professional.

3.NEUTROPHIL Level:
- 1.0 % LOWER than normal
- MILD deviation from normal range

Potential Causes: (Common causes are listed first)

Infection (Generally Bacterial, commonly - Tuberculosis, Dengue, HIV), Inflammation, Chemotherapy, Blood Cancer (rare), Leukemia (rare)

Suggestions:

Acute cases will resolve naturally.

If chronic/severe, professional assistance is required: Follow up with your healthcare provider for prescriptions/further testing

4.HAEMOGLOBIN Level:
- 7.69 % LOWER than normal
- MILD deviation from normal range

Potential Causes: (Common causes are listed first)

Anemia, Iron or
Vitamin B-12 or folate deficiency,
Inherited Diseases (thalassemia),
Bleeding

Suggestions:

For Treating Mild Anaemia -

B-12 Deficiency: Meat, fish, eggs, dairy products, yeast extract

Folate Deficiency: green vegetables such as broccoli, Brussels sprouts and peas.

Iron Deficiency:Spinach, Meat, eggs, Fortified Bread, Beans, Dal

For Supplemental Injections/Tablets, contact your healthcare provider.

More serious symptoms require professional consultation

## 8.6 GUI

**Backend**: app.py consists of the code from all the modules above, with additional functions to create pdf and hande the web components.

app.py 9+ ● index.html result.html

app.py > ...

```python
app = Flask(__name__)
def image_proc(image_path,pred_json): ···
# Function to pass the image to the Roboflow API
def pass_to_roboflow(image_path): ···


def pass_to_yolo(image_path): ···

def extract_numeric_info(text): ···

# Function to check if a string is numeric
def is_numeric(value): ···

# Function for report generation
def generate_report(df): ···

# Function for PDF creation
def create_pdf(report): ···
```

app.py 9+ ● index.html result.html

app.py > ...

```python
@app.route('/', methods=['GET', 'POST'])
def home():
    if request.method == 'POST':
        # Get the uploaded image file from the request
        image_file = request.files['image']

        # Save the image file to a temporary location
        image_path = 'tmp/uploaded_image.jpg'
        image_file.save(image_path)

        # Pass the image to the Roboflow API
        output = pass_to_roboflow(image_path)

        output_yolo= pass_to_yolo(image_path)

        ocr_output=image_proc(image_path,output)

        # Generate report
        report = generate_report(ocr_output)

        # Create a PDF
        pdf_path = create_pdf(report)

        # Render the result page with the PDF path
        return render_template('result.html', pdf_path=pdf_path, image_path=image_path)

    return render_template('index.html')
```

```python
@app.route('/image/<path:filename>')
def get_image(filename):
    return send_file('/tmp/' + filename, mimetype='image/jpg')

@app.route('/download_pdf')
def download_pdf():
    pdf_path = request.args.get('pdf_path')
    return send_file(pdf_path, as_attachment=True)

if __name__ == '__main__': ...
```

**Frontend**: We have 2 pages for the above application, index.html (Homepage) and result.html to show the output.

app.py 9+ | index.html | result.html

templates > index.html > html > head > style > body

```html
        }
        #logo {
            width: 500px;
            height: auto;
            display: block;
            margin: 0 auto;
        }
    </style>
</head>
<body>
    <img src="{{url_for('static', filename='logo.png')}}" alt="Logo" id="logo">
    <h1>Hematology report data extraction and diagnosis generation</h1>
    <form method="POST" enctype="multipart/form-data" action="/">
        <input type="file" name="image" accept="image/*" required>
        <br><br>
        <input type="submit" value="Submit">
    </form>
</body>
</html>
```

app.py 9+ index.html result.html

templates > result.html > html > body

```
46  </head>
47  <body>
48      <h1>Result</h1>
49      <!--<div>
50          <h2>Sliced Images</h2>
51          {% for sliced_image in sliced_images %}
52              <img src="{{ sliced_image }}">
53          {% endfor %}
54      </div>-->
55      <div>
56          <h2>Comparison</h2>
57          <div style="display: flex; justify-content: center;">
58              <div style="flex: 1; padding: 10px;">
59                  <h3>Output from Roboflow Object detection model</h3>
60                  <img src= "{{url_for('static', filename='prediction.jpg')}}">
61              </div>
62              <div style="flex: 1; padding: 10px;">
63                  <h3>Output from YOLOv8x</h3>
64                  <img src="{{url_for('static', filename='predict/uploaded_image.jpg')}}">
65              </div>
66          </div>
67      </div>
68      <div>
69          <h2>Download PDF Report</h2>
70          <a href="{{ url_for('download_pdf', pdf_path=pdf_path) }}">Download</a>
71      </div>
72  </body>
73  </html>
```

