CS6301

MACHINE LEARNING

PROJECT ON **Non-Invasive**

Anemia detection

(*From ACM April 2022 Paper:* iNAP: A Hybrid Approach for Non-Invasive Anemia-Polycythemia Detection in the IoMT)

Abstract

The project presents a novel, self-sufficient model called iNAP to address the shortcomings of anemia detection. The proposed model captures fingernail images using a smartphone camera and automatically extracts the fingernails as the regions of interest. A novel algorithm extracts the dominant color by analyzing color spectroscopy of the extracted portions and accurately predicts blood hemoglobin level. A less than a certain threshold value is categorized as anemia while a greater than that is non-anemic. The model incorporates machine learning and image processing techniques allowing easy smartphone implementation. Furthermore, a novel brightness adjustment algorithm is developed, allowing robustness to a wide illumination range and the type of device used. The proposed IoMT framework allows virtual consultations between physicians and patients, as well as provides overall public health information. The model thereby establishes itself as an authentic and acceptable replacement for invasive and clinically based hemoglobin tests by leveraging the feature of self-anemia diagnosis.

Introduction

Hematology is the study of blood and its related diseases. In medical terms this field is inclusive of blood disorders such as anemia, sickle-cell anemia, hemophilia, leukemia, and lymphoma, among others. Hemoglobin is a protein in the Red Blood Cells (RBCs) tasked with delivering oxygen to different organs and tissues in the body and transporting carbon dioxide back to the lungs. A healthy level of hemoglobin is therefore primarily required for the proper functioning of the body. However, increased red blood cell destruction due to pancreatic diseases, severe blood loss due to a significant injury or trauma, or an iron-deficient diet for a prolonged period, causes the hemoglobin level to drop below an optimal level. Clinically this condition is termed "Anemia". Therefore, we can define anemia as the dearth of blood hemoglobin (Hb).

To overcome the shortcomings of traditional invasive techniques of anemia detection, researchers shifted to a new category that does not involve any injection mechanism. They collectively constitute the "non-invasive" method of blood hemoglobin measurement. The significant advantage of these methods is their operational flexibility. With the advent of non-invasive methods, blood hemoglobin estimation became accessible through economical electronic gadgets, which implied that most of the population from low-middle income countries or rural areas could be effectively screened for anemia.

