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An Automated System for the Classification of Fasting Lipid Profile Parameters using Image Processing withDeep Learning

Samuel Awuhe [1], Patience Orukpe2
[1]PhD Student, Department of Electrical/Electronic Engineering, University of Benin, Benin City, Edo State, Nigeria
[2]Professor, Department of Electrical/Electronic Engineering, University of Benin, Benin City, Edo State, Nigeria

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ABSTRACT— The disorder of lipid profile is a major modifiable risk factor for cardiovascular diseases including obesity, heart disease, diabetes, cancers etc. The abnormality in fasting lipid profile parameters such as total cholesterol, triglycerides, high-density lipoprotein cholesterol and low-density lipoprotein cholesterol accounts for millions of deaths annually. However, much attention has not been given to lipid profile testing probably because of lack of awareness due to limited testing machines or chemistry analyzers at health care centers especially in third world countries like Nigeria. Some of these analyzers are relatively expensive and are operated by well-trained chemical pathologists. Therefore, developing a deep learning based system for classifying lipid profile parameters will provide another means of carrying out fast lipid profile testing for early and proper management of lipid profile disorder. This is because the proposed deep learning model is software based and can be deployed on laptop, desktop or smart phone for use at health care centers where there are limited resources to procure analyzers. The deep learning model, which applies transfer learning using squeezenet CNN, was trained on lipid profile dataset. The trained model produced an accuracy of 90.6%, which shows that such a method can be deployed for lipid testing.

KEYWORDS—Convolutional neural network, Low-density lipoprotein cholesterol, Squeezenet, Transfer learning, Dataset

I. INTRODUCTION

The disorder of lipoprotein metabolism, which results in high lipid profile, is a major modifiable risk factor for several chronic non-infectious diseases including Coronary Heart Diseases (CHDs) and stroke [1]. Lipid profile disorder is caused by elevated levels of Total Cholesterol (TC) in the blood, an increase in blood Triglyceride (TG) levels, high levels of Low-Density Lipoprotein Cholesterol (LDL-C) and reduced High-Density Lipoprotein Cholesterol (HDL-C) levels [2].

Abnormality in lipid profile accounts for more than four million deaths annually [3]. The study of lipid profile disorder has become imperative since lipid level variations in the blood of humans are known to play a major role in several diseases affecting millions of people including obesity [4], diabetes [9], hypertension [10] and cancers [11].

The pattern of lipids or fats in the blood is referred to as lipid profile and the progressive hardening of arteries is caused by lipid deposits in the arteries of an adult[5]. Therefore, screening for lipid profile abnormality in children and adults as a major risk factor for CHDs is very important. Lipid profile test is usually employed by physicians for screening lipid profile disorders. The test uses a blood component called serum or plasma for estimating levels of lipid parameters in the blood. The lipid parameter samples are normally prepared in white plastic containers called cuvettes or test tubes and are analyzed by chemistry analyzers, spectrophotometer or photometers for further interpretation of results by experienced chemical pathologists.

Recently, Computer-Aided Diagnosis (CAD) has been applying data mining techniques to interpret medical records and it has been found to improve the accuracy of diagnosis, which can be used to predict the risk of lipid profile disorder in subjects [6]. Deep learning convolutional neural networks have also recorded some breakthrough in computer vision and image processing which automatically extract the features required for image classification [7]. Deep learning feature extraction using convolutional neural network has demonstrated good classification performance in the field of machine learning [8]. Therefore, with the application of machine learning (ML) algorithms in health care

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system, the process of analyzing samples of lipid profile parameters during lipid profile testing with chemistry analyzers to determine the concentration of lipid levels in the blood can be automated.