# Chapter 9
# Testing

## Module 1: Object detection model comparison:

| | mAP (%) | Precision (%) | Recall (%) | Training time | Epochs |
|---|---|---|---|---|---|
| ROBOFLOW 2.0 OBJECT DETECTION (FAST) | 98.4 | 90.4 | 94.7 | 1Hr | 790 |
| YOLOv8x | 96.5 | 92.1 | 88.7 | 1.202 Hr | 269 |

Table 9.1. Object detection model comparison

YOLOv8 result

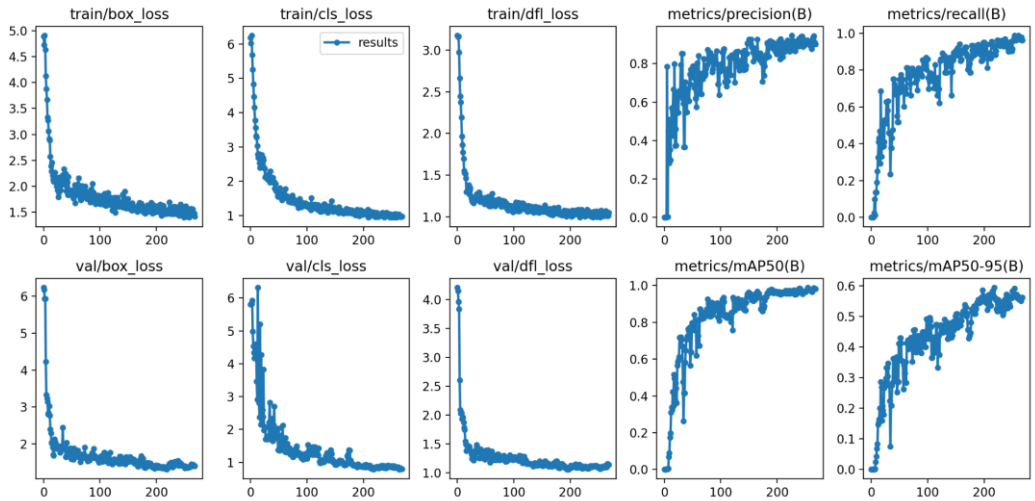



Fig 9.1. YOLOv8x result

ROBOFLOW 2.0 OBJECT DETECTION (FAST) result

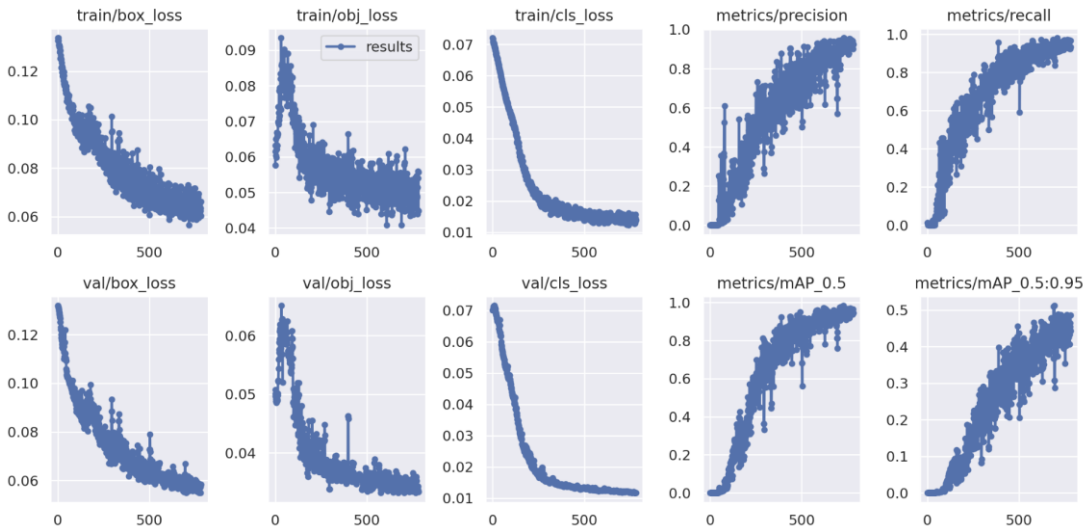