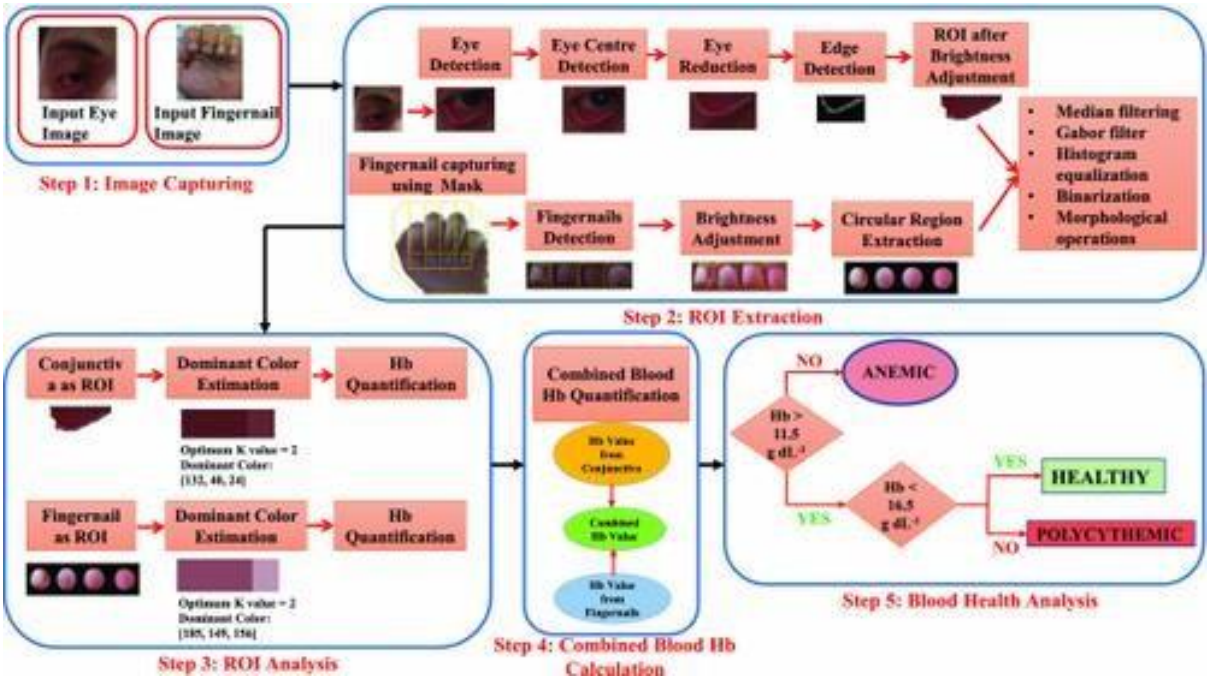
Problem Statement

Around the globe, 1.62 billion people are anemic, which corresponds to 25% of the entire world population, and it is the low and middle-income populations which make up the majority. Worldwide among the female, male, and children population, anemia is highly prevalent among women and children (47.4%) and relatively less prevalent in adult males (12.7%) [24]. Data from the World Health Organization (WHO) regional estimates indicate that the highest number of anemia affected individuals are in Southeast Asia (about 315 million individuals). In India, 21.7% of the male and 53.24% of the female population are clinically termed as anemic [9]. Anemia is predominant in pregnant women, malnourished children, and older adults (more than 60 years of age). Therefore, anemia constitutes a significant threat to public health, making its fast and efficient detection primarily important. Traditionally blood hemoglobin is measured by the syringe injection and blood extraction method. Techniques based on similar concepts collectively constitute the “invasive” method of blood hemoglobin measurement. However, they are excruciating, protracted, dicey, and involves the expertise of trained physicians. All these factors make the invasive method unobtainable and unfeasible for peripheral people living especially in low-middle income countries (LMC), resulting in unchecked blood hemoglobin levels among most of their population.

Overall Objective:

This project is aimed towards contributing to the non-invasive blood hemoglobin measurement domain. We have proposed a model that automatically extracts multiple regions of interest for a highly accurate prediction. The fingernail images are captured as inputs. Then, employing image processing, a prediction of the patient's blood hemoglobin level is made. The prediction is numerically quantified, similar to the Gold Standard method of hemoglobin measurement. Based on the standard thresholds mentioned, participants have been grouped into anemic, and healthy categories. The data set used for the study is appropriately balanced with equal proportions of all three categories and a wide age range. Finally, using the obtained predictions and the IoMT platform, we will implement the feature of virtual consultations and provide accurate statistical information regarding the surveyed area's overall public health that can be utilized by the health administrators.

System Model (Block Diagram):



Code:

We have used Python as the programming language to code for our project.

Data pre-processing

- Getting the dataset

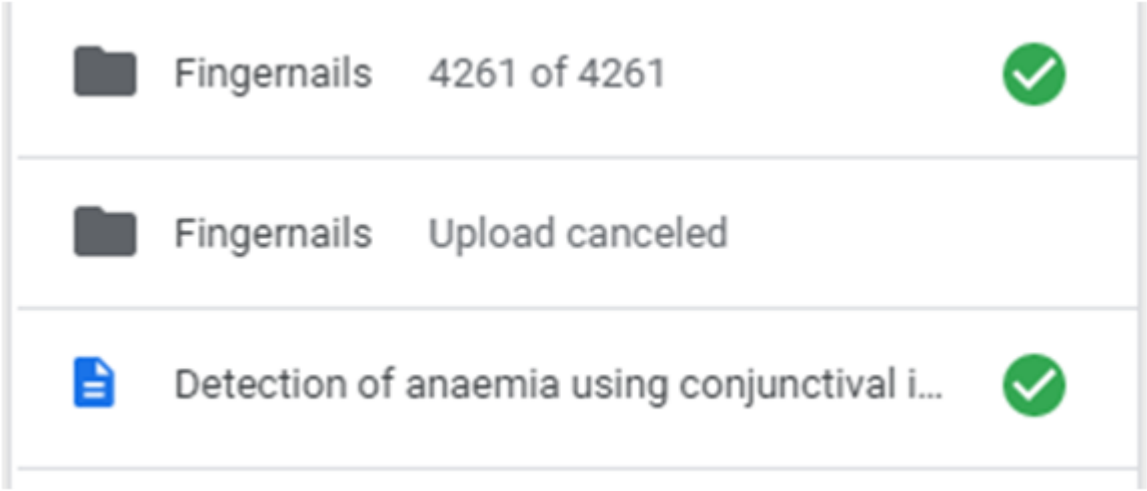
  Source link for Fingernails dataset:

  https://data.mendeley.com/datasets/2xx4j3kjg2

- Importing the Libraries

```
import tensorflow
import keras
import os
from skimage import io
import numpy as np
import pandas as pd
import csv
from google.colab.patches import cv2_imshow
from sklearn.model_selection import train_test_split
import matplotlib.pyplot as plt
import math
```

- Importing the datasets



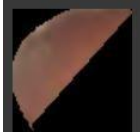
All files are first uploaded to google drive

The drive is then mounted in google colab, where it can then be accessed in the code.