II. SIGNIFICANCE OF THE PROPOSED SYSTEM

Abnormality in lipid profile is an underlying risk factor for some abnormal medical conditions such as obesity, diabetes, hypertension, arthritis and cancers. These diseases affect millions of people globally as stated by the World Health Organization report [3]; but there are limited fast and simple machines to analyze samples of lipid profile parameters during lipid profile testing especially in third world countries like Nigeria. The biochemistry analyzers found in well-established hospitals cannot be used without the assistance of well-trained and experienced chemical pathologists who understand how to operate these machines. Besides, these analyzers are relatively expensive and are not affordable by primary health care systems especially in rural and semi-urban areas. Therefore, developing a deep learning model for easy classification of lipid profile parameters can provide another means of carrying out lipid profile testing. The deep learning model is software-based and can be deployed on a laptop, desktop or smartphone for easy classification of blood lipid parameters. This will solve the problem of procuring an analyzer, which in most cases requires the services of a well-trained chemical pathologist for its operation. The deep learning model will provide widespread lipid profile testing opportunities for people to know the concentrations of their blood lipids for prompt and proper management without allowing their condition to degenerate into terminal illnesses [9-11].

III. LITERATURE REVIEW

This review is on some previous studies involving the measurement of lipid profile parameters.

Sapkota and Thapa [12] investigated the pattern of abnormal lipid profile to establish correlation between lipid profile and glycemic parameters such as fasting blood sugar, postprandial blood sugar and glycated haemoglobin in type-II diabetic patients. The result of the study proved that glycemic parameters were significantly elevated and that the most common pattern of abnormal lipid profile was decreased HDL-C and high level of TG. This study did not apply computer-aided diagnosis to classify levels of HDL-C and TG for predicting abnormal lipids in type-II diabetic patients.

Habiba et al.[13] investigated the association of abnormal lipids and the social economic status on non-diabetic children for the risk of developing type-II diabetes. They collected data on race, family history, body mass index percentile, blood pressure and presence of neck pigment from 149 non-diabetic children divided into high risk and low risk groups. Blood samples were drawn and tested for lipid profile in all the participating subjects. The findings of the study indicated that abnormal lipids of low HDL-C ($P<0.001$) and elevated TG ($P=0.02$) were significantly higher in the high-risk group showing a strong correlation with type-II diabetes risk. However, the abnormality of other lipid makers such as TC, LDL-C and high blood glucose levels was not significantly different among high risk and low risk groups.

Li et al. [14]carried out studies on traditional and novel lipid indices in predicting coronary severity by Gensini Score (GS) in 1605 non-lipid lowering drug treatment patients. All patients underwent clinical examinations and the concentrations of TC, TG, HDL-C and LDL-C were measured using biochemistry analyzer through the process of enzymatic array and turbid metric immunoassay. Findings from the study established that patients with higher GS belonged to the group of old people, people with hypertensions, people with diabetes, people with abnormal lipid profile and smokers.

Suneja et al.[15]investigated the correlation between serum uric acid and lipid profile in patients with untreated abnormal lipid profile. The study consisted of 70 patients of untreated abnormal lipid profile and 70 healthy people as control group. Anthropometric, physiological and biochemical parameters were used in the study. The association between uric acid level and other parameters in lipid profile were assessed by Pearson's correlation coefficient. The findings from the study showed significant higher levels of uric acid in subjects with abnormal lipid profile.

Najafipour et al. [16] investigated the association of coronary artery disease (CAD) risk factors and the prevalence of abnormal lipid profile. The epidemiological research involved the data of 5558 individuals based on baseline demographic variables and lipid measurements. Total cholesterol was measured using standard methods with enzymatic method and triglyceride was measured through standard spectrophotometric technique. High-density lipoprotein cholesterol was measured enzymatically and low-density lipoprotein was calculated using the Friedewald formula. The results of the study showed that the prevalence of undiagnosed abnormal lipid profile was 16.8% and 13.2% was diagnosed with abnormal lipid profile.

Wsoo and Hama [17] compared the accuracy of the concentrations of serum TC, TG and HDL-C between single beam visible Spectrophotometer and

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Reflotron analyzer. Ten individuals from Rania General Hospital Kurdistan, Iraq were selected for the study and 4-5 ml of blood samples were collected from the subjects after fasting for 9-10 hours. The serum samples were separated from the clotted blood by centrifugation at 4000 rpm for 10 minutes and were analyzed by visible Spectrophotometer and Reflotron analyzer. Significant differences were observed in the concentrations of the serum samples of TC, TG and HDL-C between the two approaches. The Spectrophotometric method produced mean values of 208.20 mg/dl, 198.60 mg/dl and 25.72 mg/dl for serum TC, TG and HDL-C respectively. The mean values of serum TC, TG and HDL-C for the Reflotron method were 182.20 mg/dl, 183.40 mg/dl and 30.33 mg/dl respectively. The results of TC and TG using the Spectrophotometric method were significantly higher than the results obtained by using the Reflotron method. However, the result of serum HDL-C produced by the Reflotron method was higher than the concentration of HDL-C measured by using Spectrophotometer. The study concluded that lipid profile measurement using Spectrophotometer was more accurate than lipid profile measurement using the Reflotron procedure.