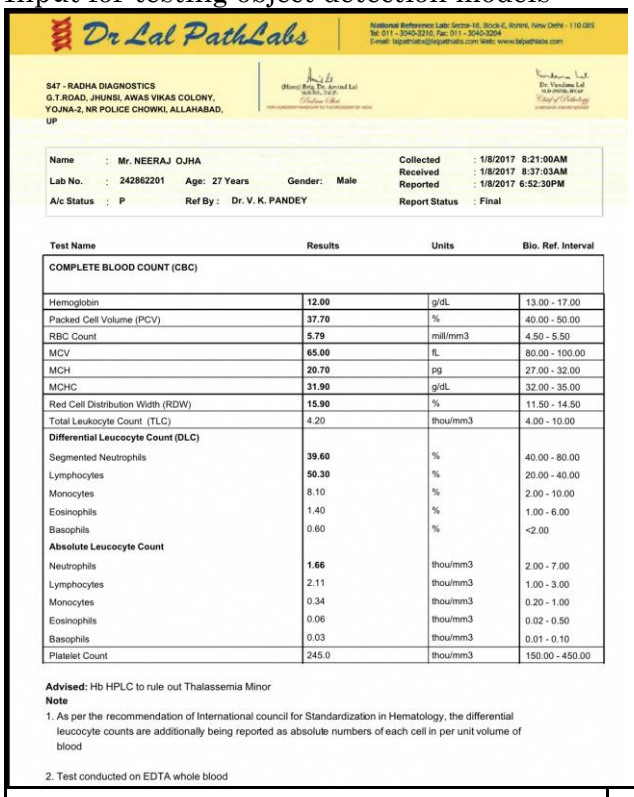



Fig 9.2. Roboflow 2.0 Object detection (fast) result

Input for testing object detection models:



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G.T.ROAD, JHUNSI, AWAS VIKAS COLONY,
YOJNA-2, NR POLICE CHOWKI, ALLAHABAD,
UP

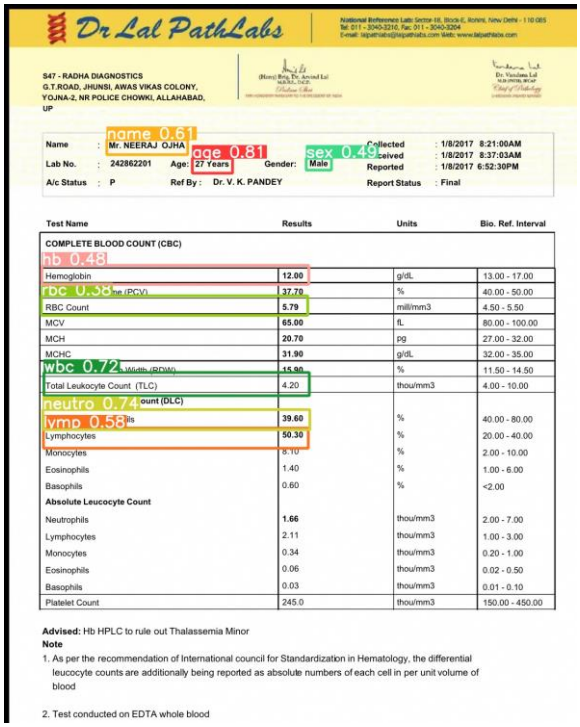
Name : Mr. NEERAJ OJHA
Lab No. : 242862201 Age: 27 Years Gender: Male
A/c Status : P Ref By : Dr. V. K. PANDEY

Collected : 1/8/2017 8:21:00AM
Received : 1/8/2017 8:37:03AM
Reported : 1/8/2017 6:52:30PM
Report Status : Final

