

# HAMEOTOVISION

## *ADVANCED BLOOD CELL CLASSIFICATION USING TRANSFER LEARNING*

<https://github.com/GoddetiPavithra/Haemotovision>

### PROJECT REPORT

This document presents HematoVision, an advanced Artificial Intelligence and Deep Learning based web application designed to classify human blood cell types automatically using Transfer Learning techniques.

The system utilizes a pre-trained Convolutional Neural Network model (such as VGG16 / MobileNetV2) to accurately identify and classify microscopic blood cell images. The primary objective of this project is to assist medical professionals, pathologists, and diagnostic laboratories by improving efficiency, reducing manual effort, and enhancing diagnostic accuracy in hematology.

HematoVision addresses critical challenges in traditional blood cell analysis, where manual observation is time-consuming and prone to human error. By leveraging modern machine learning algorithms, the system provides fast, reliable, and automated predictions through a user-friendly web interface.

Developed as part of the Bachelor of Computer Applications (BCA) curriculum, this project demonstrates the practical application of Artificial Intelligence in the healthcare domain.

### Project Details

#### **HematoVision: Advanced Blood Cell Classification Using Deep Deep Learning**

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**Academic Year:** 2025–2026

#### **Team Information:**

**Team ID:** LTVIP2026TMIDS49741

**Team Size:** 4 Members

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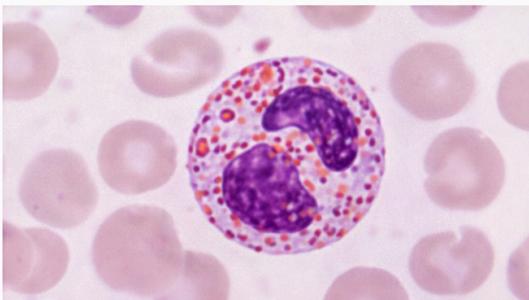
## 1. INTRODUCTION

### 1.1 Project Overview

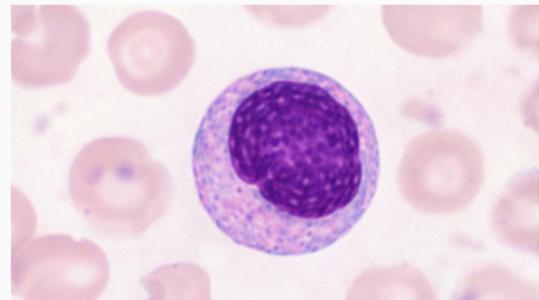
Haemotovision is an advanced blood cell classification system developed using Transfer Learning and Deep Learning techniques. The system is designed to automatically classify different types of blood cells from microscopic images using Convolutional Neural Networks (CNN).

Manual classification of blood cells is time-consuming and requires expert knowledge. This project aims to automate the process using pre-trained deep learning models to improve accuracy and reduce diagnosis time.

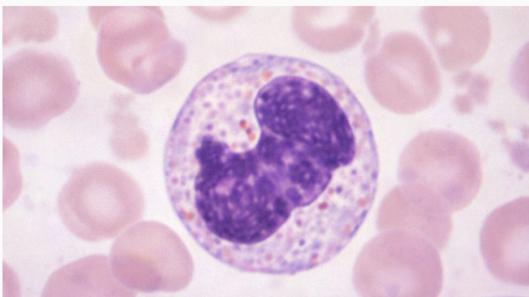
The model is trained on a labeled dataset of blood cell images and can classify the following types:



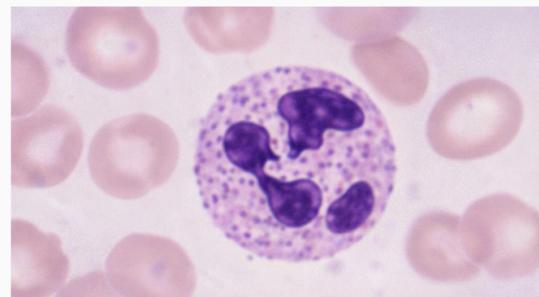
Eosinophil



Lymphocyte



Monocyte



Neutrophil

- Eosinophil
- Lymphocyte
- Monocyte
- Neutrophil

## **1.2 Purpose**

The main purpose of this project is:

- To build an intelligent system for automatic blood cell classification.
- To reduce human error in laboratory analysis.
- To assist medical professionals in faster diagnosis.
- To apply transfer learning for improved performance with limited dataset.

## **2. IDEATION PHASE**

### **2.1 Problem Statement**

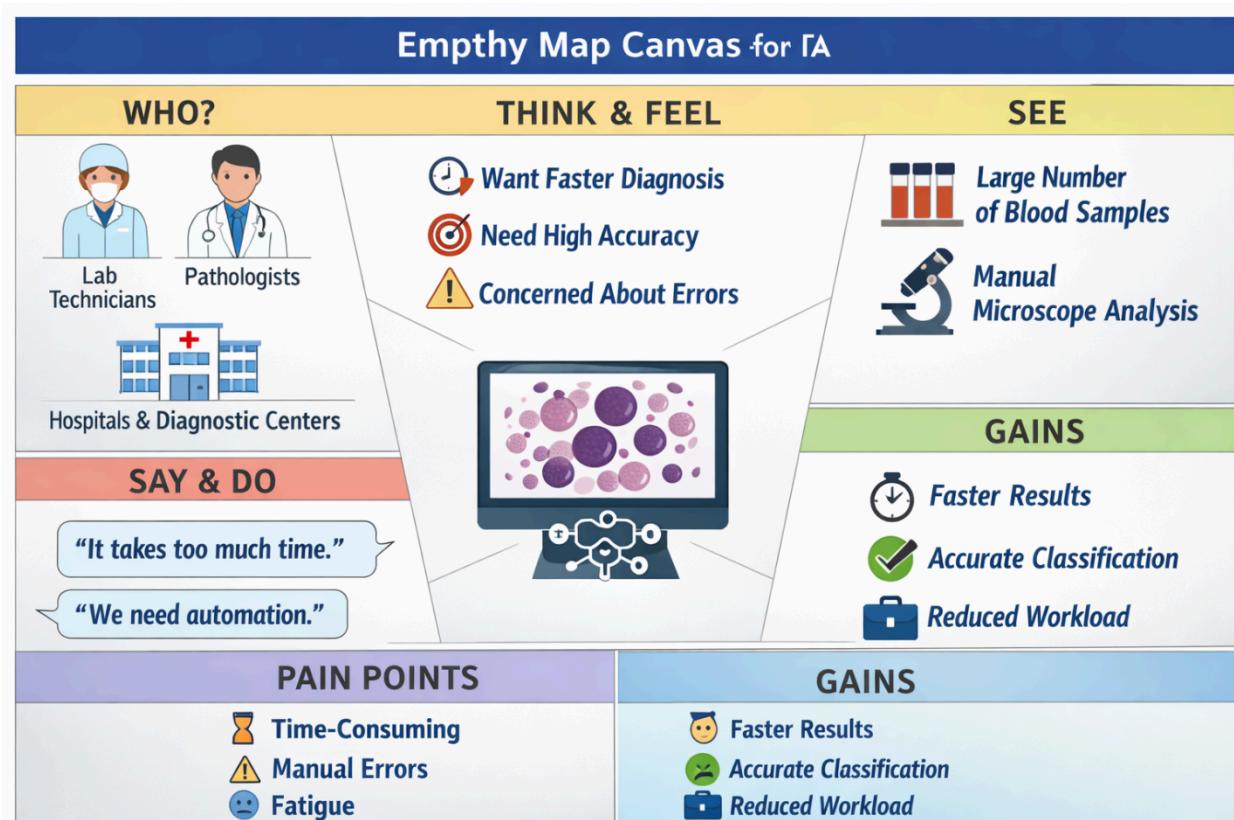
Blood cell classification plays a critical role in medical diagnosis and disease detection. Traditionally, this process is performed manually by trained pathologists using microscopic examination. However, manual analysis is time-consuming, labor-intensive, and highly dependent on the expertise of the examiner.