All the images in the fingernail dataset can be accessed as well, as shown from this example

```
myImg = io.imread("drive/MyDrive/Fingernails/Fingernails/Anemic-FN-056.png")
cv2_imshow(myImg)
```

```
myImg = cv2.imread("drive/MyDrive/Fingernails/Fingernails/Non-Anrmic-FN-195.png")
#print(myImg)
cv2_imshow(myImg)
print(myImg)
cv2_imshow(cv2.cvtColor(myImg, cv2.COLOR_BGR2RGB))
```



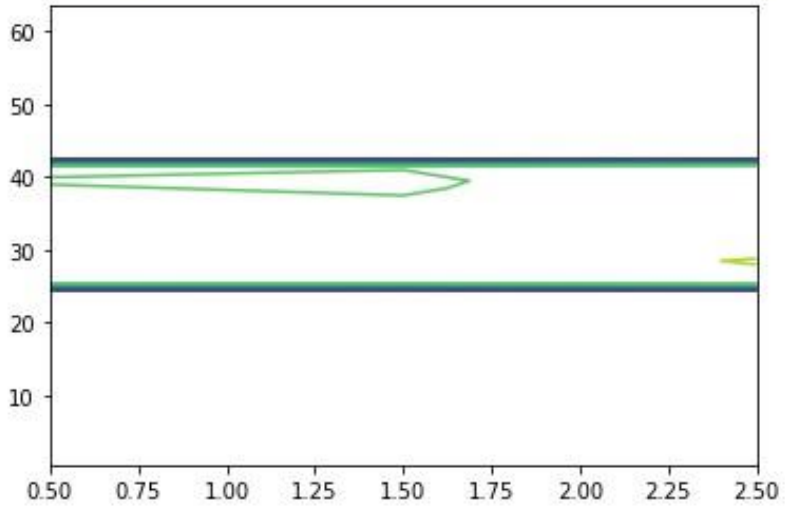
Handling the data

```
def load_data(data_dir):
  images=[]
  dc=[]
  anemic=[]
  i=j=0
  for pics in os.listdir(data_dir):
    if pics[0:3]=='Non':
      #if i==100:
      #  continue
      anemic.append(1)
      #i+=1
    else:
      #if j==100:
      #  continue
      anemic.append(0)
      #j+=1
    print(i,j)
    img=cv2.imread(os.path.join(data_dir,pics),1)
    img=AdaptBrightness(img)
    d = DominantColors(img)
    clrs=d.dominantColors()
    dc.append(d.MAXFREQ)
    img=cv2.resize(img, (200,200), interpolation = cv2.INTER_AREA)
    images.append(np.array(img))

    #if i==100 and j==100:
    #  break
  return images,dc,anemic
```

```
imgs,dc,anemic=load_data("drive/MyDrive/Fingernails/Fingernails")
```

```
[18] plt.contour(cv2.cvtColor(myImg, cv2.COLOR_BGR2RGB)[0], origin = "image")
```

```
<matplotlib.contour.QuadContourSet at 0x7f4bd75dee50>
```



