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# Sickle Cell Anemia Detection Using Convolutional Neural Network

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**ABSTRACT:** Sickle Cell Anemia (SCA) is a prevalent genetic blood disorder characterized by abnormal hemoglobin causing red blood cells to take on a distinct sickle shape. Early and accurate detection of SCA is essential for effective treatment and management. This study presents an innovative approach to SCA detection utilizing Convolutional Neural Networks (CNNs), a class of deep learning algorithms known for their effectiveness in image analysis tasks. The proposed method involves the use of microscopic images of blood smears from patients. These images are preprocessed to enhance contrast, normalize intensities, and remove noise. Subsequently, CNN architectures are employed to automatically extract hierarchical features from the blood smear images. The trained CNN model learns discriminative features directly from the images, effectively capturing subtle differences between normal and sickled red blood cells (RBCs).

**KEYWORDS:** Sickle Cell Anemia, convolutional neural network, deep learning, image analysis, blood smear images, early detection, diagnostic tool.

## I. INTRODUCTION

Sickle Cell Anemia (SCA) is a hereditary blood disorder caused by a genetic mutation that affects the structure of hemoglobin, the protein responsible for carrying oxygen in red blood cells. This genetic alteration leads to the distinctive sickle shape of red blood cells (RBCs) and results in various complications, including pain, anemia, organ damage, and a decreased lifespan. Traditionally, SCA diagnosis involves manual examination of blood smears under a microscope to identify the characteristic sickled RBCs. However, this process can be time-consuming, labor-intensive, and subject to inter-observer variability. As technology advances, there is a growing interest in leveraging machine learning techniques, particularly Convolutional Neural Networks (CNNs), to automate and enhance the SCA detection process.

Convolutional Neural Networks are a class of deep learning algorithms designed to process and analyze visual data, such as images and videos. They have demonstrated remarkable success in various image analysis tasks, including object recognition, image segmentation, and medical image classification.

## II. OBJECTIVES

To develop and evaluate a Convolutional Neural Network (CNN)-based method for the automatic detection of Sickle Cell Anemia (SCA) from microscopic blood smear images.

This study aims to contribute to the advancement of automated SCA detection using CNNs, potentially revolutionizing the way SCA is diagnosed, increasing accessibility to diagnostics, and improving patient outcomes.

## III. EXISTING SYSTEM

Gather a dataset containing relevant features for each patient. Choose the most relevant features that are likely to influence the presence of sickle cell Anemia Split the dataset into training and testing sets. The training set is used to train the SVM model, and the testing set is used to evaluate its performance. Choose an appropriate kernel function for your SVM. Common choices include linear, polynomial, and radial basis function (RBF) kernels. Train the SVM model using the training data. The model will learn to differentiate between patients with sickle cell anemia and those without

based on the provided features .Evaluate the trained model using the testing data. Common evaluation metrics for classification problems include accuracy, precision, recall, F1-score, and ROC curves .Once the model is trained and evaluated, it can be used to predict whether new patients have sickle cell anemia based on their feature data.

### 3.1 ARCHITECTURE OF EXISTING SYSTEM

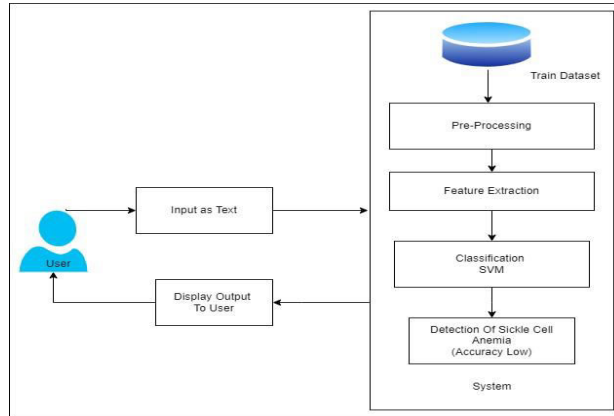


Figure 3.1: System Architecture

### 3.2 LIMITATIONS OF EXISTING SYSTEM

SVMs are sensitive to the scale of input features.

SVMs, especially non-linear kernels, require a relatively large amount of data to perform well.

Training SVMs, especially with non-linear kernels, can be computationally intensive, making them less suitable for real-time applications or large-scale datasets.