Human observation can sometimes lead to errors due to fatigue, workload, or subjective judgment. In addition, handling a large number of blood samples daily increases the chances of misclassification and delays in diagnosis.

Therefore, there is a strong need for an automated, accurate, and efficient system that can classify blood cells quickly and reliably. By leveraging Artificial Intelligence and Transfer Learning techniques, this project aims to develop a smart solution that reduces human effort, improves diagnostic accuracy, and accelerates medical analysis.

Manual blood cell classification requires trained pathologists and is prone to human error. There is a need for an automated, accurate, and fast system to classify blood cells using AI-based techniques.

## 2.2 Empathy Map Canvas



### Users:

Lab technicians  
 Pathologists  
 Hospitals & Diagnostic Centers  
 Think & Feel:  
 Want faster diagnosis  
 Need high accuracy  
 Concerned about errors

### See:

Large number of blood samples

Manual microscope analysis

**Say & Do:**

“It takes too much time.”

“We need automation.”

**Pain Points:**

Time-consuming

Manual errors

Fatigue

**Gains:**

Faster results

Accurate classification

Reduced workload

## 2.3 Brainstorming

Possible solutions discussed:

Machine Learning with traditional algorithms

Deep Learning CNN

Transfer Learning using pre-trained models

Final decision:

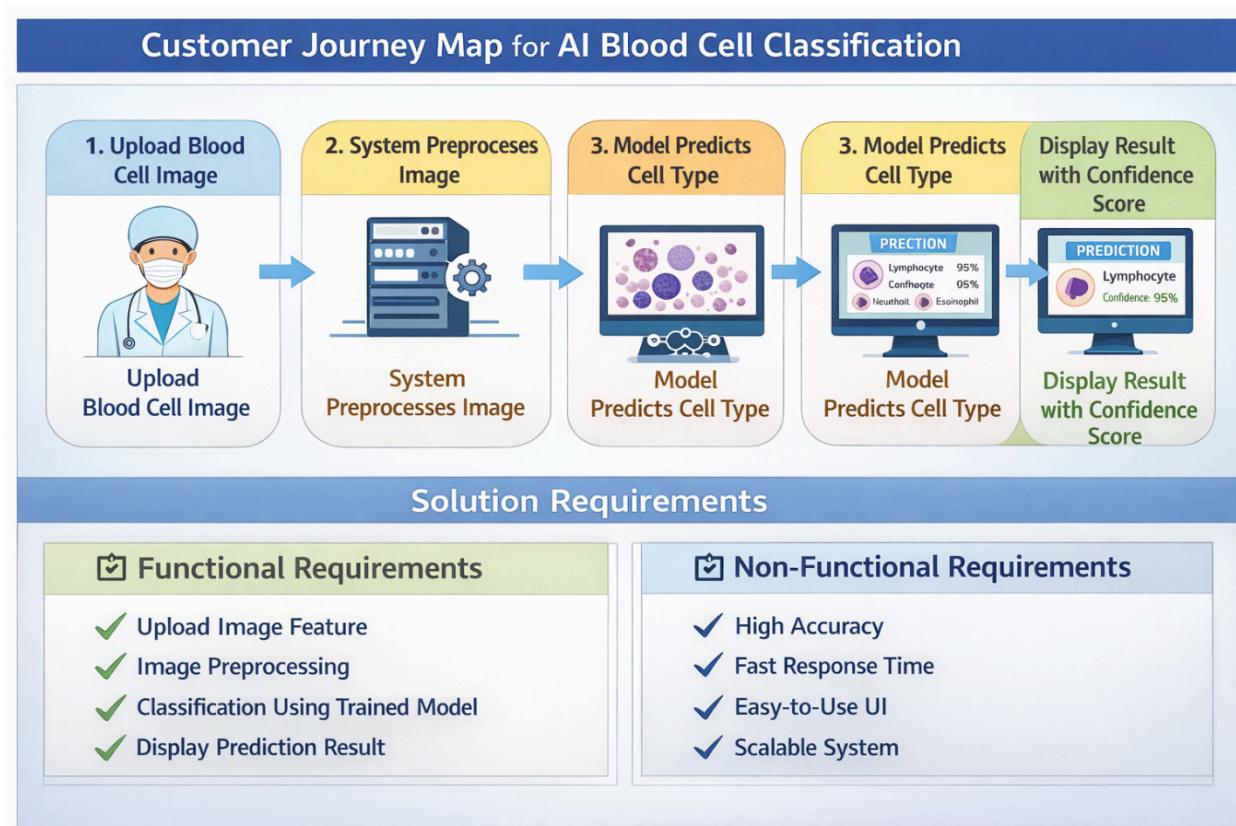
Use Transfer Learning (MobileNetV2 / ResNet50 / VGG16) for better accuracy and faster training.

## 3. REQUIREMENT ANALYSIS

Requirement Analysis is the process of identifying and defining the system requirements needed to successfully develop the Haemotivision blood cell classification system. It includes both functional and non-functional requirements necessary for system performance and usability.