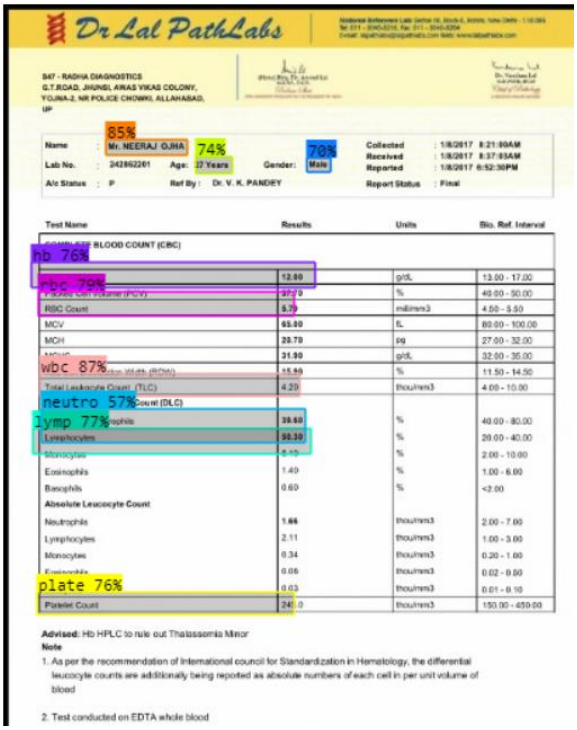
| Test Name | Results | Units | Bio. Ref. Interval |
|---|---|---|---|
| COMPLETE BLOOD COUNT (CBC) | | | |
| Hemoglobin | 12.00 | g/dL | 13.00 - 17.00 |
| Packed Cell Volume (PCV) | 37.70 | % | 40.00 - 50.00 |
| RBC Count | 5.79 | mill/mm3 | 4.50 - 5.50 |
| MCV | 65.00 | fL | 80.00 - 100.00 |
| MCH | 20.70 | pg | 27.00 - 32.00 |
| MCHC | 31.90 | g/dL | 32.00 - 35.00 |
| Red Cell Distribution Width (RDW) | 15.90 | % | 11.50 - 14.50 |
| Total Leukocyte Count (TLC) | 4.20 | thou/mm3 | 4.00 - 10.00 |
| Differential Leucocyte Count (DLC) | | | |
| Segmented Neutrophils | 39.60 | % | 40.00 - 80.00 |
| Lymphocytes | 50.30 | % | 20.00 - 40.00 |
| Monocytes | 8.10 | % | 2.00 - 10.00 |
| Eosinophils | 1.40 | % | 1.00 - 6.00 |
| Basophils | 0.60 | % | <2.00 |
| Absolute Leucocyte Count | | | |
| Neutrophils | 1.66 | thou/mm3 | 2.00 - 7.00 |
| Lymphocytes | 2.11 | thou/mm3 | 1.00 - 3.00 |
| Monocytes | 0.34 | thou/mm3 | 0.20 - 1.00 |
| Eosinophils | 0.06 | thou/mm3 | 0.02 - 0.50 |
| Basophils | 0.03 | thou/mm3 | 0.01 - 0.10 |
| Platelet Count | 245.0 | thou/mm3 | 150.00 - 450.00 |

Advised: Hb HPLC to rule out Thalassemia Minor
Note
1. As per the recommendation of International council for Standardization in Hematology, the differential leucocyte counts are additionally being reported as absolute numbers of each cell in per unit volume of blood
2. Test conducted on EDTA whole blood

YOLOv8x output




ROBOFLOW 2.0 OBJECT DETECTION (FAST) output



Inference: Comparing both the models, going through the output and the evaluation metrics, we can notice that Roboflow 2.0 object detection model performs better.. In the above comparison of the predicted objects, we can notice the higher confidence and accuracy in the Roboflow 2.0 model compared to the YOLOv8x.
Conclusion: Based on the results obtained by training the roboflow 2.0 object detection (fast) and YOLOv8x model, we chose to go with roboflow 2.0 due to the following reasons:

- Better mAP and recall score
- Comparable precision score
- Faster
- Direct API provision for easier deployment