IV. THE PROPOSED SYSTEM

The proposed system consists of an image acquisition system for capturing the images of lipid profile samples,thepre-processingstageand the application of deep learning algorithm for training images, which could produce a model for classifying blood lipid parameters.

V. IMPLEMENTATION OF PROPOSED SYSTEM

The implementation of the system for the classification of lipid profile parameters applies transfer learning with squeezenetpre-trained convolutional neural network for training images in the lipid profile dataset. The squeezenet pre-trained convolutional neural network (CNN) trains the images of lipid samples captured by the camera of an android phone to produce amodel for classifying lipid profile parameters. The block diagram of the proposed system implementation is shown in Fig. 1.

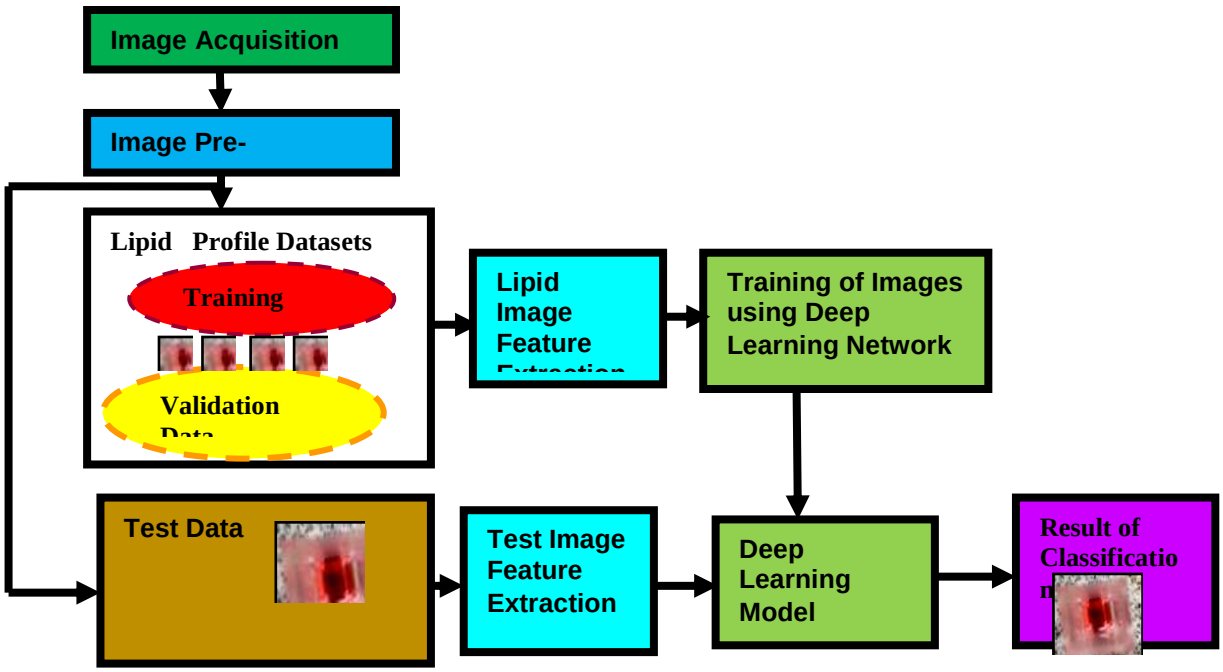

Fig. 1:Block diagram of the proposed model

VI. MATERIALS AND METHODS

The practical implementation of this system involves the connection of a techno android phone, which was connected to an HP Elite Book laptop through a universal serial port cable. The sample images of the lipid profile parameters were captured by the camera of the android phone and transferred to the laptop and adataset was created using these images. Squeezenet CNN was trained on the sample images in the lipid profile dataset to produce a model. New images of lipid parameters were captured by the techno phone and were used as test images against

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the trained model.