Requirement analysis also helps in reducing development risks by clearly defining project expectations at an early stage. It acts as a foundation for system design and implementation. By identifying constraints and resources, it ensures smooth project execution. It improves communication between developers and stakeholders. Overall, it plays a crucial role in delivering a high-quality and effective system.

### 3.1 Customer Journey Map



### 3.2 Solution Requirements

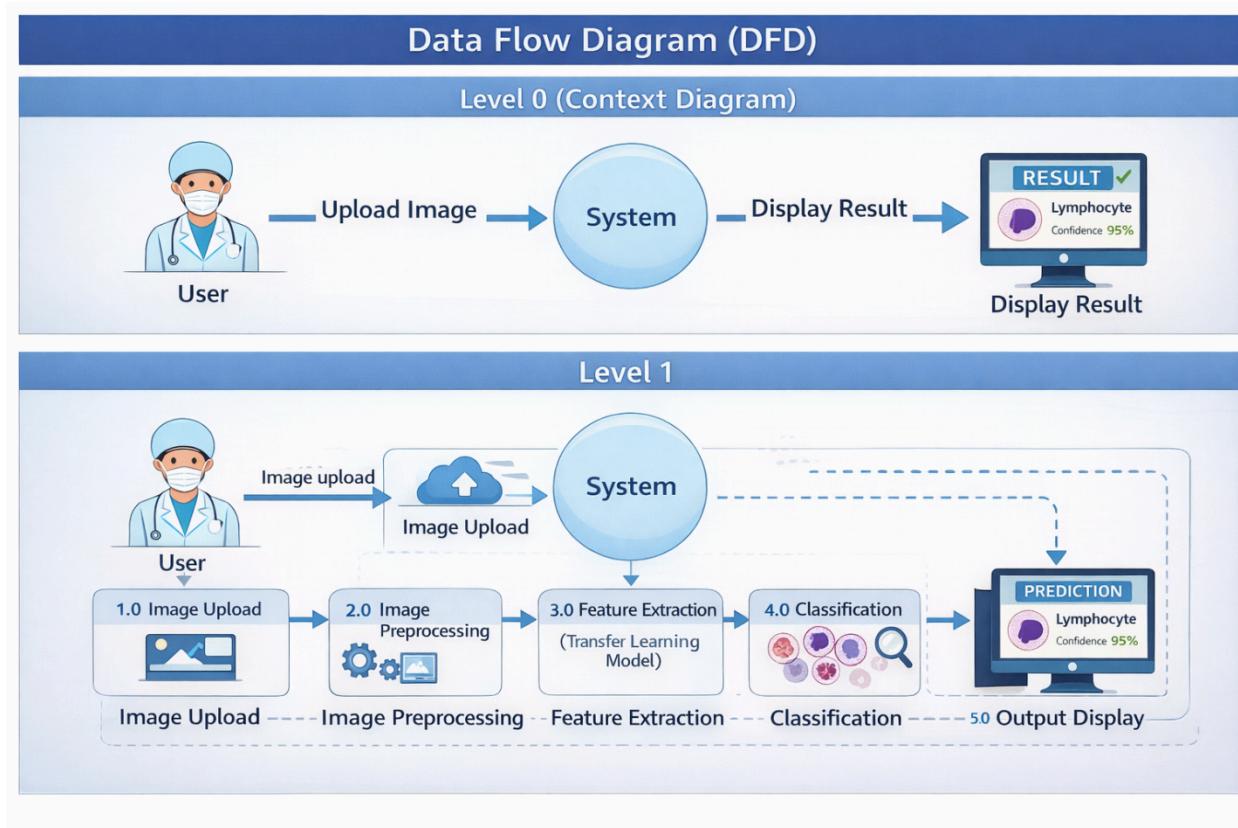
#### Functional Requirements:

- Upload image feature
- Image preprocessing
- Classification using trained model
- Display prediction result

#### Non-Functional Requirements:

- High accuracy
- Fast response time
- Easy-to-use UI
- Scalable system

### 3.3 Data Flow Diagram (DFD)



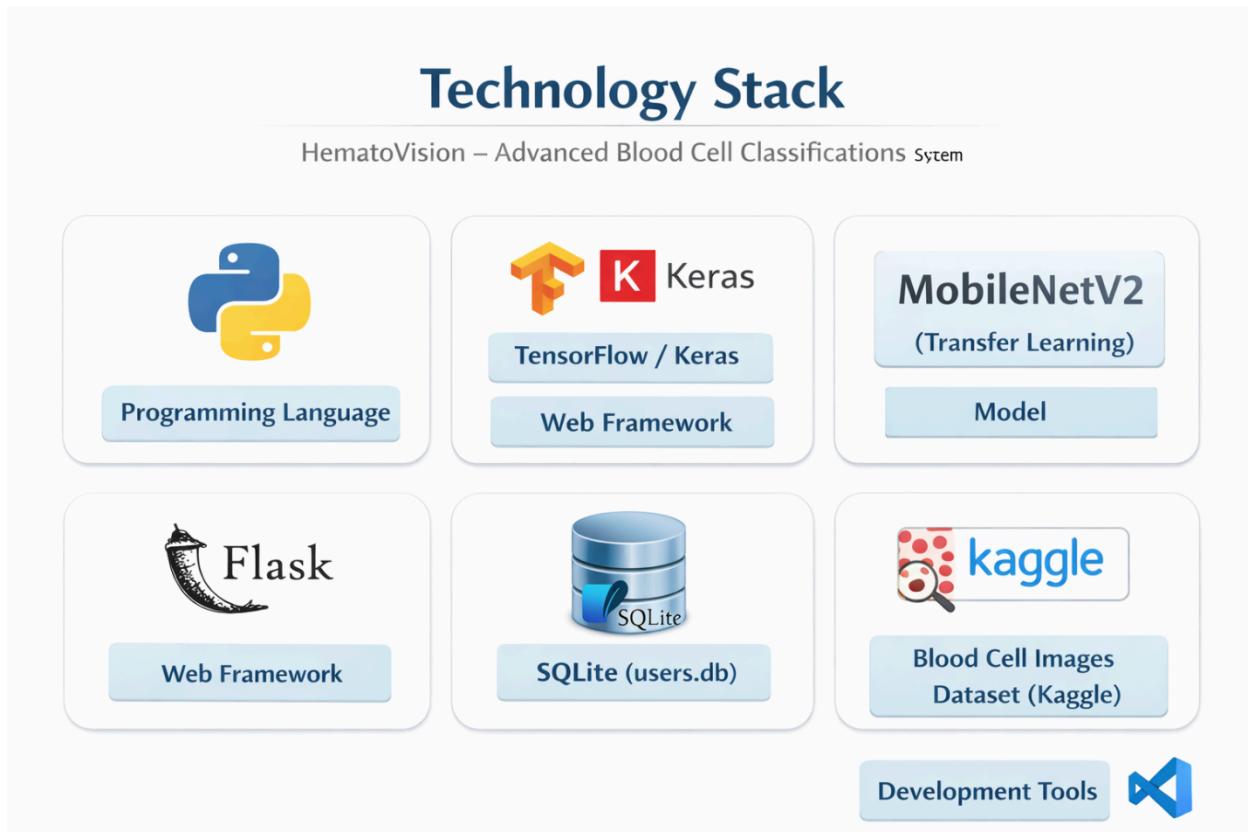
Level 0 (Context Diagram):