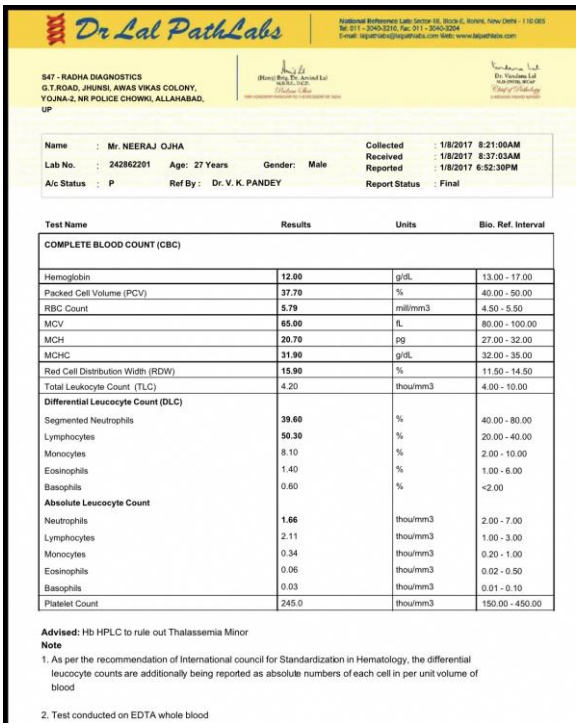
## Module 2: OCR comparison:

Image chosen for testing:

```
import os
from PIL import Image
import easyocr
import cv2
import pytesseract
import pandas as pd
import re
reader = easyocr.Reader(['en'])
```

```
WARNING:easyocr.easyocr:Downloading detection model, please wait. This may take
Progress: |                                        | 100.0% Complete
Progress: |                                        | 100.0% Complete
```

```
[16] original_image=Image.open('a.jpg')
     display(original_image)
```



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YOJNA-2, NR POLICE CHOWKI, ALLAHABAD,
UP

| | | | | | |
|---|---|---|---|---|---|
| Name | : Mr. NEERAJ OJHA | | | Collected | : 1/8/2017 8:21:00AM |
| Lab No. | : 242862201 | Age: 27 Years | Gender: Male | Received | : 1/8/2017 8:37:03AM |
| | | | | Reported | : 1/8/2017 6:52:30PM |
| A/c Status | : P | Ref By : Dr. V. K. PANDEY | | Report Status | : Final |

| Test Name | Results | Units | Bio. Ref. Interval |
|---|---|---|---|
| COMPLETE BLOOD COUNT (CBC) | | | |
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| RBC Count | 5.79 | mill/mm3 | 4.50 - 5.50 |
| MCV | 65.00 | fL | 80.00 - 100.00 |
| MCH | 20.70 | pg | 27.00 - 32.00 |
| MCHC | 31.90 | g/dL | 32.00 - 35.00 |
| Red Cell Distribution Width (RDW) | 15.90 | % | 11.50 - 14.50 |
| Total Leukocyte Count (TLC) | 4.20 | thou/mm3 | 4.00 - 10.00 |
| **Differential Leucocyte Count (DLC)** | | | |
| Segmented Neutrophils | 39.60 | % | 40.00 - 80.00 |
| Lymphocytes | 50.30 | % | 20.00 - 40.00 |
| Monocytes | 8.10 | % | 2.00 - 10.00 |
| Eosinophils | 1.40 | % | 1.00 - 6.00 |
| Basophils | 0.60 | % | <2.00 |
| **Absolute Leucocyte Count** | | | |
| Neutrophils | 1.66 | thou/mm3 | 2.00 - 7.00 |
| Lymphocytes | 2.11 | thou/mm3 | 1.00 - 3.00 |
| Monocytes | 0.34 | thou/mm3 | 0.20 - 1.00 |
| Eosinophils | 0.06 | thou/mm3 | 0.02 - 0.50 |
| Basophils | 0.03 | thou/mm3 | 0.01 - 0.10 |
| Platelet Count | 245.0 | thou/mm3 | 150.00 - 450.00 |

**Advised:** Hb HPLC to rule out Thalassemia Minor
**Note**
1. As per the recommendation of International council for Standardization in Hematology, the differential leucocyte counts are additionally being reported as absolute numbers of each cell in per unit volume of blood
2. Test conducted on EDTA whole blood

### EasyOCR output

```
[13] ocr_result = reader.readtext('a.jpg',detail=0)

     ocr_result
```

```
['Natonal Reterence Lob: Sector-[8. Block E Roh
ni New Dcthl:',
 'Ki0 085',
 '8 Dr Lal PathLals',
 'Exai: 121pot-32toapetrOansc',
 '3m032cbwwlaipachlabs com',
 'LL',
 '547',
 'RADHA DIAGNOSTICS',
 '(Honv)',
```

