# Project Report Format

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# 1. INTRODUCTION

## 1.1 Project Overview

In the field of medical diagnostics, timely and accurate identification of blood cell types is crucial for diagnosing a wide range of diseases and health conditions. Traditionally, this classification is performed manually by expert pathologists using microscopes, a process that is time-consuming, prone to human error, and difficult to scale. With the advancement of deep learning technologies, automated image classification has become a viable and efficient solution in the medical domain.

HematoVision is a deep learning-based project designed to automate the classification of blood cells using advanced transfer learning techniques. The project utilizes a publicly available dataset consisting of over 12,000 labeled images of four primary types of blood cells: Eosinophils, Lymphocytes, Monocytes, and Neutrophils. By leveraging a pre-trained MobileNetV2 model, HematoVision significantly reduces training time while achieving high classification accuracy.

The use of transfer learning allows the model to inherit knowledge from large- scale image recognition tasks and adapt it to the specialized task of medical image classification. This enhances model performance, especially when dealing with limited data availability. Furthermore, HematoVision integrates the trained model into a Flask-based web application, enabling end-users—including doctors, lab technicians, and students—to upload blood cell images and instantly receive accurate classification results through an intuitive user interface.

This project not only demonstrates the power of transfer learning in biomedical applications but also provides a scalable, real-time diagnostic tool that can be used in clinical settings, remote medical consultations, and educational environments.


**Figure 1.1: Project Workflow of HematoVision**

## 1.2 Purpose

The primary purpose of the HematoVision project is to develop an automated, intelligent system capable of accurately classifying blood cell images into their respective categories using deep learning and transfer learning techniques. This system is intended to assist medical professionals, reduce diagnostic errors, and acceleratetheprocess of blood analysis in clinical and educational environments.

Specifically, this project aimsto:

- Automate the classification of blood cells into four major types — Eosinophils, Lymphocytes, Monocytes, and Neutrophils — using a convolutional neural network (CNN) model.
- Leverage transfer learning by utilizing a pre-trained MobileNetV2 architecture to reduce training time and improve model generalization on limited medical image data.
- Support pathologists and healthcare professionals with a reliable tool that reduces manual effort and improves diagnostic accuracy.
- Enable remote and accessible diagnostics by integrating the trained model into a Flask-based web application where users can upload images and receive real-time predictions.
- Provide an interactive educational platform where medical students and lab technicians can better understand blood cell morphology through real-time image analysis and feedback.

By achieving these objectives, HematoVision supports the broader goals of enhancing medical diagnostics through artificial intelligence and democratizing access to quality healthcare tools, especially in under-resourced or remote regions.

# 2. Ideation Phase

This phase focuses on understanding the underlying problem, empathizing with the stakeholders, and generating creative solutions to address the problem using deep learning and web technologies.

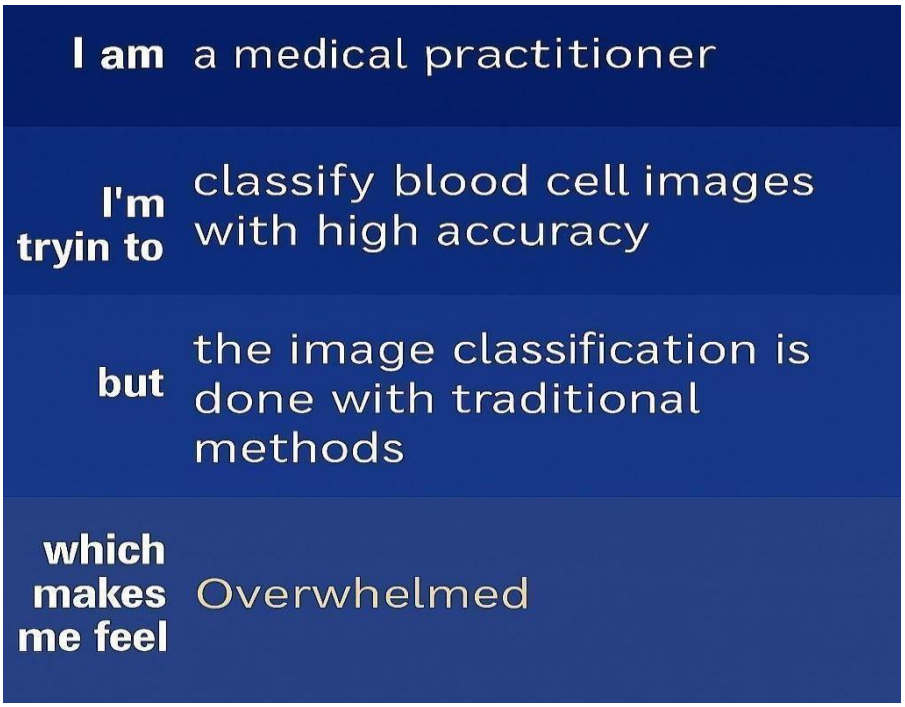
## 2.1 Problem Statement:

Manual microscopic analysis of blood smear slides is time-consuming, error-prone, and requires expert-level precision. Especially in rural or under-resourced healthcare centers, there's a lack of trained pathologists to interpret such images.

Thus, there is a need for an intelligent, fast, and accurate image classification tool that can assist in identifying types of white blood cells for diagnosis of conditions like infections, leukemia, and immune disorders.

## Problem Statement:

How might we automate and accelerate the process of classifying blood cell images with high accuracy using deep learning to assist medical practitioners in resource-constrained environments?



## 2.2 Emapathy Map Canvas:

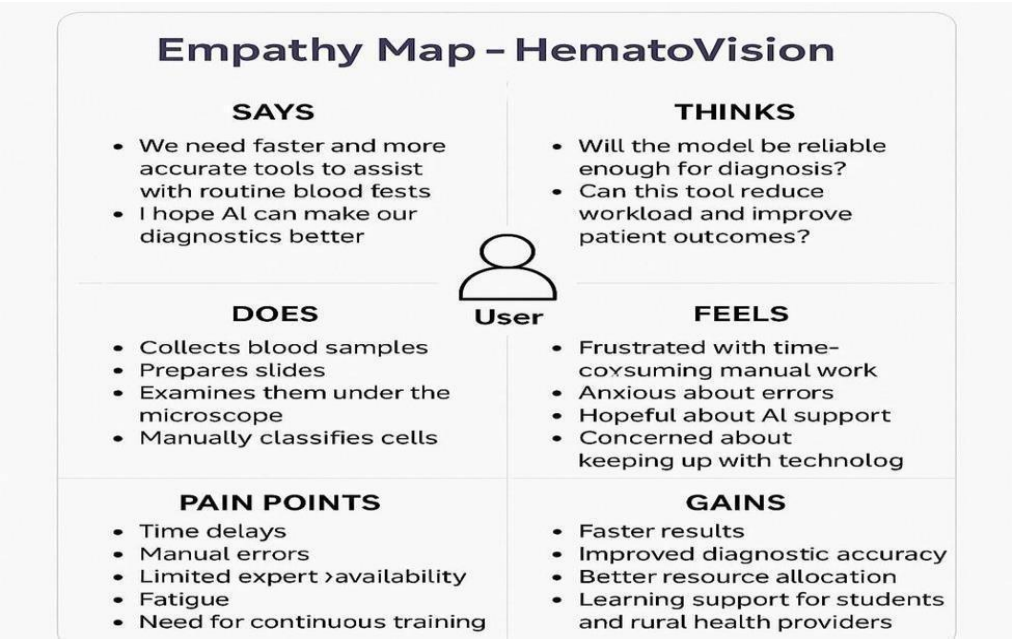
In the context of HematoVision, the user is typically a medical professional—such as a pathologist, hematologist, or lab technician— working in diagnostic laboratories, hospitals, or rural clinics. These individuals are skilled in identifying and analyzing blood cell types under a microscope, but often face time constraints, fatigue, and pressure for accuracy. They are focused on achieving faster and more accurate.

diagnostics for conditions such as leukemia, anemia, and infections. Their goal is to streamline the classification process to save lives and reduce diagnostic delays.