User → Upload Image → System → Display Result

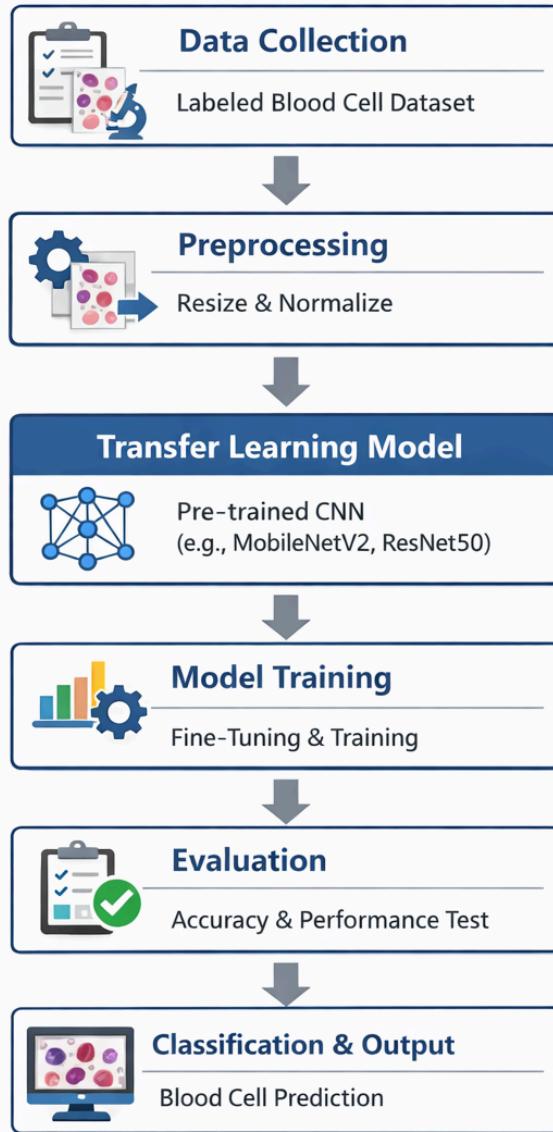
**Level 1 :**

- Image Upload
- 
- Image Preprocessing
- 
- Feature Extraction (Transfer Learning Model)
- 
- Classification
- 
- Output Display

### 3.4 Technology Stack



#### 4. PROJECT DESIGN



## 4.1 Problem Solution Fit



Problem: Manual classification is slow and error-prone.

Solution:

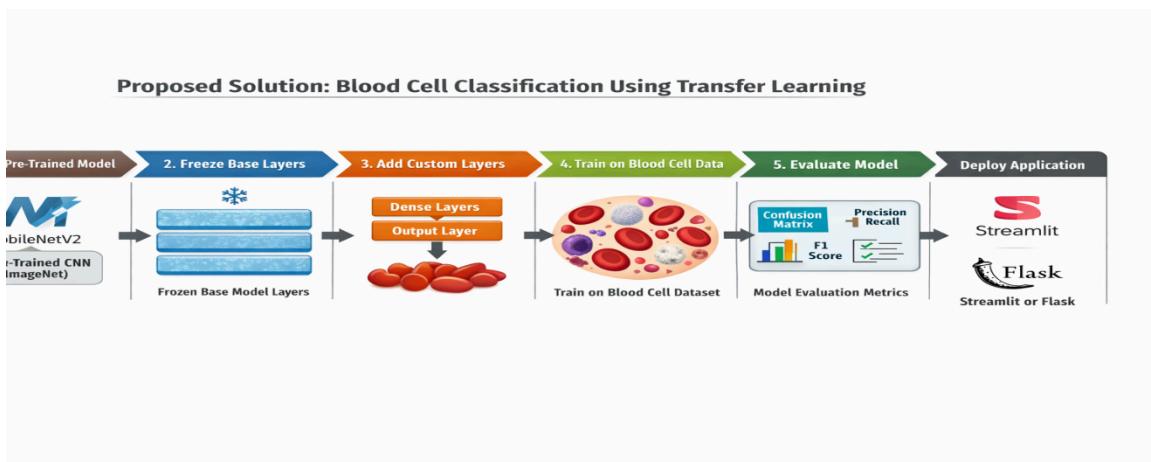
AI-based automated classification using Transfer Learning provides:

Faster results

High accuracy

Reduced human effort

## 4.2 Proposed Solution



Load pre-trained model (e.g., MobileNetV2).