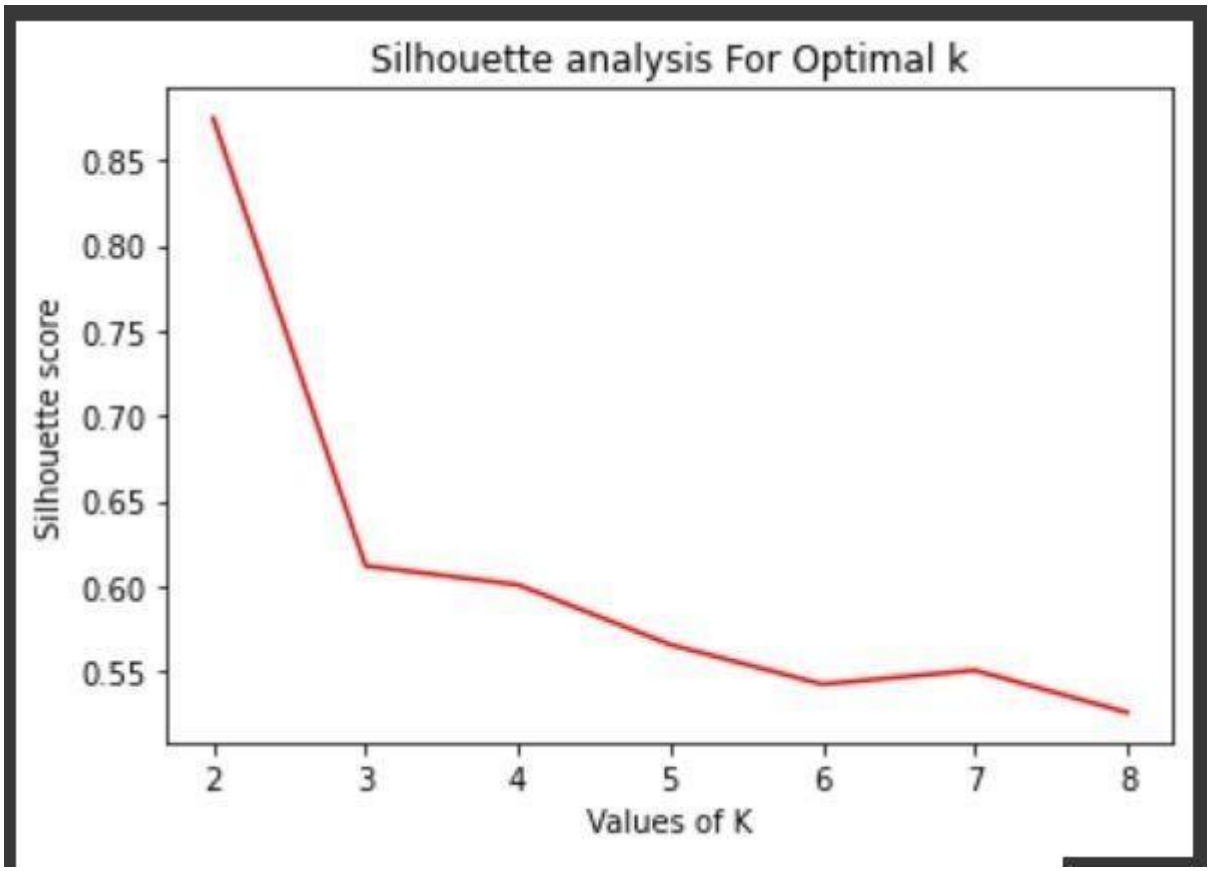
Splitting the data

```
from sklearn.neural_network import MLPClassifier
from sklearn.datasets import make_classification
from sklearn.model_selection import train_test_split
import pandas as pd
import numpy
dc1=numpy.array(dc).T
df1 = pd.DataFrame(dc, columns = ['R','G','B'])
X_train, X_test, y_train, y_test = train_test_split(df1, anemic, train_size=0.6)
```

Silhouette Analysis:

Silhouette analysis can be used to study the separation distance between the resulting clusters. The silhouette plot displays a measure of how close each point in one cluster is to points in the neighboring clusters and thus provides a way to assess parameters like number of clusters visually.

Prior to using K Means Clustering, silhouette score is used to find the optimal k value for each image.



K means Clustering:

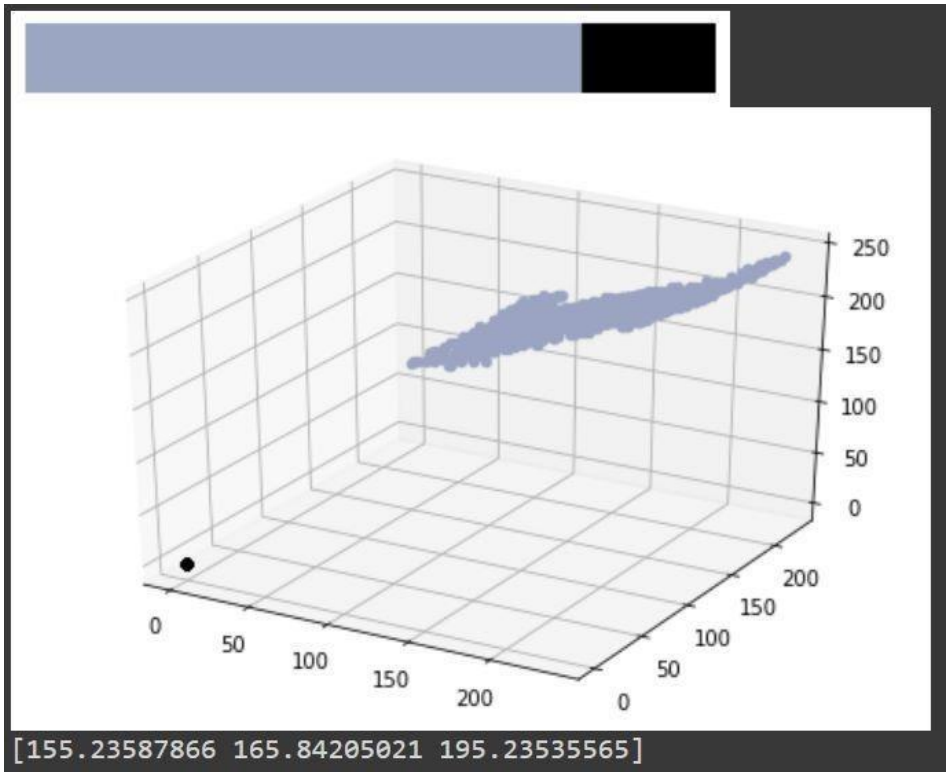
```
[ ]  import cv2
     from sklearn.cluster import KMeans
     import pandas as pd
     import matplotlib.pyplot as plt
     import seaborn as sns
     import sklearn
     from sklearn.cluster import KMeans
     from sklearn.metrics import silhouette_score
     import matplotlib.pyplot as plt
     from mpl_toolkits.mplot3d import Axes3D

     class DominantColors:

         CLUSTERS = None
         IMAGE = None
         COLORS = None
         LABELS = None
         MAXFREQ = None

         def __init__(self, image, clusters=3):
             self.CLUSTERS = clusters
             self.IMAGE = image

         def dominantColors(self):
             #img = cv2.imread(self.IMAGE)
             img = cv2.cvtColor(self.IMAGE, cv2.COLOR_BGR2RGB)
             img = img.reshape((img.shape[0] * img.shape[1], 3))
             self.IMAGE = img
             range_n_clusters = [2, 3, 4, 5, 6, 7, 8]
             silhouette_avg = []
             for num_clusters in range_n_clusters:

             # initialise kmeans
               kmeans = KMeans(n_clusters=num_clusters)
```