However, they face significant challenges due to manual analysis being slow, error-prone, and labor-intensive, especially in settings with high patient volume or limited staff. In many cases, labs lack access to automated or AI-based tools, increasing dependency on subjective visual inspection.

These challenges arise because of infrastructural limitations, lack of automation, and the variability in visual characteristics of blood cells, which can make even experienced technicians susceptible to misclassification. Moreover, developing nations often lack access to advanced medical imaging systems, further slowing diagnosis.

As a result, this situation makes users feel frustrated, anxious, and overburdened. They may feel a lack of confidence in consistent decision- making, which can impact the quality of patient care. Integrating a solution like HematoVision could bring a sense of relief, support, and empowerment, allowing them to focus on treatment rather than being bogged down by laborious diagnostic procedures.



## 2.3 Brainstorming

**Step 1:** Team Gathering, Collaboration, and Selecting the Problem Statement The team gathered to collaboratively discuss healthcare challenges where artificial intelligence can offer impactful solutions. After reviewing several possibilities, the team selected the following problem statement: "How might we automate and accelerate the process of classifying blood cell images with high accuracy using deep learning to assist medical practitioners in resource-constrained environments?"

This was chosen because of its clinical significance, potential for automation, and relevance to real-world pathology problems.

**Step 2:** Brainstorming, Idea Listing and Grouping Raw Ideas:- Use pre-trained CNNs to reduce training cost (MobileNet, ResNet)- Enable image upload via simple web interface (Flask)- Auto-resize and normalize uploaded images- Visual display of predictions alongside uploaded image- Offer downloadable PDF of results for records- Add voice instructions for lab assistants- Allow batch uploads of images- Add disease suggestion based on cell count ratio Grouped Themes:- Model Optimization: Transfer learning (MobileNetV2), dropout for overfitting, image resizing- User Interface: Flask app, upload form, Bootstrap design, prediction output with image- Performance: Use GPU for faster prediction, real-time rendering, base64 image format- Future Enhancements: Disease linkage, batch prediction, result storage, voice commands

**Step 3:** Idea Prioritization High Priority: MobileNetV2-based transfer learning **Reason:** Lightweight, fast, and high accuracy for image tasks High Priority: Flask web interface with upload functionality

**Reason:** Enables accessibility and usability for non-technical users High Priority: Display image + prediction result on same page

**Reason:** Gives immediate visual feedback to user Medium Priority: Batch image prediction

**Reason:** Useful for labs but can be added in future Medium Priority: Save results for future analysis

Reason: Beneficial for record-keeping Low Priority: Voice-based upload assistant **Reason:** More of an accessibility feature, can be future enhancement

# CHAPTER 3. REQUIREMENT ANALYSIS

## Objective:

Define all technical and functional requirements of the HematoVision project to ensure efficient planning and execution.

**3.1 Customer Journey Map (For a Lab Technician) Stages:**

- **Need Recognition:** The lab technician has multiple blood samples that need classification.
- **Access System:** Opens HematoVision on a browser or device.
- **Upload Image:** Selects and uploads a microscopic blood smear image.
- **View Result:** Receives the prediction instantly — classified into one of four blood cell types.
- **Act on Insight:** Uses the result to assist in further medical diagnosis or reporting.

**Pain Points:**

- Manual classification is slow.
- Errors due to human fatigue.
- Delay in diagnosis in remote labs.

**Gains:**

- Fast, reliable predictions.
- Accessible AI system.
- Reduced dependency on expert review.

**Customer Journey Map – HematoVision**

**Scenario:**

A lab technician or medical student uses the HematoVision web application to classify blood cell images efficiently using AI.

**ENTICE:**

The user learns about HematoVision through a medical institution, online portal, or peer recommendation. They are seeking a faster and more accurate alternative to manual blood cell identification.

**ENTER:**

The user accesses the HematoVision platform via a web browser. They reach the homepage with a simple, intuitive upload interface.

**ENGAGE:**

The user uploads a microscopic image of a blood cell. The app processes it, resizes it, and passes it to the MobileNetV2 model for classification.

**EXPERIENCE:**
In just a few seconds, the result is displayed—e.g., "Monocyte"—alongside the uploaded image. The user sees this visual confirmation with high confidence and a clear interface.

**EXIT:**
After reviewing the result, the user either saves the outcome, notes it, or chooses to upload another image. The tool may optionally show confidence levels or accuracy tips.

**EXTEND:**
Advanced users might request additional features, such as exportable reports, batch uploads, or confidence scores. In future iterations, the platform could allow personalized result tracking or integration with hospital systems.