## IV. PROPOSED SYSTEM

### ARCHITECTURE

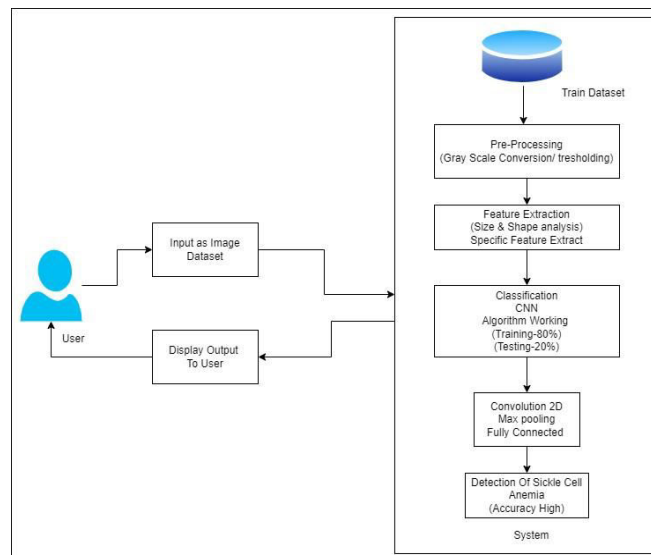


Figure 4.1: Proposed Architecture

### 4.1 Module

- Admin
- In this module,the Admin has to log in by using valid user name and password.

After login successful he can do some operations such as View All Users and Authorize,

- View and Authorize Users
- In this module, the admin can view the list of users who all registered. In this, the admin can view the user's details such as, user name, email, address and admin authorizes the users.
- End User
- In this module, there are n numbers of users are present. User should register before doing any operations. Once user registers, their details will best or to the database. After registration successful ,he has to login by using authorized user name and password.

## 4.2 SOFTWARE REQUIREMENT SPECIFICATION

### 4.2.1 Requirement Analysis

#### 4.2.1.1 Functional Requirements

System Feature1(Functional Requirement)

**Admin:** Admin module will be on web module. Admin will verify user information and allow or reject to user. Load the Data set.

**User:** User registers into system with personal information. Automatically user verification request send to admin. After verification user can login into system.

System Feature2(Functional Requirement)

**System:** By using CNN algorithm, Enhance Machine learning techniques like CNN for the Sickle cell anemia detection.

## 4.2.2 EXTERNAL INTERFACE REQUIREMENT

### 4.2.2.1 User Interface

- Application of Sickle cell anemia detection.

### 4.2.2.2 Hardware Interfaces:

**RAM :** 8GB

As we are using Machine Learning Algorithm and Various High Level Libraries Laptop

RAM minimum required is 8 GB.

Hard Disk : 40 GB

Processor : Intel i5 Processor

Spyder IDE that Integrated Development Environment is to be used and data loading should be fast hence Fast Processor is required

### 4.2.4 Database Requirements

SQLITE

### 4.2.5 Software Requirements(Platform Choice)

- Operating system : Windows 7 or more.
- Coding Language : python
- IDE : Spyder

### 4.2.6 Hardware Requirements

- System : Intel I3 Processor and above.
- Hard Disk : 20 GB
- Ram : 8GB

## 4.3 DESIGN PHASE

In Data Flow Diagram ,we Show that flow of data in our system in DFD0 we show that base DFD in which rectangle present input as well as output and circle show our system ,In DFD1 we show actual input and actual output of system input of our system is text or image and output is rum or detected like wise in DFD 2 we present operation of user as well as admin.