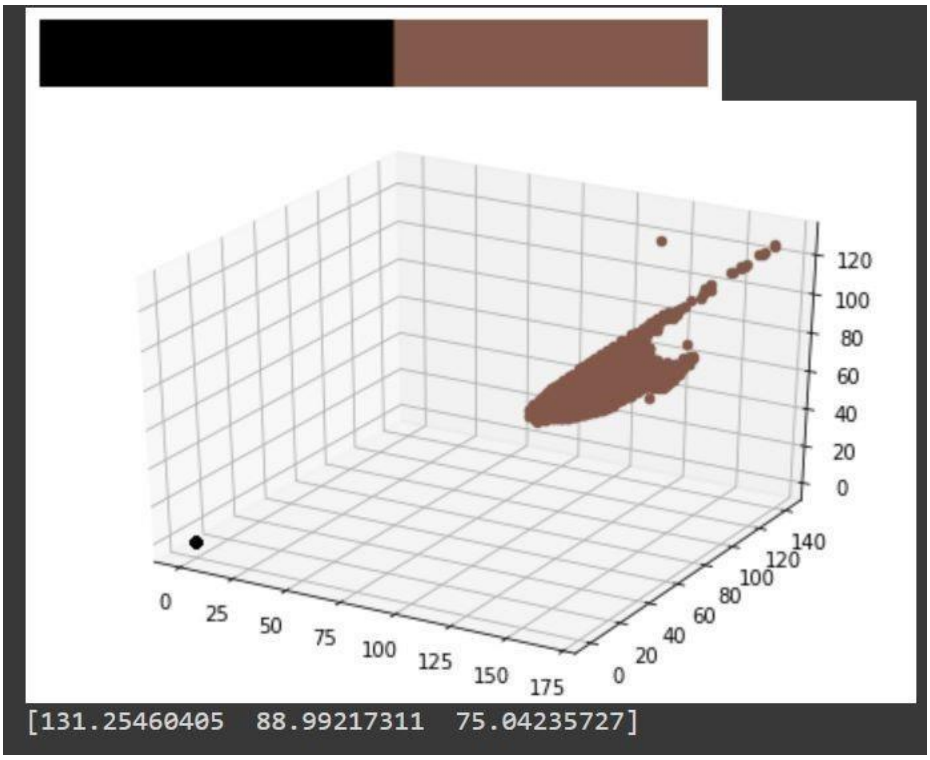
```
[ ]
            kmeans.fit(img)
            cluster_labels = kmeans.labels_

            # silhouette score
            silhouette_avg.append(silhouette_score(img, cluster_labels))
        k=range_n_clusters[silhouette_avg.index(max(silhouette_avg))]
        self.CLUSTERS=k
        kmeans = KMeans(n_clusters = k)
        kmeans.fit(img)
        self.COLORS = kmeans.cluster_centers_
        self.LABELS = kmeans.labels_
        self.calcmaxfreq()
        return self.COLORS.astype(int)
    def calcmaxfreq(self):
        #labels form 0 to no. of clusters
        numLabels = np.arange(0, self.CLUSTERS+1)

        #create frequency count tables
        (hist, _) = np.histogram(self.LABELS, bins = numLabels)
        hist = hist.astype("float")
        hist /= hist.sum()

        #appending frequencies to cluster centers
        colors = self.COLORS
        #descending order sorting as per frequency count
        colors = colors[(-hist).argsort()]
        hist = hist[(-hist).argsort()]
        if colors[0].astype('int')[0] == 0 and colors[0].astype('int')[1] == 0 and colors[0].astype('int')[2] == 0:
          self.MAXFREQ=colors[1]
        else:
          self.MAXFREQ=colors[0]
    def plotHistogram(self):

        #labels form 0 to no. of clusters
        numLabels = np.arange(0, self.CLUSTERS+1)
```

```
[ ]         #create frequency count tables
            (hist, _) = np.histogram(self.LABELS, bins = numLabels)
            hist = hist.astype("float")
            hist /= hist.sum()

            #appending frequencies to cluster centers
            colors = self.COLORS
            #descending order sorting as per frequency count
            colors = colors[(-hist).argsort()]
            hist = hist[(-hist).argsort()]
            #creating empty chart
            chart = np.zeros((50, 500, 3), np.uint8)
            start = 0
            if colors[0].astype('int')[0] == 0 and colors[0].astype('int')[1] == 0 and colors[0].astype('int')[2] == 0:
              self.MAXFREQ=colors[1]
            else:
              self.MAXFREQ=colors[0]
            #creating color rectangles
            for i in range(self.CLUSTERS):
                end = start + hist[i] * 500

                #getting rgb values
                r = colors[i][0]
                g = colors[i][1]
                b = colors[i][2]

                #using cv2.rectangle to plot colors
                cv2.rectangle(chart, (int(start), 0), (int(end), 50), (r,g,b), -1)
                start = end

            #display chart
            plt.figure()
            plt.axis("off")
            plt.imshow(chart)
            plt.show()
```

```
        def rgb_to_hex(self, rgb):
            return '#%02x%02x%02x' % (int(rgb[0]), int(rgb[1]), int(rgb[2]))

        def plotClusters(self):
            #plotting
            fig = plt.figure()
            ax = Axes3D(fig)
            for label, pix in zip(self.LABELS, self.IMAGE):
                ax.scatter(pix[0], pix[1], pix[2], color = self.rgb_to_hex(self.COLORS[label]))
            plt.show()


    dc = DominantColors(myImg)
    colors = dc.dominantColors()
    dc.plotHistogram()
    dc.plotClusters()
    print(dc.MAXFREQ)
```

Output:


250
200
150
100
50
0
0
50
100
150
200
0
50
100
150
200
[155.23587866 165.84205021 195.23535565]