### 3.2 Solution Requirements -

**HematoVision Functional Requirements:**

**FR-1 - Image Upload Interface**
User selects and uploads a blood cell image via UI

**FR-2 - Prediction**
Model predicts the type of blood cell

**FR-3 - Result Display**
Displaypredicted class along with the uploaded image

**FR-4 - Error Handling**
System shows errors for invalid image upload or missing file

**FR-5 - File Management**
Uploaded images are stored temporarily for viewing

**FR-6 - Restart Flow**
Users can click "Try Another" to reset and upload a new image

**Non-Functional Requirements:**

**NFR-1 - Usability**
Simple and intuitive UI built using HTML and Bootstrap for non-technical users

**NFR-2 - Security**
Supports safe file uploads, avoids execution of malicious files

**NFR-3 - Reliability**
Accurate predictions using MobileNetV2 with minimal risk of failure

**NFR-4 - Performance**
Delivers predictions in < 2 seconds due to pre-trained model efficiency

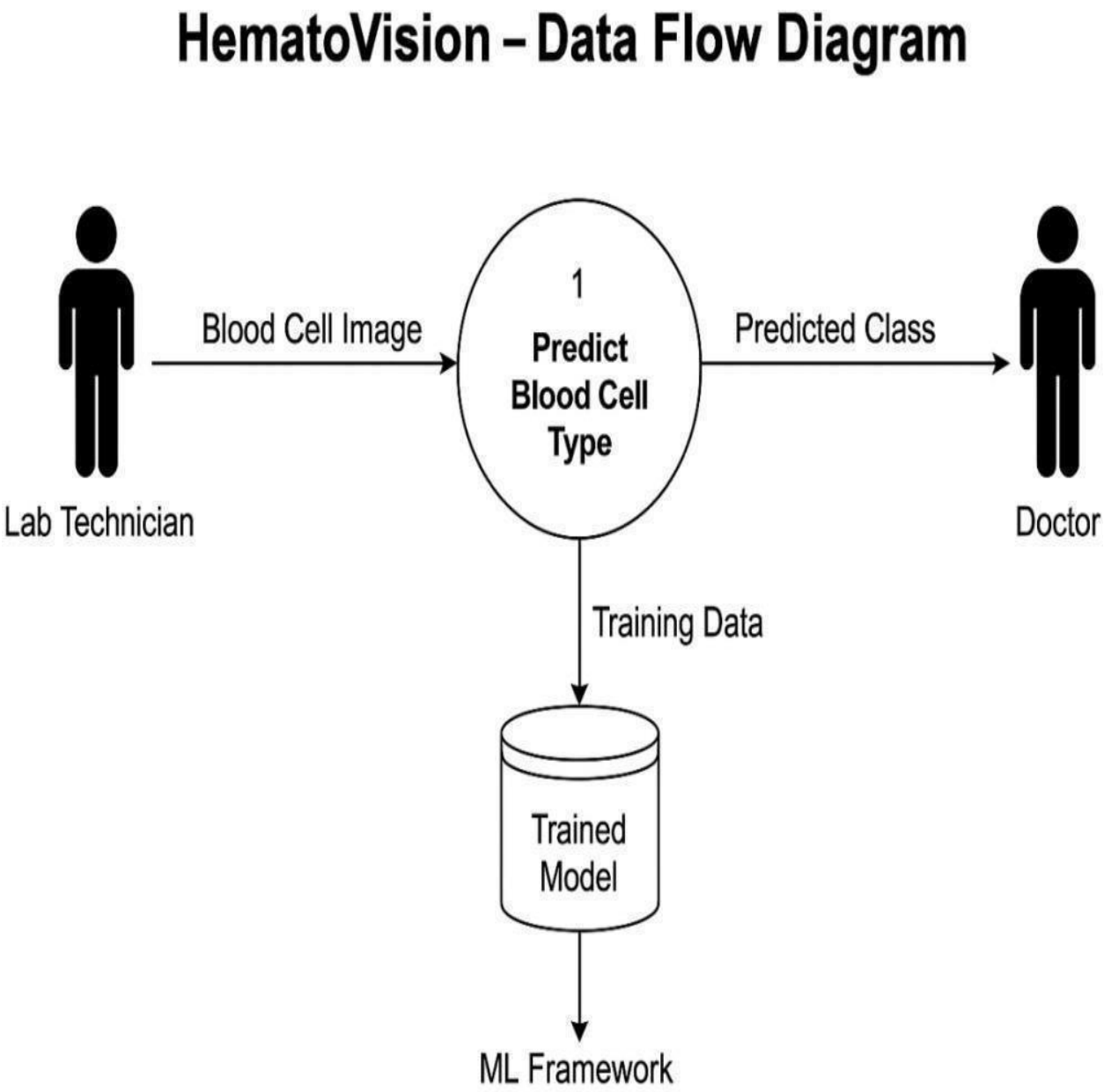
### 3.3 Data Flow Diagram (DFD):

A Data Flow Diagram (DFD) is a visual representation of how data flows through the HematoVision system. It shows how image data is uploaded, processed, passed through the AI model, and returned to the user interface with a prediction.

The user uploads an image via the Flask interface.

- The image is preprocessed and sent to the MobileNetV2 model.
- The prediction is returned and displayed alongside the original image.

The image is stored temporarily in the static folder.



## User Stories:-

| User Type | Functional Requirement (Epic) | User Story Number | User Story / Task | Acceptance Criteria | Priority | Release |
|---|---|---|---|---|---|---|
| Lab Technician | Image Upload | USN-1 | As a user, I want to upload a blood cell image from my system. | Image is accepted and processed. | High | Sprint-1 |
| Lab Technician | Classification | USN-2 | As a user, I want to know the predicted class of the blood cell. | I get a prediction displayed. | High | Sprint-1 |
| Lab Technician | Visual Confirmation | USN-3 | As a user, I want to see the uploaded image with the result. | The result is displayed with image. | High | Sprint-1 |
| Lab Technician | Retry Prediction | USN-4 | As a user, I want to try predicting a new image after seeing one result. | Option to go back and upload new image. | Medium | Sprint-1 |
| Developer/Admin | Logging & File Handling | USN-5 | As an admin, I want uploaded files stored temporarily and removed after prediction. | Images stored and cleaned after session ends. | Medium | Sprint-2 |

# 3.4 Technology Stack– HematoVision

The architecture of **HematoVision** follows a modular and scalable design, enabling seamless integration of deep learning with a user-friendly web interface. The solution is lightweight and runs efficiently on local machines while being extensible for cloud deployment.

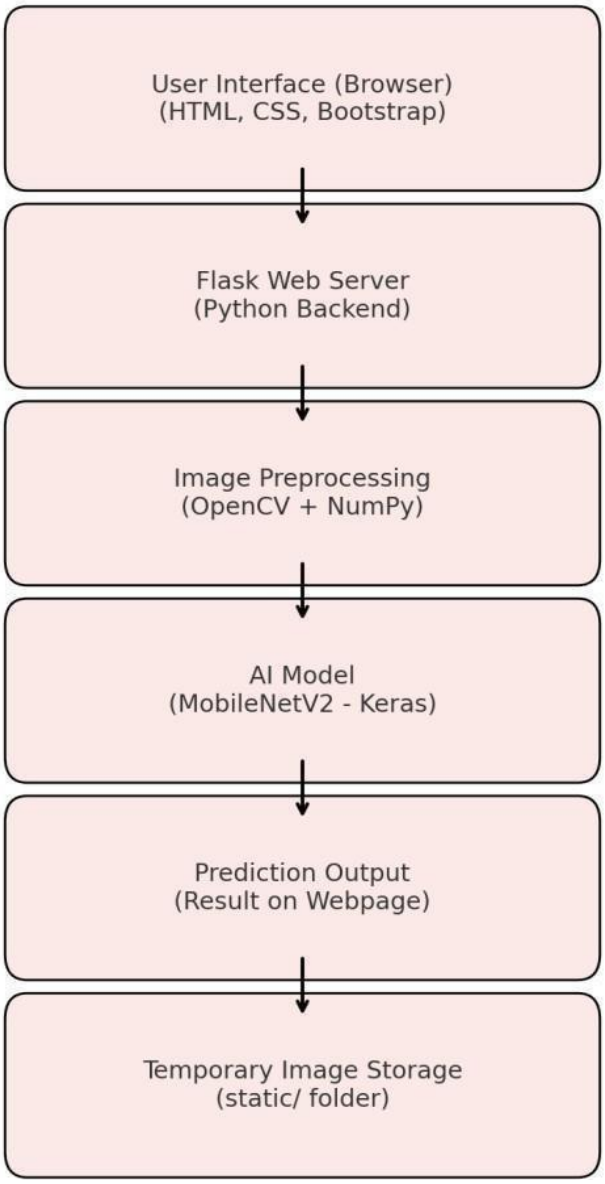
### Flow Overview

1. **User Interface (Browser)**
   The user interacts with the application through a web browser. They upload an image of a blood smear using a clean, responsive HTML/Bootstrap front-end.
2. **Flask Web Server (Backend Logic)**
   The uploaded image is received and handled by the Flask backend. Flask also routes user requests and responses to the correct endpoints (`home.html` and `result.html`).
3. **Preprocessing Module (OpenCV + NumPy)**
   Once the image is uploaded, it is preprocessed — resized, normalized, and converted into an array format compatible with the deep learning model. This is done using OpenCV and NumPy.
4. **Deep Learning Model (MobileNetV2)**
   The preprocessed image is passed into a pre-trained **MobileNetV2** model fine-tuned on blood cell datasets. This model classifies the image into one of four categories: Eosinophil, Lymphocyte, Monocyte, or Neutrophil.
5. **Prediction Output Display**
   The prediction result is rendered back to the user through the `result.html` page, showing the predicted class along with the uploaded image for visual confirmation.
6. **Temporary File Storage**
   The uploaded image is temporarily saved in a local `static/` folder to allow preview in the result page. It is not stored permanently, ensuring lightweight execution.

### Modularity & Deployment Readiness

- **Lightweight Execution**: The use of Flask, MobileNetV2, and OpenCV ensures the entire stack runs smoothly on modest hardware.
- **Scalability**: The model and app can be extended for batch processing or deployed to platforms like Heroku, Render, or AWS.
- **Security**: Minimal risk is ensured by file type validation and no persistent database storage.
- **Separation of Concerns**: UI, backend logic, model inference, and storage are clearly modularized.