### Tesseract output

```
pytesseract.pytesseract.tesseract_cmd = r'/usr/bin/tesseract'

img=cv2.imread('a.jpg',1)
print(pytesseract.image_to_string(img))
```

```
S47 - RADHA DIAGNOSTICS
G.T.ROAD, JHUNSI, AWAS VIKAS COLONY, Sedum hee
YOJNA-2, NR POLICE CHOWKI, ALLAHABAD, Sa
aoamNesa
uP
Name Mr. NEERAJ OJHA
Lab No. 242862201 Age: 27 Years Gender: Male
Alc Status : P RefBy: Dr.V.K. PANDEY
Test Name Results
```

| | |
|---|---|
| "'Rrkea", | COMPLETE BLOOD COUNT (CBC) |
| 'Dc. Anin { Lal', | |
| 'Dr Vindan_ Lall', | Hemoglobin |
| 'MRnIn', | Packed Cell Volume (PCV) |
| 'DCr', | RBC Count |
| 'G.TROAD, JHUNSI; AWAS VIKAS COLONY_', | |
| 'Whooramdr', | (Hony) Brig. De, Arvind Lal |
| 'TATot Oer', | Mis ber. |
| '{di', | |
| 'YOJNA-2, NR POLICE CHOWKI, ALLAHABAD_', | Collected |
| 'UP', | Received |
| 'Name', | Reported |
| 'Mr: NEERAJ OJHA', | |
| 'Collected', | Report Status |
| '1/8/2017  8.21.OOAM', | |
| 'Received', | Units |
| '1/8/2017  8.37:03AM', | |
| 'Lab No_', | gldL |
| '242862201', | % |
| 'Age:', | |
| '27 Years', | mill/mm3 |
| 'Gender:', | |
| 'Male', | Vandana Lat |
| 'Reported', | Dr. Vandana Lal |
| '1/8/2017 6.52:30PM', | Nip ear |
| 'Alc Status', | Chiff Dibetgy |
| 'Ref By', | |
| 'Dr. V.K PANDEY', | : 1/8/2017 8:21:00AM |
| 'Report Status', | 18/2017 8:37:03AM |
| 'Final', | : 1/8/2017 6:52:30PM |
| 'Test Name', | |
| 'Results', | |
| 'Units', | |
| 'Bio. Ref: Interval', | : Final |
| 'COMPLETE BLOOD COUNT (CBC)', | |
| 'Hemoglobin', | Bio. Ref. Interval |
| '12.00', | |
| 'gldL', | 13.00 - 17.00 |
| '13.00 - 17.00', | 40.00 - 50.00 |
| 'Packed Cell Volume (PCV)', | 4.50 - 5.50 |
| '37.70', | 80.00 - 100.00 |
| '40.00', | |
| '50.00', | |
| 'RBC Count', | |
| '5.79', | 27.00 - 32.00 |
| 'milllmm3', | |
| '4.50 - 5.50', | |
| 'MCV', | |
| '65.00', | Red Cell Distribution Width (RDW) |
| '80.00', | Total Leukocyte Count (TLC) |
| '100.00', | Differential Leucocyte Count (DLC) |
| 'MCH', | Segmented Neutrophils |
| '20.70', | Lymphocytes |
| 'pg', | |
| '27.00', | Monocytes |
| '32.00', | |
| 'MCHC', | Eosinophils |
| '31.90', | |
| 'gldL', | Basophils |
| '32.00', | |
| '35.00', | Absolute Leucocyte Count |
| 'Red Cell Distribution Width (RDW)', | |
| '15.90', | Neutrophils |
| '11.50 _', | |
| '14.50', | Lymphocytes |
| 'Total Leukocyte Count (TLC)', | |
| '4.20', | Monocytes |
| 'thoulmm3', | Eosinophils |
| '4.00 -', | |
| '10.00', | Basophils |
| 'Differential Leucocyte Count (DLC)', | |
| 'Segmented Neutrophils', | % |
| '39.60', | |
| '40.00 - 80.00', | thou/mm3 |
| 'Lymphocytes', | |
| '50.30', | % |
| '20.00 - 40.00', | % |
| 'Monocytes', | % |
| '8.10', | % |
| '2.00 - 10.00', | % |