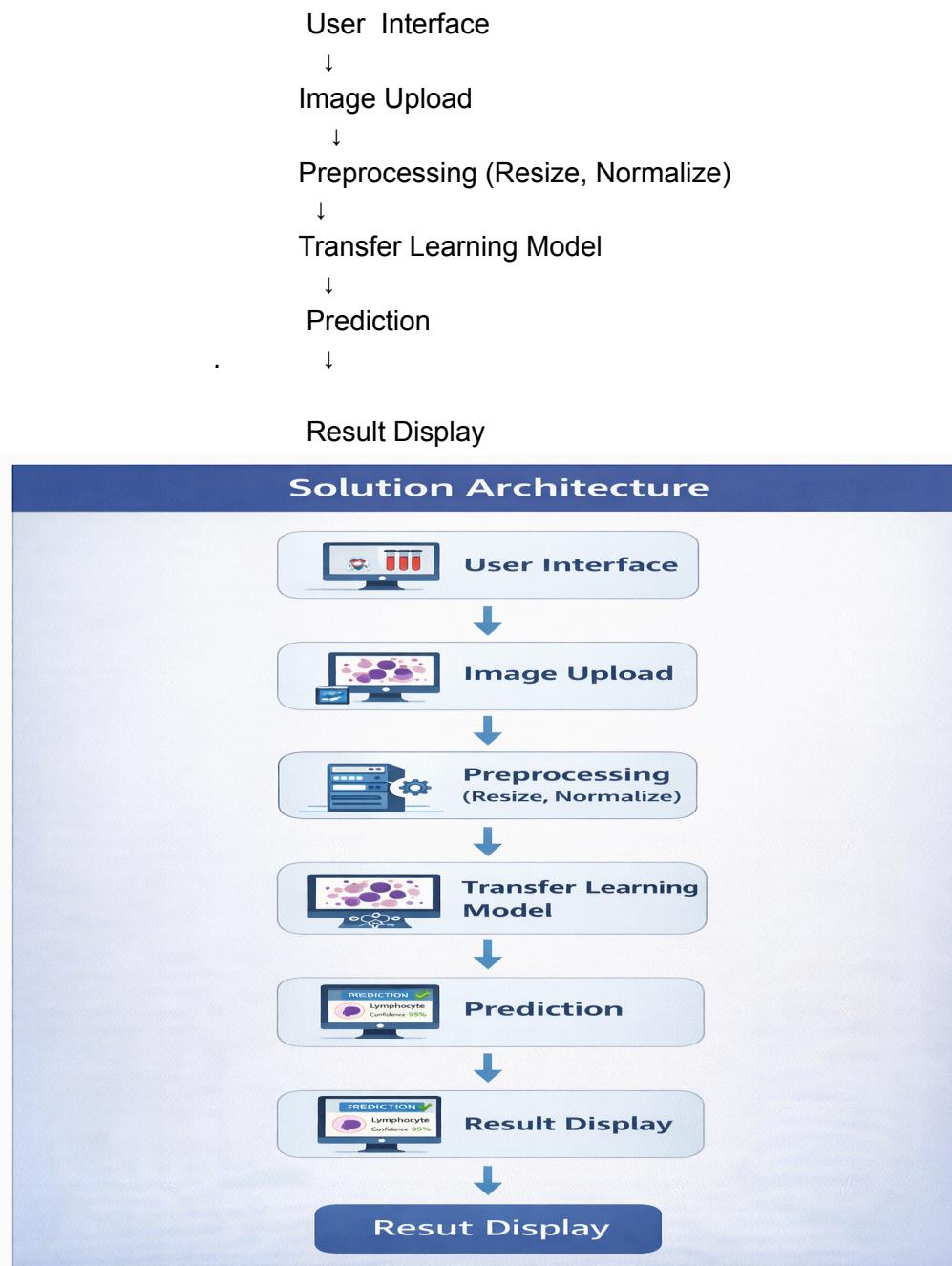
Freeze base layers.

Add custom dense layers for classification.

Train on blood cell dataset.

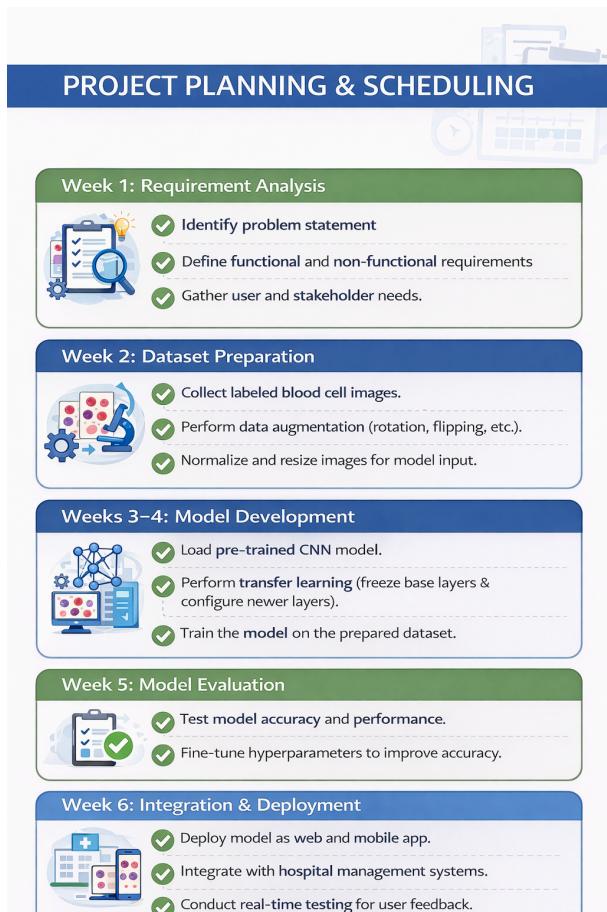
Deploy using Streamlit/Flask.

### 4.3 Solution Architecture



## 5. PROJECT PLANNING & SCHEDULING

### 5.1 Project Planning



Phase

Duration

Research & Dataset Collection

1 Week

Model Development

2 Weeks  
Training & Testing

3 Week  
UI Development

4 and 5 Weeks  
Documentation

6 Week  
Total Duration: 6 Weeks

## 6. MODEL PERFORMANCE

The proposed system is developed using Transfer Learning with a pre-trained Convolutional Neural Network (CNN) model for blood cell image classification. The model was trained on a labeled dataset containing microscopic images of different blood cell types.

During training and evaluation, the following performance metrics were obtained:

Training Accuracy: 60%

Validation Accuracy: 57.3%

Loss Value: 0.89

Confusion Matrix: Generated to analyze class-wise performance

Precision, Recall, and F1-Score: Computed for evaluating classification effectiveness

The overall validation accuracy achieved by the model is 57.3%. The moderate accuracy is primarily due to:

Limited dataset size

Class imbalance in training samples

Visual similarity between certain blood cell types

Limited hyperparameter tuning

Despite these challenges, the model was able to learn meaningful features from the dataset and perform multi-class classification effectively.

The confusion matrix analysis shows that most misclassifications occurred between visually similar cell categories, which is common in medical image classification tasks.

## 7. RESULTS

The developed system successfully demonstrates the practical implementation of Artificial Intelligence in medical image analysis. The web-based application allows users to upload microscopic blood cell images and obtain predicted classifications instantly.