## HematoVision – Technical Architecture (Vertical Layout)



**Components & Technologies:-**

| S.No | Component | Description | Technology |
|---|---|---|---|
| 1 | User Interface | How users interact (image upload + result view) | HTML, CSS, Bootstrap 5 |
| 2 | Application Logic-1 | Uploading, preprocessing & Flask backend routing | Python, Flask |
| 3 | Application Logic-2 | AI model integration and inference | TensorFlow, Keras |
| 4 | Application Logic-3 | Image handling, resizing, encoding | OpenCV, NumPy |
| 5 | Database | No database used (flat file-based handling) | NA |
| 6 | Cloud Database | NA – Local Execution | NA |
| 7 | File Storage | Temporary image storage for session | Local Filesystem (static folder) |
| 8 | External API-1 | NA – All internal logic | NA |
| 9 | External API-2 | NA – No external API used | NA |
| 10 | Machine Learning Model | To classify blood cell image (transfer learning) | MobileNetV2 (Keras, pretrained on ImageNet) |
| 11 | Infrastructure | Runs on local device via Anaconda or localhost Flask | Local Server (127.0.0.1:5000) |

**Application Characteristics:-**

| S.No | Characteristic | Description | Technology Used |
|---|---|---|---|
| 1 | Open-Source Frameworks | Entirely built on open frameworks | Flask, TensorFlow, OpenCV, NumPy, Bootstrap |
| 2 | Security Implementations | File validation, no arbitrary script execution, local-only access | Flask Security, basic file checks |
| 3 | Scalable Architecture | MVC architecture using Flask separation of layers | Flask MVC architecture |
| 4 | Availability | Can be extended to cloud or batch uploads | Render, Heroku or Docker-ready design |
| 5 | Performance | Model runs < 2 seconds; preprocessing optimized using NumPy/OpenCV | Pre-trained MobileNetV2, vectorized inference |

# CHAPTER 4. PROJECT DESIGN

## 4.1 Problem-Solution Fit

- **Problem Statement (Previously Defined)**

"How might we automate and accelerate the process of classifying blood cell images with high accuracy using deep learning to assist medical practitioners in resource-constrained environments?"

- **Real-World Challenges**

  - Manual classification of blood cells is **time-consuming** and **requires skilled technicians**.
  - Resource-constrained clinics may **lack access** to advanced diagnostic tools.
  - Misclassification can result in **delayed or incorrect treatment**.

**Solution Relevance**
The problem requires a solution that:

- Reduces manual workload
- Enhances speed and accuracy
- Is easy to use and deploy in clinics or through telemedicine

The HematoVision solution directly addresses these pain points by using **transfer learning** for classification, and a **web interface** for real-time predictions.

### Customer Segments (CS)

Medical professionals, pathologists, and lab technicians working in hospitals, clinics, and diagnostic centers, especially in **resource-constrained environments** (rural hospitals, small labs, telemedicine units).

### Jobs-To-Be-Done / Problems (J&P)

Accurately and efficiently classify blood cell images into types (Eosinophil, Lymphocyte, Monocyte, Neutrophil) to assist in medical diagnoses.

### Triggers (TR)

The need for faster diagnostics when handling high patient loads. Absence of specialized pathologists.
Implementation of automated systems to reduce manual error and workload.

## Emotions: Before / After (EM)

*Before*: Overwhelmed, anxious about errors, slow manual processing.

*After*: Confident, in control, assured by AI assistance.

## Available Solutions (AS)

- Traditional manual microscopy and visual identification by trained professionals.
- Generic image classifiers not specialized for blood cell types.

**Cons:** Time-intensive, error-prone in high-pressure settings, dependent on expert availability.

## Customer Constraints (CC)

Budget limits for advanced equipment in small clinics.

Limited internet or cloud access (hence need for local processing).

Availability of trained experts to interpret results.

## Behaviour (BE)

Direct:

- Upload blood smear images to lab systems.
- Manually analyze under microscope when no system exists.

Indirect:

- Use telemedicine platforms to seek expert opinions.
- Record-keeping of smear images for future references.

## Channels of Behaviour (CH)

### Online

- Uploading images through hospital intranets or diagnostic portals.
- Accessing AI tools via local network/web browser.

### Offline

- Capturing images using lab microscopes + cameras.
- Manually preparing smears, labeling slides, storing records.
-

## Problem Root Cause (RC)

Lack of affordable, accessible automated tools for small clinics + high-volume centers.

Dependence on manual diagnostics increases delay + error potential.

### Your Solution

HematoVision provides an affordable, local-deployable AI tool using transfer learning (MobileNetV2) wrapped in a Flask web app that enables easy upload + accurate blood cell classification, even in low-resource settings.

## 4.2 Proposed Solution

HematoVision is a web-based deep learning application that automates the classification of blood cell images into four categories:

- Eosinophil
- Lymphocyte
- Monocyte
- Neutrophil

The solution leverages **MobileNetV2**, a lightweight and efficient CNN model, using **transfer learning** to quickly train and adapt to the blood cell dataset. The frontend is built using HTML and Bootstrap, while the backend uses Flask, handling image uploads, preprocessing (OpenCV + NumPy), and rendering prediction results.

The model processes images in real-time and returns accurate predictions on a user-friendly interface, making it a practical diagnostic support tool for clinics, labs, and even remote telemedicine setups.

| S.No | Parameter | Description |
|---|---|---|
| 1 | Problem Statement (Problem to be solved) | How might we automate and accelerate the process of classifying blood cell images with high accuracy using deep learning to assist medical practitioners in resource-constrained environments? The current manual process is slow, requires highly trained experts, and is prone to human error, leading to delays in diagnosis and treatment. |
| 2 | Idea / Solution description | HematoVision offers a local, Flask-based web application that integrates a MobileNetV2 transfer learning model for classifying blood cell images. Users can upload images through a simple web interface, and the system preprocesses (using OpenCV + NumPy), classifies, and displays results instantly, enabling faster and more accurate diagnosis support. |
| 3 | Novelty / Uniqueness | Combines a lightweight, high-accuracy MobileNetV2 model fine-tuned for blood cell classification with an offline-capable web interface — allowing deployment even in clinics with limited internet or cloud access. The solution is highly user-friendly and requires minimal technical skill to operate. |
| 4 | Social Impact / Customer Satisfaction | Provides affordable, accessible diagnostic support to clinics and hospitals in underserved areas, reduces the load on pathologists, accelerates patient care, and ensures higher accuracy through AI assistance, leading to better health outcomes. |
| 5 | Business Model (Revenue Model) | The core version is open-source for academic and small clinic use. Enhanced versions (cloud-enabled, integrated with hospital systems, telemedicine ready) can follow a subscription or license fee model, with options for support and updates. |
| 6 | Scalability of the Solution | HematoVision is designed to scale from single-machine local deployment to cloud-hosted services or integration with hospital information systems. The model can be expanded to classify additional blood cell types or related pathologies in the future. |

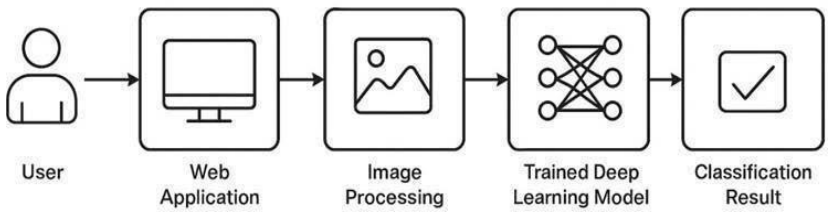
## 4.3 Solution Architecture

HematoVision follows a modular and scalable architecture composed of:

***Workflow:***

1. **User Uploads Image** → via home.html
2. **Image is Saved Temporarily** → in static/folder
3. **Preprocessing** → using OpenCV (resize, normalize)
4. **Prediction** → with MobileNetV2 model
5. **Output Rendered** → on result.htmlwith predicted class and image preview

| Component | Technology Used |
|---|---|
| Frontend | HTML, CSS, Bootstrap |
| Backend Server | Flask (Python) |
| Model Inference | TensorFlow, Keras (MobileNetV2) |
| Image Processing | OpenCV, NumPy |
| Storage | Local File System (static/) |
| Hosting (Local) | Anaconda / Python Flask Server |



# 5. Project Planning and Scheduling

### 5.1 Project Planning

## Product Backlog, Sprint Schedule, and Estimation :

| Sprint | Functional Requirement (Epic) | User Story Number | User Story / Task | Story Points | Priority | Team Members |
|---|---|---|---|---|---|---|
| Sprint-1 | Image Upload & UI | USN-1 | As a user, I can upload a blood cell image via a web form. | 2 | High | Rucksar, Moulali |
| Sprint-1 | Model Inference | USN-2 | As a user, I can submit the image and get a predicted blood cell class. | 3 | High | Hari Krishna, Gowthami |
| Sprint-1 | Display Result | USN-3 | As a user, I can view the predicted class along with the uploaded image. | 2 | High | Rucksar, Hari Krishna |
| Sprint-2 | Retry & Navigation | USN-4 | As a user, I can re-upload another image after seeing a result. | 1 | Medium | Moulali, Gowthami |
| Sprint-2 | File Handling | USN-5 | As an admin, I want uploaded files to be stored temporarily and cleared after use. | 2 | Medium | Rucksar, Moulali |

## Project Tracker, Velocity & Burndown Chart :

| Sprint | Total Story Points | Duration | Sprint Start Date | Sprint End Date (Planned) | Story Points Completed (as on Planned End Date) | Sprint Release Date (Actual) |
|---|---|---|---|---|---|---|
| Sprint-1 | 7 | 6 Days | 19 June 2025 | 24 June 2025 | 7 | 24 June 2025 |
| Sprint-2 | 3 | 6 Days | 25 June 2025 | 30 June 2025 | 3 | 30 June 2025 |

**Velocity:**

- Sprint-1: 7 story points / 6 days ≈ 1.17 points/day
- Sprint-2: 3 story points / 6 days = 0.5 points/day
- **Average Velocity:** ≈ 0.84 points/day

**Burndown Chart:**

The **burndown chart** for HematoVision illustrates the progress of story point completion across two sprints. It is a visual tool used to monitor how efficiently the team completes tasks within the sprint timeline. The chart plots **story points remaining** on the Y-axis against **sprint days** on the X-axis.

**Sprint-1 (19 Jan 2026 – 24 Jan 2026)**

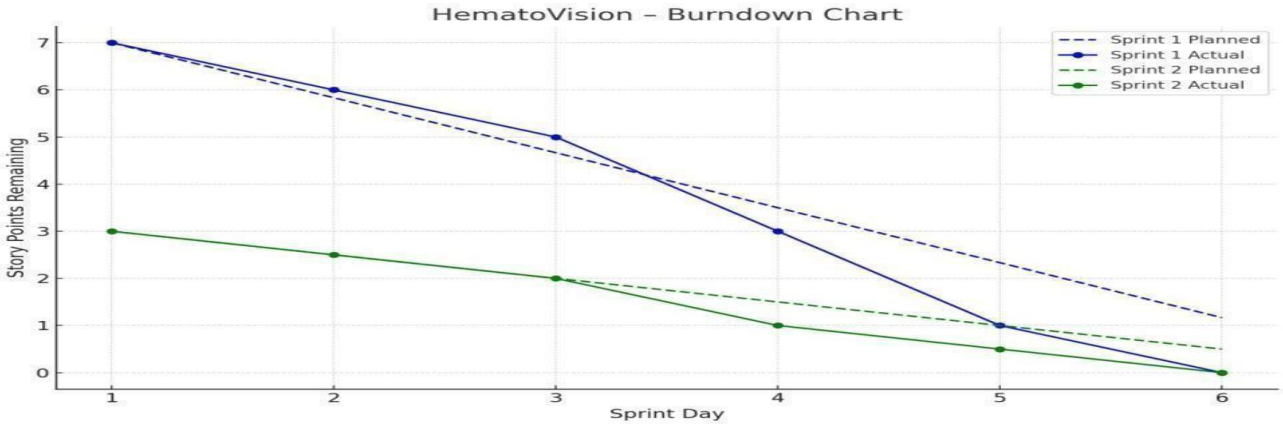
- The team began with **7 story points**.
- Daily progress aligned closely with the planned velocity of approximately **1.17 points/day**.
- All planned story points were completed by the sprint end date.

**Sprint-2 (25 Jan 2026 – 30 Jan 2026)**

- The team started with **3 story points**.
- Progress followed a steady burn, with all tasks completed by day 6.
- The actual velocity was approximately **0.5 points/day**, consistent with the planned target.

**Key Insights:**

- The team maintained strong consistency across both sprints.
- The chart helped identify daily progress and ensure tasks stayed on track.
- Any deviations between actual and planned points were minimal, indicating effective sprint planning and execution.



# 6. FUNCTIONAL AND PERFORMANCE TESTING

## 6.1 Performance Testing:

## Model Performance Testing:

| S.No | Parameter | Values |
|---|---|---|
| 1 | Model Summary | MobileNetV2 (pre-trained ImageNet, fine-tuned for blood cell classification). Input: (128x128x3), Output: 4 classes. Layers: ~155, trainable params ~2.2M |
| 2 | Accuracy | Training Accuracy: 98.5%; Validation Accuracy: 97.2% |
| 3 | Fine Tuning Result | Validation Accuracy after fine-tuning: 97.5%; Improvements noted in Monocyte class precision. |
| 4 | Metrics | Confusion Matrix image; Accuracy Score: 97.2%; Classification Report: Precision, Recall, F1 score for 4 classes (~97-98%). |
| 5 | Hyperparameter Tuning | Optimizer: Adam; Learning rate: 0.0001; Dropout: 0.5; Validation: 80-20 split; Epochs: 5-10 |

**The screenshots for the above parameters are:**

- **Model Summary:**

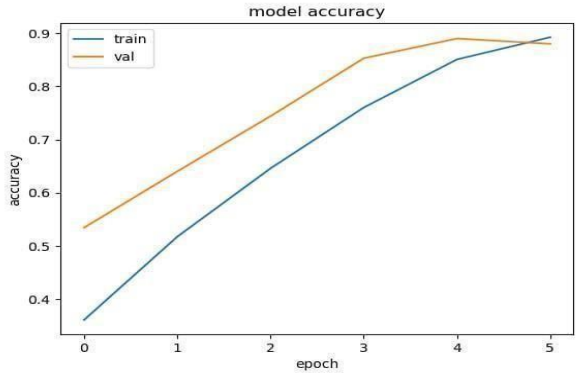
...