A. Data Collection

In this research, albino rats were used because it has been found in literature that some biomedical studies in mice or rat models have provided grounds for similar studies to be replicated in humans [18].

The study was performed on 300 out of the 345 albino rats enrolled for the experiment. The 345 rats (males and females) weighing 150g to 200g were obtained from an in- house breeding colony in Makurdi and were taken to the Department of Biochemistry at University of Agriculture, Makurdi. The rats were fed with local feeds prepared with maize for 10 to 14 weeks, kept on a twelve-hour day/night cycle and were housed in sterile micro isolator cages outside the Biochemistry laboratory. At the end of the 14^{th} week, 45 of the rats died leaving 300 animals. The 300 rats were divided into two groups consisting of 240 rats randomly selected for lipid development inducement and another group of 60 rats was used as control. The solution to inject 240 rats was prepared by dissolving 7 g of poloxamer 407 in 52 ml of cold normal saline.

After 2 weeks, the 240 subjects injected with the solution of poloxamer 407 were not fed for 12 hours before blood samples were taken in the morning of the next day. Professional chemical pathologist from the Department of Biochemistry took blood samples from the heart through cardiac puncture using sterile syringe and needle for each rat in preparation for serum. Each serum sample was separated from blood by centrifugation at 400 rpm for 10 minutes, stored at temperatures of +2 to 5℃ and the analysis was carried out in 48 hours. Serum TC, TG and HDL-C sample concentrations were analyzed using a standard ultraviolet/visible spectrophotometer which was operated at a wavelength of 500 nm whereas the concentrations of LDL-C samples were calculated using the direct method.

B. Acquisition of Lipid Profile Images

The camera of a techno phone running on android software with 3GB RAM, 16GB ROM, 1440×720 screen resolution, 13MP rear camera and a frequency of 1.3GHz specification was used for capturing the samples of lipid profile parameters as images. The concentration of the captured samples were grouped according to the results of samples analyzed on the ultraviolet/visible spectrophotometer.

C. Preprocessing of Lipid Profile Images

The image were down-sampled and resized to fit the input image requirement of the squeenet architecture. The bicubic interpolation method of the imresize function was implemented as one of the methods employed by image resizing technique. In this interpolation method, the output pixel value is the weighted average of pixels in the nearest 4×4 neighborhood in an image. The implementation of bicubic interpolation makes the resampled images to be smother with fewer interpolation artefacts.

D. Dataset

The images of lipid parameter samples were classified based on the US National Cholesterol Education Program (NCEP) Expert Panel Report [21]. The lipid profile dataset is made up of four lipid parameters namely TC, TG, HDL-C and LDL-C. Each lipid parameter was divided into three subclasses. The samples of each lipid parameter were classified based on the level or concentration of such a lipid parameter in the blood. The samples of TC for example, were classified into samples whose concentrations were regarded as being at borderline high, high or normal in the blood. Similarly, the concentrations of TG and HDL-C lipid parameter samples were classified as being at borderline high, high or normal. However, the concentrations of HDL-C lipid parameter samples were classified as being at borderline low, low or normal. Based on this classification, the lipid profile dataset contains twelve classes. Each class in the dataset contains seventy-five (75) images bringing the total of images in the dataset to nine hundred (900). Examples of images in the dataset are shown in Fig. 2.

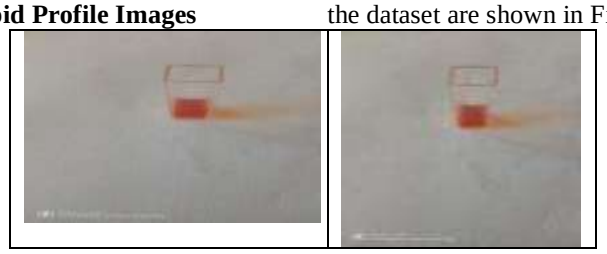

Fig. 2: Images of cholesterol samples

E. Image Feature Extraction

Feature detection and extraction from static and dynamic scenes have become an active area of research in computer vision and image processing. The concept of image feature detection and description refers to the process of identifying interest

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or key points that can be used to represent the content of an image such as corners, edges, ridges and blobs. Feature detection is a process of selecting regions of an image with unique content such as corners or blobs. The key to feature detection is to identify image features that remain locally invariant so that such features can be detected in the presence of scale changes or rotation. Feature extraction is an important aspect of image classification and detection. The similarity between two images can be determined through vector representation of image features. In a color image for example, the various features or properties used to represent an image are color, texture, shape and so on [19].