| | |
|---|---|
| 'Eosinophils',<br>'1.40',<br>'1.00 - 6.00',<br>'Basophils',<br>'0.60',<br>'<2.00',<br>'Absolute Leucocyte Count',<br>'Neutrophils',<br>'1.66',<br>'thoulmm3',<br>'2.00 - 7.00',<br>'Lymphocytes',<br>'2.11',<br>'thoulmm3',<br>'1.00 - 3.00',<br>'Monocytes',<br>'0.34',<br>'thoulmm3',<br>'0.20 - 1.00',<br>'Eosinophils',<br>'0.06',<br>'thoulmm3',<br>'0.02 - 0.50',<br>'Basophils',<br>'0.03',<br>'thoulmm3',<br>'0.01 - 0.10',<br>'Platelet Count',<br>'245.0',<br>'thoulmm3',<br>'150.00',<br>'450.00',<br>'Advised: Hb HPLC to rule out Thalassemia Minor',<br>'Note',<br>'1. As per the recommendation of International council for Standardization in Hematology, the differential',<br>'leucocyte counts',<br>'additionally',<br>'reported as absolute numbers ofeach cell in per unit volume of',<br>'blood',<br>'2. Test conducted on EDTA whole blood',<br>'Vi ',<br>'617td',<br>'J',<br>'being',<br>'are'] | thou/mm3<br>thou/mm3<br>thou/mm3<br>thou/mm3<br><br>thou/mm3<br><br>32.00 - 35.00<br>11.50 - 14.50<br>4.00 - 10.00<br><br>40.00 - 80.00<br>20.00 - 40.00<br>2.00 - 10.00<br>1.00 - 6.00<br><2.00<br><br>2.00 - 7.00<br>1.00 - 3.00<br>0.20 - 1.00<br>0.02 - 0.50<br>0.01 - 0.10<br><br><br>Platelet Count<br><br>thou/mm3<br><br><br><br><br>150.00 - 450.00<br><br><br><br>Advised: Hb HPLC to rule out Thalassemia Minor<br>Note<br><br>1. As per the recommendation of International council for Standardization in Hematology, the differential<br>leucocyte counts are additionally being reported as absolute numbers of each cell in per unit volume of<br><br>blood<br><br>2. Test conducted on EDTA whole blood |

Inference: Going through the direct output by the OCR's, we can notice a accurate and cleaner output from the EasyOCR compared to the Tesseract.

Conclusion: Based on the results obtained from direct comparison of EasyOCR and Tesseract, we chose to go with EasyOCR due to the following reasons:

- Higher accuracy
- Cleaner output
- Slightly faster

# Chapter 10
# Conclusion

Our research has demonstrated that utilising deep learning OCR models for blood report scanning may be a successful method of gathering pertinent information for illness prediction models. In the study on haematology report OCR models, the efficiency of several strategies for automated text extraction from haematology reports was investigated. Utilising its object identification capabilities, the YOLOv8 model proved to be a reliable and effective method for identifying text areas within the reports. The whole computer vision workflow was streamlined by the full platform offered by Roboflow for data storage, annotation, and model training. On the other hand, Tesseract OCR and EasyOCR OCR models showed their language support and convenience of use, allowing accurate text extraction from the reports. The best OCR model to use will rely on a variety of criteria, including project-specific objectives, resource availability, and performance requirements. Each technique has its own advantages. Overall, by utilising OCR technology, this project improved the automation and effectiveness of haematology report processing.

# Chapter 11
# Future prospect

Future scope for this study includes exploring more advanced OCR models and algorithms, using more advanced data pre-processing techniques, and testing on a larger dataset with a wider variety of report formats. Additionally, incorporating more features and data such as patient demographics, medical history, and other laboratory results could help implement a better disease prediction model.

- Broader and more varied data set: The performance of the object detection and OCR models may be evaluated more thoroughly by expanding the dataset to include a wider and more varied collection of haematology papers.
- Multi-modal Information Integration: Including additional data with the extracted text, such as patient demographics, medical history, or other test findings, can provide the reports a more complete analysis. The creation of more complex illness prediction models may be made possible by the integration of different modalities, such as pictures or time-series data.
- Real-time Processing and Deployment: For applications that need quick results, real-time processing of haematology reports may be essential.
- Advanced OCR Models: Researching more sophisticated OCR models, such as those based on advanced deep learning (Transformer) architectures, may enhance the reliability and accuracy of the text extraction procedure.
- Better Data Pre-processing: Using cutting-edge data pre-processing methods including picture enhancement modification can increase the accuracy of OCR.

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