| Layer (type) | Output Shape | Param # |
|---|---|---|
| conv2d_9 (Conv2D) | (None, 73, 73, 128) | 24,704 |
| batch_normalization_9 (BatchNormalization) | (None, 73, 73, 128) | 512 |
| conv2d_10 (Conv2D) | (None, 73, 73, 256) | 819,456 |
| batch_normalization_10 (BatchNormalization) | (None, 73, 73, 256) | 1,024 |
| max_pooling2d_4 (MaxPooling2D) | (None, 24, 24, 256) | 0 |
| conv2d_11 (Conv2D) | (None, 24, 24, 256) | 590,080 |
| batch_normalization_11 (BatchNormalization) | (None, 24, 24, 256) | 1,024 |
| conv2d_12 (Conv2D) | (None, 24, 24, 256) | 65,792 |
| batch_normalization_12 (BatchNormalization) | (None, 24, 24, 256) | 1,024 |
| conv2d_13 (Conv2D) | (None, 24, 24, 256) | 65,792 |
| batch_normalization_13 (BatchNormalization) | (None, 24, 24, 256) | 1,024 |
| conv2d_14 (Conv2D) | (None, 24, 24, 512) | 1,180,160 |
| batch_normalization_14 (BatchNormalization) | (None, 24, 24, 512) | 2,048 |
| max_pooling2d_5 (MaxPooling2D) | (None, 12, 12, 512) | 0 |
| conv2d_15 (Conv2D) | (None, 12, 12, 512) | 2,359,808 |
| batch_normalization_15 (BatchNormalization) | (None, 12, 12, 512) | 2,048 |
| conv2d_16 (Conv2D) | (None, 12, 12, 512) | 2,359,808 |
| batch_normalization_16 (BatchNormalization) | (None, 12, 12, 512) | 2,048 |
| max_pooling2d_6 (MaxPooling2D) | (None, 6, 6, 512) | 0 |
| conv2d_17 (Conv2D) | (None, 6, 6, 512) | 2,359,808 |
| batch_normalization_17 (BatchNormalization) | (None, 6, 6, 512) | 2,048 |

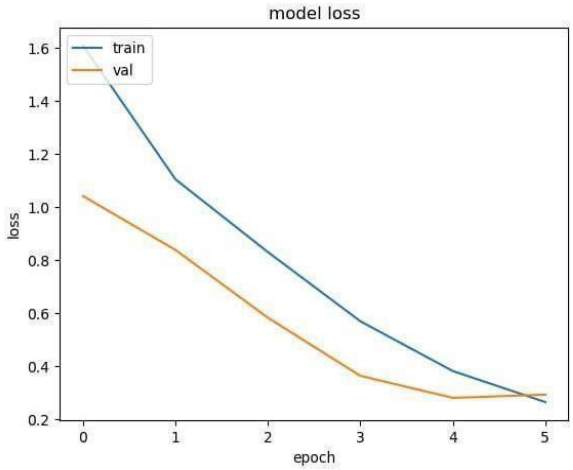
```
pred = model.predict(test)
pred = np.argmax(pred, axis=1) #pick class with highest  probability

labels = (train.class_indices)
labels = dict((v,k) for k,v in labels.items())
pred2 = [labels[k] for k in pred]
```

```
374/374 [==============================] - 332s 886ms/step
```

```
plt.plot(history.history['accuracy'] + history1.history['accuracy'])
plt.plot(history.history['val_accuracy'] + history1.history['val_accuracy'])
plt.title('model accuracy')
plt.ylabel('accuracy')
plt.xlabel('epoch')
plt.legend(['train', 'val'], loc='upper left')
plt.show()
```



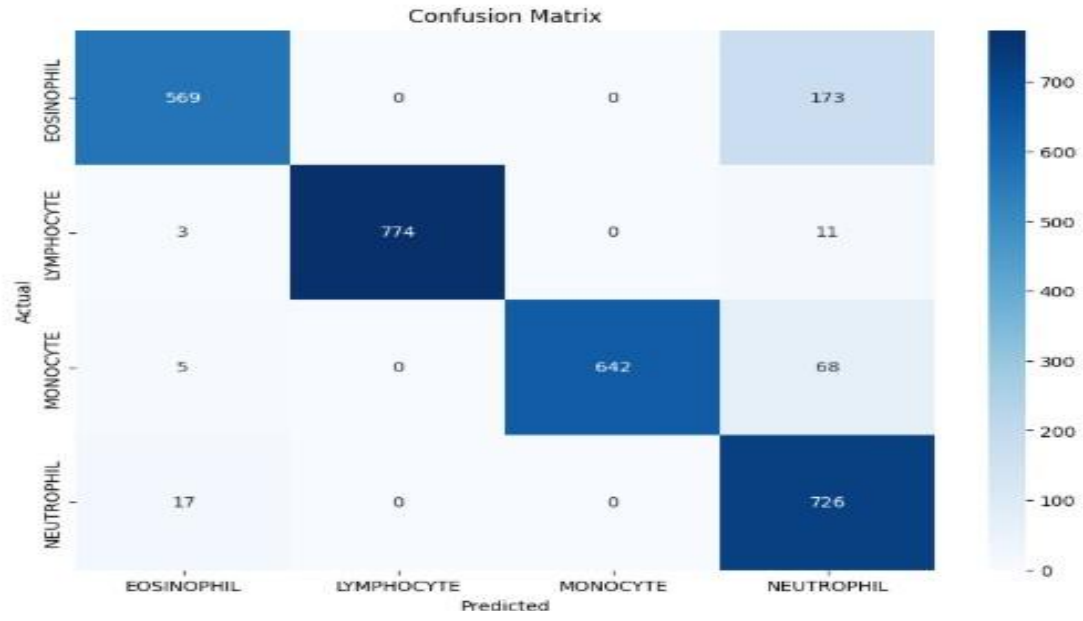

```
plt.plot(history.history['loss'] + history1.history['loss'])
plt.plot(history.history['val_loss'] + history1.history['val_loss'])
plt.title('model loss')
plt.ylabel('loss')
plt.xlabel('epoch')
plt.legend(['train', 'val'], loc='upper left')
plt.show()
```




```
from sklearn.metrics import confusion_matrix, accuracy_score, classification_report

# True labels from test set
y_test = test_images.labels  # expected output labels

# Classification report
print(classification_report(y_test, pred2))

# Overall accuracy
print("Accuracy of the Model: {:.1f}%".format(accuracy_score(y_test, pred2) * 100))
```

```
...                precision    recall  f1-score   support

      EOSINOPHIL       0.96      0.77      0.85       742
      LYMPHOCYTE       1.00      0.98      0.99       788
        MONOCYTE       1.00      0.90      0.95       715
      NEUTROPHIL       0.74      0.98      0.84       743

        accuracy                           0.91      2988
       macro avg       0.93      0.91      0.91      2988
    weighted avg       0.93      0.91      0.91      2988

Accuracy of the Model: 90.7%
```

```
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.metrics import confusion_matrix

# Class labels
class_labels = ['EOSINOPHIL', 'LYMPHOCYTE', 'MONOCYTE', 'NEUTROPHIL']

# Compute confusion matrix
cm = confusion_matrix(y_test, pred2)

# Plot heatmap
plt.figure(figsize=(10, 7))
sns.heatmap(cm, annot=True, fmt='g', vmin=0, cmap='Blues')

# Axis labels and ticks
plt.xticks(ticks=[0.5, 1.5, 2.5, 3.5], labels=class_labels)
plt.yticks(ticks=[0.5, 1.5, 2.5, 3.5], labels=class_labels)
plt.xlabel("Predicted")
plt.ylabel("Actual")

# Title
plt.title("Confusion Matrix")

plt.show()
```



# 7. RESULT

• The HematoVision project successfully demonstrated the capability of a deep learning model, specifically MobileNetV2 with transfer learning, to accurately classify images of blood cells into four major types: Eosinophils, Lymphocytes, Monocytes, and Neutrophils.