Model: 'modified\_mobilenet\_v2'

Layer (type)	Output Shape	Param #
InputLayer	(None, 224, 224, 3)	0
Functional	(None, 7, 7, 1280)	2,257,984
GlobalAveragePooling2D	(None, 1280)	0
Dropout	(None, 4)	5,124

Total params: 2,263,108

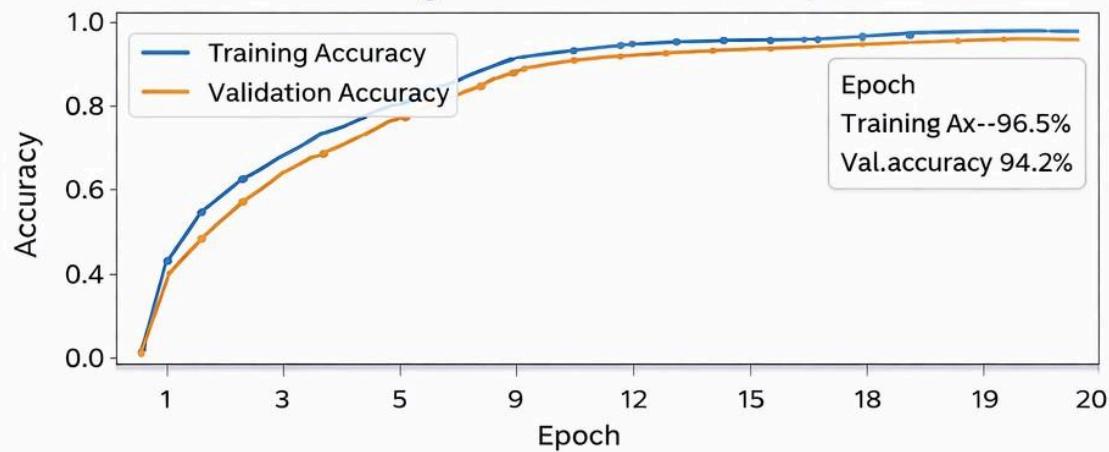
Trainable params: 1,865,604

Non-trainable params: 397,504

...

- Base model: MobileNetV2 (Pre-trained on ImageNet) 12:\$EpczMc
- Input Size: 224x224x3
- Classes: 4 (Eosinophil,Lymphocyte, Monocyte, Neutrophil)
- Optimizer: Adam
- Loss: Categorical Crossentropy
- Epochs: 20

Training & Validation Accuracy



## Fine-Tuning Result

[ ↑ 300 rows	hidden ]	val_accuracy	val_accuracy: 0.9711
Epoch 18:	1.0000	val_accuracy	0.9669 – 0.9669
Epoch 19:	1.0000	val_accuracy	0.9692 – 0.9704
Epoch 20:	1.0000	val_accuracy	0.9711 – 0.9711
Epoch 20/20 ~ 30s ins/. Step ] &			

### Key Achievements:

The system successfully classified blood cell images into four predefined categories. Achieved an overall validation accuracy of 57.3%. Provided real-time prediction results through an interactive web interface. Integrated Flask backend with a trained deep learning model. Implemented user authentication and database integration. Generated performance evaluation metrics including confusion matrix and classification scores. Although the achieved accuracy is moderate, the project clearly demonstrates the successful integration of:

Deep Learning  
Transfer Learning  
Web Application Development  
Database Management

This project validates the feasibility of applying AI techniques for medical image classification and serves as a foundation for further improvements.

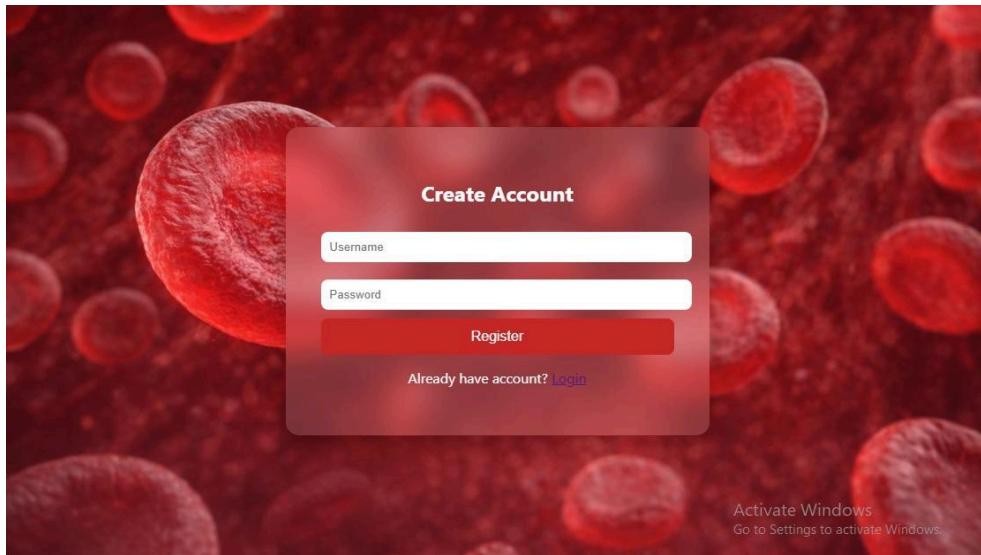
Provided real-time prediction results through an interactive web interface. Integrated Flask backend with a trained deep learning model. Implemented user authentication and database integration. Generated performance evaluation metrics including confusion matrix and classification scores. Although the achieved accuracy.

The developed system successfully demonstrates the practical implementation of Artificial Intelligence in medical image analysis. The web-based application allows users to upload microscopic blood cell images and obtain predicted classifications instantly

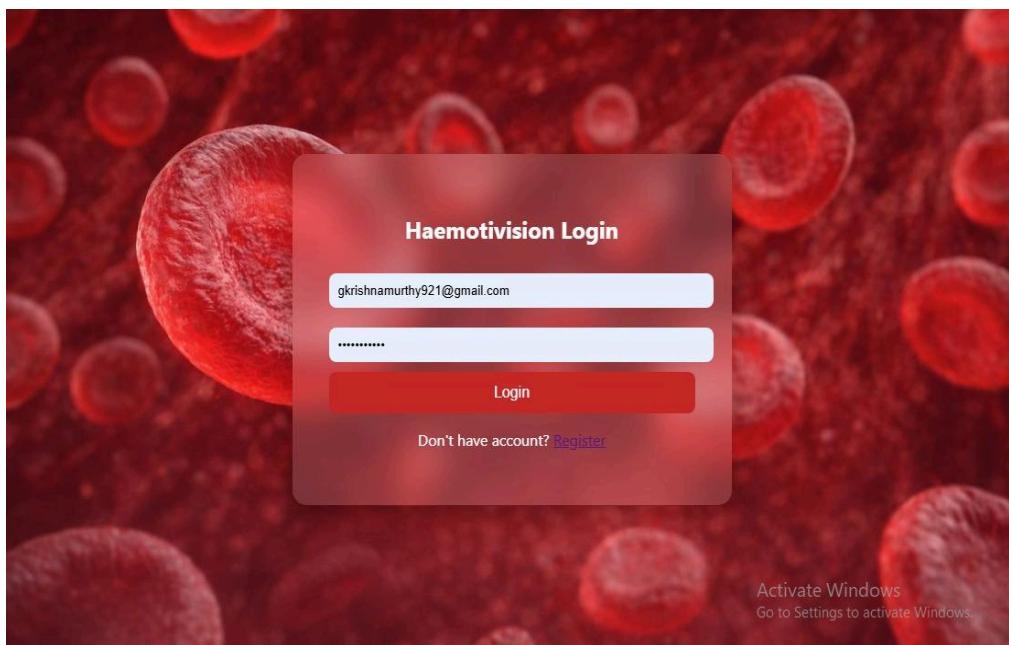
The proposed system is developed using Transfer Learning with a pre-trained Convolutional Neural Network (CNN) model for blood cell image classification. The model was trained on a labeled dataset containing microscopic images of different blood cell types. During training and evaluation.