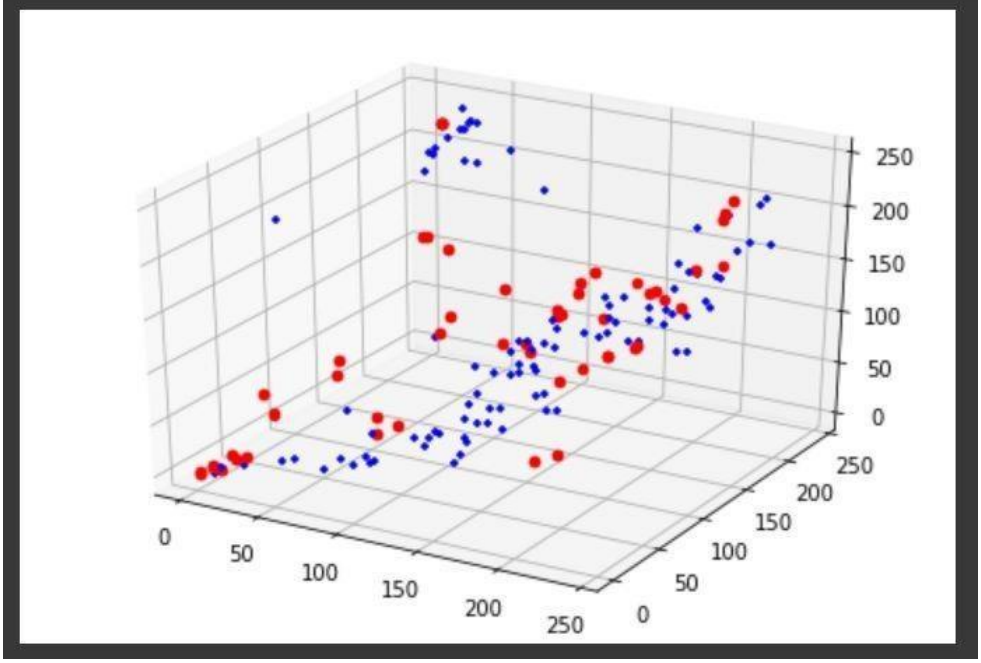

```
clf = MLPClassifier(hidden_layer_sizes=(150,100,50), max_iter=300,activation = 'relu',solver='adam',random_state=1).fit(df,anemic)
mlpanemia=clf.predict(df)
mlpanemia
```

```
array([1, 0, 1, 1, 0, 1, 0, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1,
       1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1,
       1, 1, 0, 1, 1, 0, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 1, 1,
       0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 1, 0, 0, 1, 1, 0, 1, 0, 1, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0,
       1, 1])
```

Using MLP we classified the samples as anemic or non-anemic(healthy)

For a sample of 200:

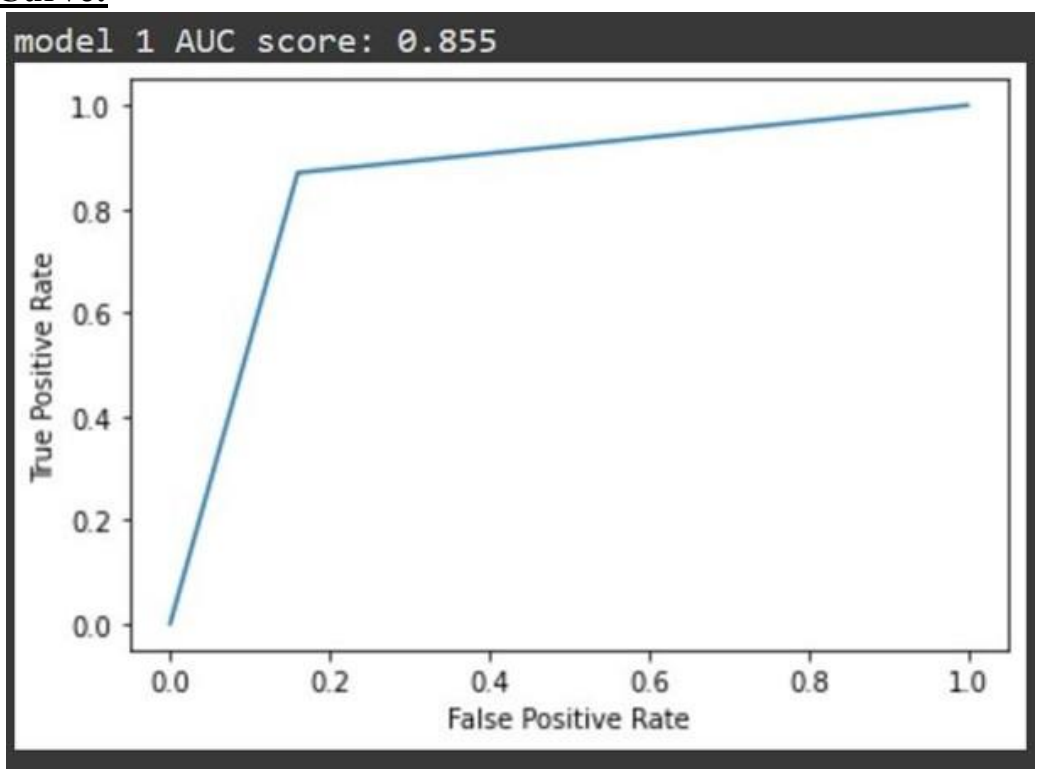
```
import numpy as np
import matplotlib.pyplot as plt

from mpl_toolkits import mplot3d
fig = plt.figure()
ax = Axes3D(fig)
dc1=dc[0:100]
dc2=dc[100:200]
for i in dc1:
  ax.scatter3D(i[0],i[1],i[2],marker='+',c='b')
for i in dc2:
  ax.scatter3D(i[0],i[1],i[2],c='r')
plt.show()
```