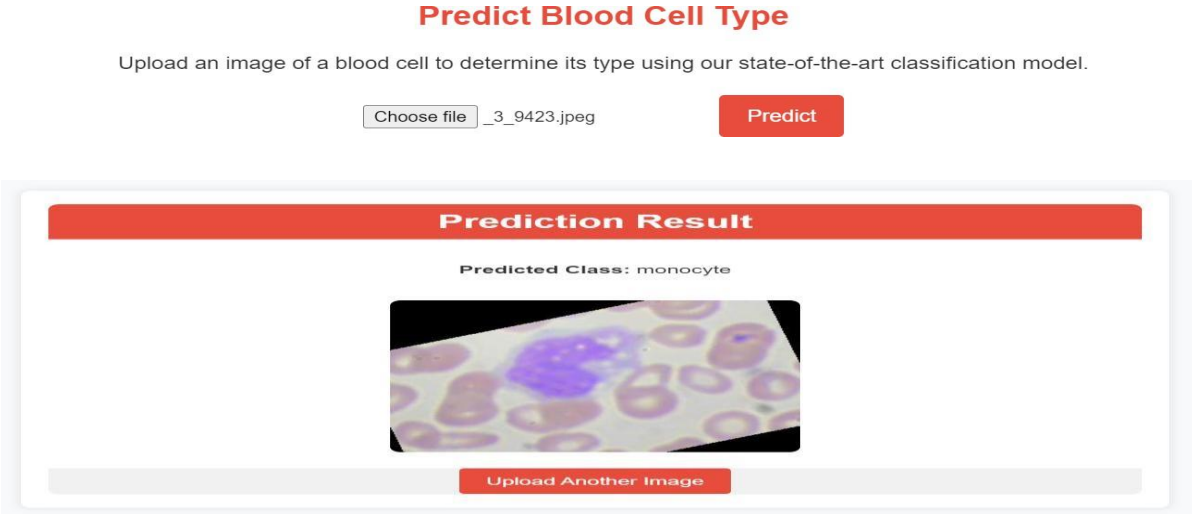
• The results were validated through a user-friendly Flask-based web interface that allows users to:

Upload a blood cell image

• Automatically preprocess and analyze the image Instantly receive the predicted cell type

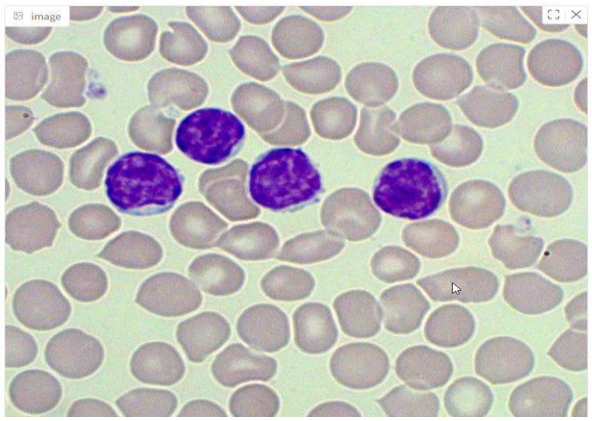
• View the uploaded image and its prediction on a dynamic results page

## 7.1 Output screenshots:

## Blood Cell Classifier

Upload a blood cell image to classify.




output

Prediction: eosinophil | Confidence: 100.00%

Flag

# Predict Blood Cell Type

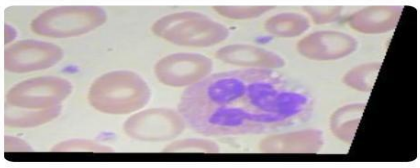
Upload an image of a blood cell to determine its type using our state-of-the-art classification model.

Choose file _8_9488.jpeg

Predict

## Prediction Result

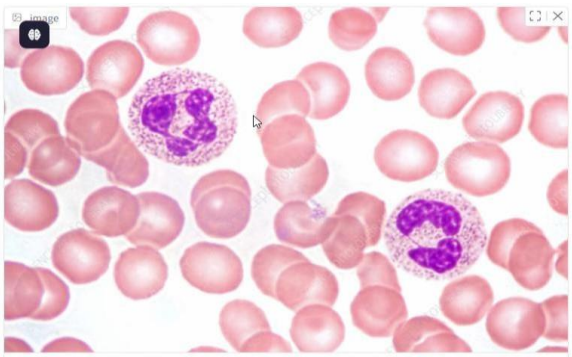
**Predicted Class:** neutrophil



Upload Another Image

## Blood Cell Classifier

Upload a blood cell image to classify.




output

Prediction: eosinophil | Confidence: 99.59%

Flag

Clear

Submit

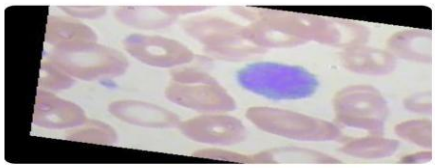
# Predict Blood Cell Type

Upload an image of a blood cell to determine its type using our state-of-the-art classification model.

Choose file _5_9201.jpeg Predict

## Prediction Result

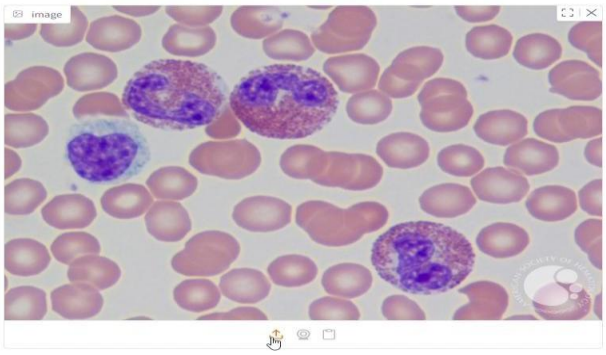
**Predicted Class:** lymphocyte



Upload Another Image

**Blood Cell Classifier**

Upload a blood cell image to classify.




output

Prediction: eosinophil | Confidence: 100.00%

Flag

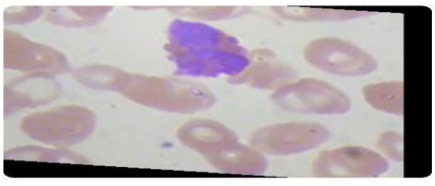
# Predict Blood Cell Type

Upload an image of a blood cell to determine its type using our state-of-the-art classification model.

Choose file _3_9885.jpeg Predict

## Prediction Result

**Predicted Class:** eosinophil



Upload Another Image

# 8. Advantages and Disadvantages

**Advantages:-**

**1. High Accuracy & Generalization:**
By leveraging MobileNetV2 (transfer learning from ImageNet), the model achieves high classification accuracy even with a moderate dataset size.
Fine-tuning helps it generalize well to new, unseen blood cell images.

**2. Reduced Training Time**
Transfer learning eliminates the need to train a model from scratch, saving time and computational resources.

**3. User-Friendly Web Application**
The Flask-based interface allows users (doctors, technicians) to upload images and get predictions without technical expertise.

**4. Portable and Lightweight**
The model size is small (MobileNetV2 is optimized for mobile/edge deployment) → can be deployed on local servers or even edge devices.

**5. Supports Resource-Constrained Settings**
No need for large, expensive diagnostic equipment — works on standard computers or low-end servers.

**Disadvantages:-**

**1. Limited Class Scope**
The model only classifies four types of blood cells (Eosinophil, Lymphocyte, Monocyte, Neutrophil).
It does not cover rare or abnormal cell types (e.g., blast cells in leukemia).

**2. Dependent on Image Quality**
The model's accuracy relies heavily on the quality and resolution of uploaded images.
Poor lighting, focus, or staining issues can lead to misclassification.

**3. No Explainability**
Deep learning models like MobileNetV2 are black-boxes → no direct insight into why a prediction was made, which may reduce trust in medical contexts.