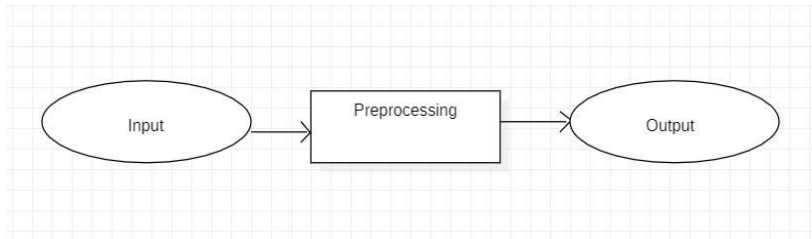


Figure 4.2: Data Flow(0) diagram

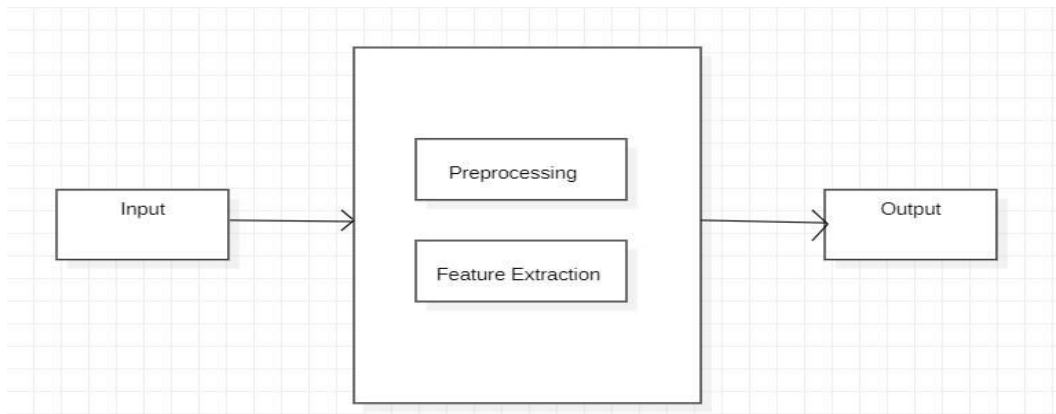


Figure 4.3: Data Flow(1) Diagram

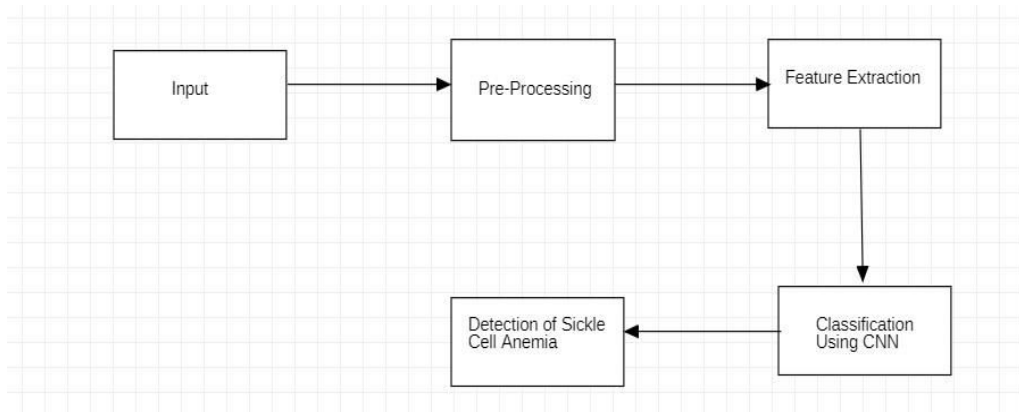


Figure 4.4: Data Flow(2) diagram

**4.3.2 Analysis Model: SDLC Model to be applied**

The software development cycle is a combination of different phases such as designing, implementing and deploying the project. These different phases of the software development model are described in this section. The SDLC model for the project development can be understood using the following figure. The chosen SDLC model is the waterfall model which is easy to follow and fits bests for the implementation of this project.

**ADVANTAGES**

- CNNs are specifically designed to extract hierarchical features from images.
- Sickle cell anemia detection often requires identifying subtle changes in cell shape and structure.
- Raditional methods of image analysis often involve manual feature extraction, which can be time-consuming and prone to human error.
- CNNs can leverage pre-trained models on large datasets for tasks related to image classification or feature extraction.



**DISADVANTAGE**

- CNNs, particularly deep architectures, require large datasets for effective training.
- Medical image datasets need to be meticulously annotated and labeled by experts, which is a labor-intensive and costly process.
- Medical images often require sophisticated preprocessing, such as noise reduction, contrast enhancement, and image registration.

**Test cases Test Result**

Test cases Test Results

Test Case ID	Test Case	Test Case I/P	Actual Result	Expected Result	Test case criteria(P/F)
001	Store Xml File	Xml file	Xml file store	Error Should come	P
002	Parse the xml file for conversion	parsing	File get parse	Accept	P
003	Attribute identification	Check individual Attribute	Identify Attributes	Accepted	P
004	Weight Analysis	Check Weight	Analyze Weight of individual Attribute	Accepted	P
005	Tree formation	Form them-Tree	Formation	Accepted	P
006	Cluster Evaluation	Check Evaluation	Should check Cluster	Accepted	P
007	Algorithm Performance	Check Evaluation	Should work Algorithm Properly	Accepted	P
008	Query Formation	Check Query Correction	Should check Query	Accepted	P

Figure 7.1: GUI TESTING

**V. FUTURE SCOPE**

The application of Convolutional Neural Networks (CNNs) for the detection of sickle cell anemia holds great promise in revolutionizing the way we diagnose, manage, and understand this complex genetic disorder. By leveraging the strengths of CNNs in image analysis and pattern recognition, we can potentially enhance early detection, automate diagnosis, and contribute to research efforts. The future of using CNNs for sickle cell anemia detection lies in advancing technology, interdisciplinary collaboration, and a deep understanding of the disease and patient needs.

**VI. CONCLUSION**

In conclusion, the proposed deep learning model, integrating histogram equalization and gray scaling for preprocessing along with data augmentation, demonstrates a promising approach for the precise classification of blood smear images into normal, sickle-shaped, and other blood components. The layered convolutional neural network effectively addresses the challenge of dataset scarcity through transformations applied via data augmentation techniques. The incorporation of histogram equalization enhances image contrast, contributing to improved model performance. The resulting 5-layer convolutional neural network proves to be a lightweight and low-complexity solution for the accurate classification of red blood cells, consequently enabling the prediction of Sickle Cell Disease. The model's capability for automatic detection and classification suggests its potential utility in clinical settings. As part of future work, enhancements in efficiency are anticipated through the implementation of advanced data augmentation techniques such as transfer learning, maintaining a commitment to maintaining a manageable level of model complexity.

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