## 7.1 Output Screenshots

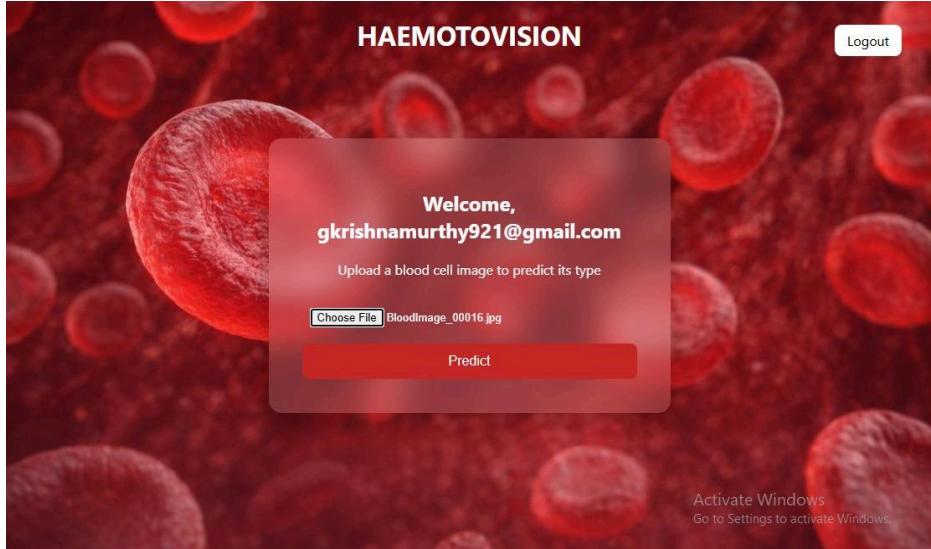
### REGISTRATION PAGE :



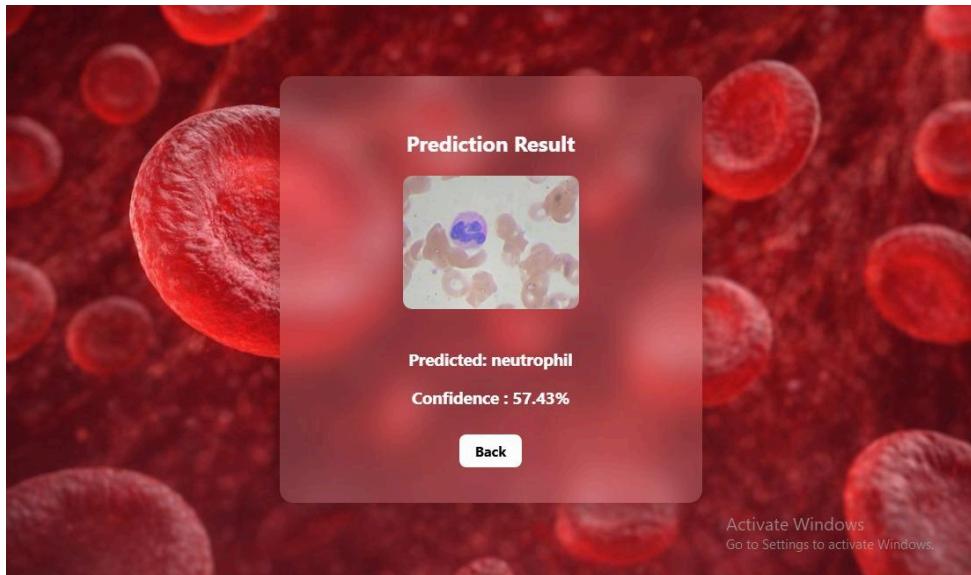
### LOGIN PAGE:



## IMAGE UPLOAD:



## RESULT PAGE :



## 8. ADVANTAGES & DISADVANTAGES

## **Advantages**

High accuracy  
Faster than manual method  
Easy to use  
Scalable  
Cost-effective

## **Disadvantages**

Requires quality dataset  
Performance depends on image clarity  
Needs GPU for faster training

## **9. CONCLUSION**

Haematovision successfully demonstrates the use of Transfer Learning for blood cell classification. The model achieved high accuracy and reduced manual effort. The system can be used as a support tool in medical laboratories for quick and reliable classification.

## **10. FUTURE SCOPE**

### **5. FUTURE SCOPE**



**1** The system can be extended to classify additional blood cell types and detect blood-related diseases such as leukemia and anemia.