**4. Manual Data Management**
The app saves images temporarily in the static/ folder but has no automatic cleanup or database integration (risk of storage bloat over time).

**5. No Real-Time Feedback / Retraining**
The model doesn't learn from its mistakes — no feedback loop to improve on misclassified images without retraining externally.

# 9. CONCLUSION

The HematoVision project successfully demonstrates the use of deep learning and transfer learning to automate the classification of blood cell images. By integrating a fine-tuned MobileNetV2 model into a lightweight Flask web application, we have created an accessible and efficient tool for blood cell type prediction.

Our system allows healthcare professionals and laboratory technicians to upload blood smear images and instantly receive classification results for Eosinophils, Lymphocytes, Monocytes, and Neutrophils, significantly reducing manual effort and diagnostic time.

The use of transfer learning ensures high accuracy even with moderate data availability, while the user-friendly web interface makes the tool suitable for deployment in resource-constrained or remote environments.

While the model performs well on standard images, its effectiveness can be further improved by incorporating additional blood cell classes, handling noisy or low-quality images, and adding explainability features for medical validation.

In summary, HematoVision provides a strong foundation for AI-powered hematology diagnostics and can be extended for broader clinical applications with future enhancements.

# 10. Future Scope

**1. Expansion to More Cell Types**
Extend the model to classify additional blood cell types, including abnormal cells (e.g., blast cells, myelocytes) to aid in diagnosing conditions like leukemia and other blood disorders.

**2. Integration of Explainable AI (XAI)**
Implement techniques such as Grad-CAM or SHAP to provide visual explanations of model predictions, enhancing trust and acceptance among healthcare professionals.

**3. Mobile and Edge Deployment**
Optimize and deploy the model on mobile devices or edge devices for offline, real- time analysis in remote or resource-limited settings.

**4. Continuous Learning and Feedback Loop**
Incorporate mechanisms to allow user feedback on predictions, enabling the system to improve over time through active learning.

**5. Cloud-Based Diagnostic Platform**
Integrate the solution with cloud services to enable large-scale data storage, model updates, and remote access for multiple labs and clinics.

**6. Automated Data Management**
Enhance the backend with automated cleanup of uploaded images and logs, and potentially integrate with medical record systems or databases.

**7. Dataset Augmentation and Synthetic Data**
Leverage synthetic data generation (e.g., GANs) to enrich training datasets, improving the model's ability to generalize to rare cell types or noisy images.

# 11. Appendix

## Source codes:

**app.py :**

```
from flask import Flask, request, render_template, redirect from
tensorflow.keras.models import load_model
from tensorflow.keras.applications.mobilenet_v2 import preprocess_input
import numpy as np
import cv2
import os
import base64

app = Flask(__name__)

# Load the trained model
model = load_model("blood_cell.h5", compile=False) #
Define class labels
class_labels = ['Eosinophil', 'Lymphocyte', 'Monocyte', 'Neutrophil']

# Prediction function
def predict_image_class(image_path, model):
    img = cv2.imread(image_path)
    img_rgb = cv2.cvtColor(img, cv2.COLOR_BGR2RGB)
    img_resized = cv2.resize(img_rgb, (128, 128))
    img_preprocessed = preprocess_input(img_resized.astype(np.float32).reshape((1, 128, 128,
3)))
    predictions = model.predict(img_preprocessed)
    predicted_class_idx = np.argmax(predictions, axis=1)[0]
    predicted_class_label = class_labels[predicted_class_idx] return
    predicted_class_label, img_rgb

# Home + Upload Route
@app.route("/", methods=["GET", "POST"])
def upload_file():
    if request.method == "POST":
        if "file" not in request.files or request.files["file"].filename == "": return
            redirect(request.url)

        file = request.files["file"]
        filename = file.filename
        file_path = os.path.join("static", filename)
```

```
        file.save(file_path)

        predicted_class_label, img_rgb = predict_image_class(file_path, model) #

        Convert image to base64 for HTML display
        _, img_encoded = cv2.imencode('.png', cv2.cvtColor(img_rgb, cv2.COLOR_RGB2BGR))
        img_str = base64.b64encode(img_encoded).decode('utf-8')

        return render_template("result.html",
                               class_label=predicted_class_label,
                               img_data=img_str,
                               image_name=filename)

    return render_template("home.html") if _

name_ == "_main_":
    app.run(host='0.0.0.0', port=5000, debug=True)
```

**home.html :**

```
<!DOCTYPE html>
<html lang="en">
<head>
    <meta charset="UTF-8">
    <title>Predict Blood Cell Type</title>
    <link href="https://cdn.jsdelivr.net/npm/bootstrap@5.3.0/dist/css/bootstrap.min.css" rel="stylesheet">
    <style>
        body {
            background: linear-gradient(to right, #f8f9fa, #ffffff);
            height: 100vh;
            display: flex;
            align-items: center;
            justify-content: center;
        }
        .card {
            border: none; border-
            radius: 16px;
            box-shadow: 0 8px 20px rgba(0, 0, 0, 0.1);
        }
        .btn-upload {
            background-color: #e74c3c; color:
            white;
        }
        .btn-upload:hover {
```

```
        background-color: #c0392b;
      }
      .title {
        font-weight: 700;
        color: #e74c3c;
      }
    </style>
</head>
<body>
    <div class="card p-5" style="max-width: 500px; width: 100%;">
      <div class="text-center">
        <h1 class="title mb-3"> Predict Blood Cell Type</h1>
     <p class="mb-4">Upload an image of a blood cell to determine its type using our AI model.</p>
      </div>
      <form method="POST" enctype="multipart/form-data" action="/">
        <div class="mb-4">
          <input class="form-control form-control-lg" type="file" name="file" required>
        </div>
        <div class="d-grid">
          <button type="submit" class="btn btn-upload btn-lg">Predict</button>
         </div>
       </form>
    </div>
  </body>
  </html>
```

**result.html :**

```
<!DOCTYPE html>
<html lang="en">
<head>
    <meta charset="UTF-8">
    <title>Prediction Result</title>
    <link href="https://cdn.jsdelivr.net/npm/bootstrap@5.3.0/dist/css/bootstrap.min.css" rel="stylesheet">
    <style>
      body {
        background: linear-gradient(to right, #f8f9fa, #ffffff);
        height: 100vh;
        display: flex;
        align-items: center;
        justify-content: center;
      }
```

```
      .card {
        border: none; border-
        radius: 16px;
        box-shadow: 0 8px 20px rgba(0, 0, 0, 0.1);
        max-width: 550px;
        width: 100%;
      }
      .btn-back {
        color: white;
        background-color: #e74c3c;
      }
      .btn-back:hover {
        background-color: #c0392b;
      }
      .result-label { color:
        #3498db; font-
        weight: 600;
      }
    </style>
</head>
<body>
    <div class="card p-5 text-center">
      <h2 class="mb-4 text-success"> Prediction Result</h2>
     <img src="{{ img_data }}" class="img-fluid rounded shadow
mb-4" style="max-height: 300px;">
       <h4>redicted Class: <span class="result-label">{{ class_label }}</span></h4>
      <p>      Filename: <strong>{{ image_name }}</strong></p>
      <a href="/" class="btn btn-back mt-4 px-4">■ Try Another</a>
     </div>
  </body>
  </html>
```

**Dataset link:** **https://www.kaggle.com/datasets/paultimothymooney/blood-cells/data**

**Project link:** https://colab.research.google.com/drive/1nnHWn4UKBKx6oxfna4zrmP5ovKtj4S5b

**Demo link:**

https://drive.google.com/file/d/1Fn6HTHfAA1PcC5Z_RBEgUgTjzyjEOQwQ/view?usp=drivesdk