F. Training Convolutional Neural Network

Deep neural networks especially CNNs have proven to give high accuracy results in the area of image recognition [22]. Some of the pre-trained convolutional neural network classification models have convolutional, subsampling and softmax layers for class probability calculation and they include alexnet, squeezenet, googlenet, resnet, densenet, mobileNetv2, xception, and inception-v3 just to mention a few [20].

In this work, transfer learning was applied to train images in the lipid dataset using squeezenet pre-trained CNN to produce a robust model for classifying fasting lipid profile parameters. The images in the dataset were split into 80% of training set and 20% of validation set. Data augmentation was applied during the training of the network to prevent squeezenet model from memorizing training data.

By applying transfer learning with squeezenet, thenew classification layer in squeezenet was designed for 12 classes of the lipid profile dataset replacing the 1000 classes in the old layers. The weight learning rate and bias learning rate factors of the last convolutional layer was increased for new layers in the networks to learn faster. An augmented lipid image datastore was applied to transform batches of training and validation data with random reflection and translation preprocessing operations to help prevent the network from memorizing details of the training lipid images. The validation frequency value of 3Hz was specified to validate the squeezenet pre-trained network once per epoch. The maximum number of epochs used for training the lipid images was 8 and a mini-batch size of 15 observations at every epoch was adopted. The initial learning rate used for training the network was specified as 2×10^{-4} and the lipid images in the training set of the dataset was made to shuffle after every epoch.

The trained squeezenet network produced a model, which was used to classify new test lipid profile sample images into different fasting lipid parameters.

VII. RESULTS

The training plot of squeezenet pre-trained CNN shown in Fig. 3used transfer learning and was trained using Stochastic Gradient Descent with Momentum (SGDM) solver optimization algorithm to update network parameters such as weight and biases to minimize the loss function.

. The plot of confusion matrix used to evaluate the accuracy of the squeezenet model is as shown in Fig. 4.

Fig. 3: Plot of trained Squeezenet model

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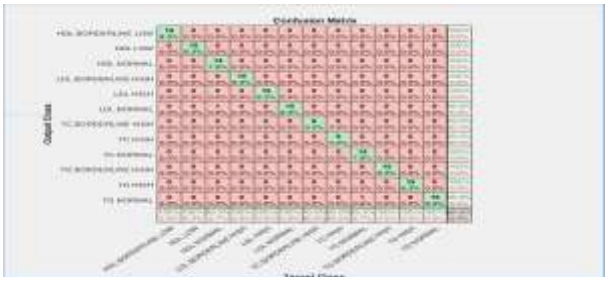

Fig. 4: Confusion matrix plot of the trained model

VIII. DISCUSSION OF RESULTS

As shown in Fig.3, the trained model reached maximum iterations of 384 in 39 minutes and 51 seconds producing an accuracy of 90.56% on validation data.The rows of the confusion matrix plot shown in Fig. 4 show the predicted class called the Output Class and the columns of the plot show the true class called the Target Class. The diagonal cells of the confusion matrix plot correspond to sample images of lipid profile parameters that were correctly classified whereas the off diagonal cells display incorrectly classified sample images of lipid parameters. The percentages of the green and red metrics in the column on the far right of the plot are the precision and false discovery rates respectively. Similarly, the percentages of the green and red metrics in the row at the bottom are called the true positive and true negative rates respectively. The cell in the bottom right of the plot comprises the percentages of green and red metrics called the overall classification accuracy and loss of samples respectively. It could be seen that the confusion matrix plot shows the overall accuracy of 90.6% and a loss of 2.6% using the 20% validation sample images, which were not used during training.

IX. CONCLUSION

This study has demonstrated that the proposed system, which applies the concepts of deep learning and image processing techniques, could be utilized effectively as another method of classifying blood lipid levels.

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