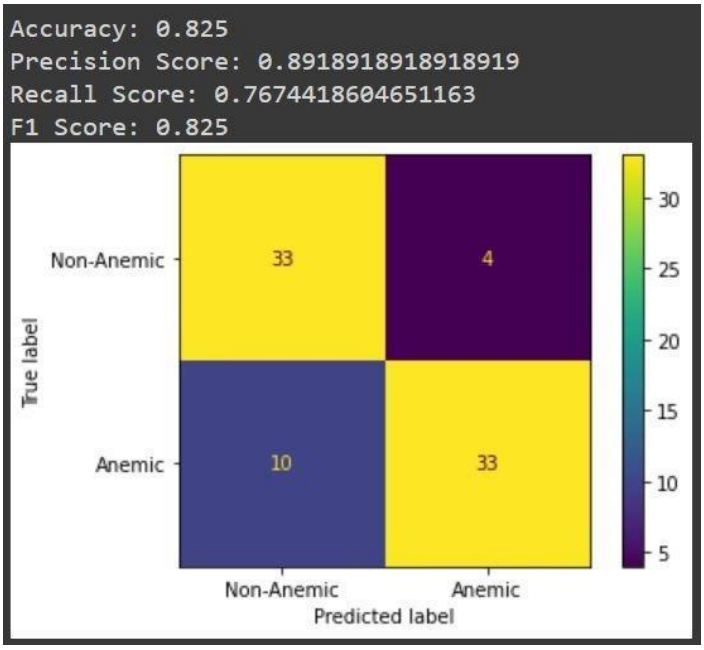
Performance Measures

```
ypred=clf1.predict(X_test)
import matplotlib.pyplot as plt
import numpy
from sklearn import metrics

actual = numpy.random.binomial(1,.9,size = 1000)
predicted = numpy.random.binomial(1,.9,size = 1000)

confusion_matrix = metrics.confusion_matrix(y_test, ypred)

cm_display = metrics.ConfusionMatrixDisplay(confusion_matrix = confusion_matrix, display_labels = ["Non-Anemic", "Anemic"])
print("Accuracy:",metrics.accuracy_score(y_test, ypred))
## Precision
print("Precision Score:",metrics.precision_score(y_test, ypred))
## Recall
print("Recall Score:",metrics.recall_score(y_test, ypred))
## F1 Score
print("F1 Score:",metrics.f1_score(y_test, ypred))
cm_display.plot()
plt.show()
```

ROC Curve:



Confusion Matrix



Conclusion:

For the project on Non-Invasive Anemia Detection based on ACM April 2022 Paper (iNAP: A Hybrid Approach for Non-Invasive Anemia-Polycythemia Detection in the IoMT), we have developed a model for Anemia detection in patients. The project involves the use of Machine Learning algorithms like K-Means Clustering and MultiLayer Perceptron (MLP) to classify individuals as either anemic or non-anemic. The fingernails image dataset has been used to obtain the results. Algorithms have been used to find out the dominant color from each image of the dataset and based on a certain threshold, KMeans and MLP algorithms have been applied to classify individuals as either anemic or non-anemic. The model has an accuracy of 0.825(82.5%), a precision score of 0.8918918918918919, a recall score of 0.7674418604651163 and a F1 score of 0.825.Thus, the project finds its application in the medical field where is applied to various scopes. Since it is a non-invasive method of anemia detection in patients, it is most preferable in the medical domain to detect anemia in patients.

References:

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