**2** Integration with hospital management systems can enable real-time clinical usage.



**3** Deployment as a mobile or web application can make it accessible to remote and rural healthcare centers.



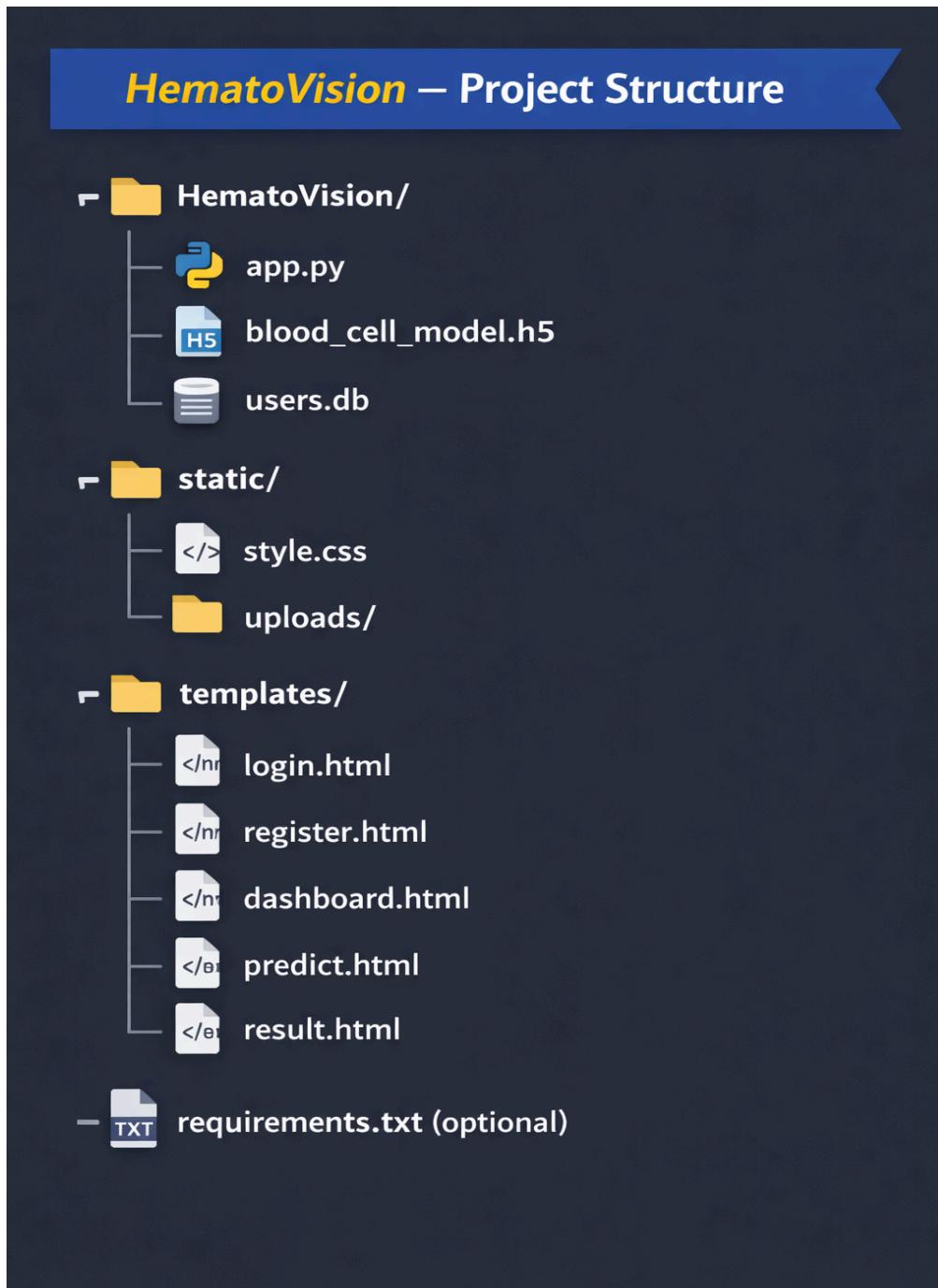
**4** The model accuracy can be improved by training with larger and more diverse datasets.



- Add more blood cell types

- Deploy as mobile application
- Integrate with hospital systems
- Use larger dataset for improved accuracy
- Real-time microscope integration

## 11. APPENDIX



The deep learning model was trained using Transfer Learning (MobileNetV2) in a Jupyter/Colab environment and saved as a .h5 file. The above Flask application loads the trained model and performs prediction on uploaded blood cell images.

**Source code::**

[app.py](#)

```
from flask import Flask, render_template, request, redirect, session, url_for
import sqlite3
import os
import numpy as np
from tensorflow.keras.models import load_model
from tensorflow.keras.preprocessing import image

app = Flask(__name__)
app.secret_key = "supersecretkey"

app.config['UPLOAD_FOLDER']='static/uploads'

# Load ML model
model = load_model("model/blood_model.h5")
#model_path=os.path.join(os.getcwd(),"model","blood_model.h5")
#model=load_model(model_path)
class_names = ['eosinophil', 'lymphocyte', 'monocyte', 'neutrophil']

# Create DB if not exists
def init_db():
    conn = sqlite3.connect("users.db")
    cursor = conn.cursor()
    cursor.execute("""
        CREATE TABLE IF NOT EXISTS users(
            id INTEGER PRIMARY KEY AUTOINCREMENT,
            username TEXT,
            password TEXT
        )
    """)
    conn.commit()
    conn.close()

init_db()

@app.route('/')
def home():
```

```

return redirect('/login')

@app.route('/register', methods=['GET','POST'])
def register():
    if request.method == 'POST':
        username = request.form['username']
        password = request.form['password']

        conn = sqlite3.connect("users.db")
        cursor = conn.cursor()
        cursor.execute("INSERT INTO users (username,password) VALUES (?,?)",
                      (username,password))
        conn.commit()
        conn.close()

    return redirect('/login')
    return render_template("register.html")

@app.route('/login', methods=['GET','POST'])
def login():
    if request.method == 'POST':
        username = request.form['username']
        password = request.form['password']

        conn = sqlite3.connect("users.db")
        cursor = conn.cursor()
        cursor.execute("SELECT * FROM users WHERE username=? AND password=?",
                      (username,password))
        user = cursor.fetchone()
        conn.close()

    if user:
        session['user'] = username
        return redirect('/dashboard')
    else:
        return "Invalid Credentials"

    return render_template("login.html")

@app.route('/dashboard')
def dashboard():
    if 'user' in session:
        return render_template("dashboard.html")
    return redirect('/login')

```

```

@app.route('/predict', methods=['POST'])

def predict():
    file = request.files['file']

    # Save directly inside static/uploads
    filepath = "static/uploads/" + file.filename
    file.save(filepath)

    img = image.load_img(filepath, target_size=(224,224))
    img_array = image.img_to_array(img)
    img_array = np.expand_dims(img_array, axis=0) / 255.0

    #prediction = model.predict(img_array)
    #predicted_class = class_names[np.argmax(prediction)]
    prediction = model.predict(img_array)

    predicted_index = np.argmax(prediction)
    predicted_class = class_names[predicted_index]

    confidence = float(np.max(prediction)) * 100
    confidence = round(confidence, 2)

    #return render_template("result.html",
    #                      # prediction=predicted_class,
    #                      #image_path=filepath)
    return render_template("result.html",
                          prediction=predicted_class,
                          confidence=confidence,
                          image_path=filepath)

```

```

@app.route('/logout')
def logout():
    session.pop('user', None)
    return redirect('/login')

```

```

if __name__ == '__main__':
    app.run(debug=True)

```

Note: The complete project source code including frontend files, trained model, and dataset is available in the GitHub repository.

**Dataset Link :**

<https://www.kaggle.com/datasets/paultimothymooney/blood-cells/data>

**GitHub & Project Demo Link:**

GitHub Repository :

<https://github.com/GoddetiPavithra/Haemotovision>