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Image Based Method for the Classification of Serum Cholesterol Concentrations using Deep Learning with Support Vector Machine

Samuel Awuhe[1], Inalegwu Bawa[2], Patience Orukpe[3]

[1]*Department of Electrical and Electronics Engineering, Federal University of Agriculture, Makurdi, Benue, Nigeria*
[2]*Department of Biochemistry, Federal University of Agriculture, Makurdi, Benue, Nigeria*
[3]*Department of Electrical/Electronic Engineering, University of Benin, Benin City, Edo, Nigeria*

Abstract - *Serum cholesterol or blood assessment have attracted attention further to the studies that has provided strong evidences that different forms of cholesterol levels are a major risk factor for cardiovascular diseases leading to death globally. However, the conventional methods of determining different forms of cholesterol levels are time consuming and are heavily reliant on medical professionals and chemistry analyzers. These are some of the major challenges experienced alongside the accuracy of results of cholesterol levels interpreted by physicians which are prone to errors. In considering artificial intelligence as a possible solution, deep learning algorithms have the ability to identify patterns in data by extracting features of the input data and as a result,* are being *used with medical imaging technologies for accurate disease diagnoses. In this work, some transfer learning models in combination with support vector machine (SVM) have been proposed to classify levels of serum cholesterol via image processing. Serum samples involving different forms of cholesterol such as total cholesterol, triglycerides, high-density lipoprotein cholesterol and low-density lipoprotein cholesterol were analyzed with their concentrations determined. Pictures/images of serum samples with cholesterol concentrations determined by enzymatic colorimetric methods were taken and the dataset of serum sample images were created. The TLS-SVM, TLR18-SVM and TLIv3-SVM models trained on the dataset of serum sample images produced classification accuracies of 86.10%, 85.60% and 87.20% respectively for different serum cholesterol concentrations.*

Key Words: Cholesterol, Confusion Matrix, Convolutional Neural Networks, Lipoprotein, Serum, Support Vector Machine, Transfer Learning.

1. INTRODUCTION

Artificial intelligence has the potential to change the field of disease diagnosis and management by carrying out classifications of some medical conditions that are difficult for human interpretation. The revolution of machine learning and image processing techniques has provided some automated systems in disease diagnosis. These computer aided diagnostic tools assist physicians in interpreting some medical conditions faster than human experts [1]. Biomedical image processing has expanded so fast in the last decades and has been an area of interdisciplinary research attracting expertise from applied mathematics, statistics, biology, computer sciences, engineering and medicine [2]. Medical imaging is a powerful tool for visualizing the internal tissues of the body and its diseases. Biomedical imaging has given rise to in vivo imaging of biological processes, molecular and cellular signaling, interactions and the movement of molecules through membranes. Biomedical imaging also offers precise tracking of intermediate products of some chemical reactions that can be used as biomarkers for disease identification, progress, and treatment responses [3]. Digital image processing is crucial in the field of medicine due to the increasing use of digital imaging systems for medical diagnosis [4]. The growth in size and number of medical images has made it possible for the use of computers to facilitate the processing and analysis of these images. Thus, computer aided diagnostics can be applied to digital images for the purpose of addressing various diagnostic problems [5].

Artificial intelligence has the potential to promote the development of disease detection by performing classification tasks that are complex for medical professionals and by speedily processing large amount of medical images used for disease detection purposes ([6]; [7]). Recently, deep learning convolutional neural networks (DLCNNs) have recorded some breakthrough in computer vision and image processing which automatically extract the features required for image identification and classification [8]. Deep learning feature extraction using convolutional neural networks (CNNs) has demonstrated good classification performance in the field of machine learning [9]. Thus, numerous studies involving imaging with machine learning techniques have been carried out to detect blood related diseases and other medical conditions.

Jewani *et al.,* [10] proposed a method based on android phone application to diagnose malaria and acute leukemia using thin blood smear through image processing and analysis. Lydia *et al.* [11] developed a deep learning convolutional neural network method using Resnet34 for malaria disease detection via malaria cell image dataset. Kermany *et al.* [12] proposed a transfer learning CNN model that uses X-ray and optical coherence tomography images to diagnose diseases and found out some treatment effects. Zhang *et al.* [13] developed neural network models for

hypertension prediction, hyperglycemia, dyslipidemia and other risk factors for chronic diseases from retinal fundus images.

According to Namara *et al.* [14], cardiovascular diseases (CVDs) remain the leading causes of death globally with a strong evidence that reduction in CVDs related deaths could be achieved for CVDs risk factors such as hypertension, abnormal blood lipid levels and so on. In view of this, cholesterol measurements are used in the diagnosis and treatments of lipid metabolism disorders which play a major role in the development of obesity [15], diabetes [16], hypertension [17] and cancers [18]. Cholesterol is quantitatively measured by a simple blood test called lipid panel or lipid profile. Lipid profile assessment is a crucial tool for diagnosing CVDs and it is a clinical test that is used for measuring different forms of cholesterol including total cholesterol (TC), triglyceride (TG), high-density lipoprotein cholesterol (HDLC) and low-density lipoprotein cholesterol (LDLC) [19]. The high-density lipoprotein cholesterol (HDLC) is termed 'good cholesterol' because excessive levels of HDLC prevents fatty build up and deposits of 'bad cholesterol' in the walls of coronary arteries which prevents artery damage and possible heart diseases. LDLC on the other hand, is part of the cholesterol left after the beneficial cholesterol has been used up by the body and it is referred to as the 'bad cholesterol' because excessive levels of LDLC in the body can build up in the walls of coronary arteries which may result to a possible cardiac arrest or stroke later in life. Several quantitative methods have been developed to determine the concentration of fasting blood cholesterol including enzymatic assays (EAs), gas chromatography (GC), classical chemical methods (CCMs), liquid chromatography (LC) and mass spectrometry (MS) [20]. Serum cholesterol is routinely analyzed by enzymatic colorimetric methods but the biochemical analysis of cholesterol is complex due to lack of technical expertise and resources to procure medical equipment especially in low income countries [21]. However, the advantages of computer aided diagnosis using machine learning with image processing to determine the concentrations of blood or serum cholesterol have not been fully utilized.

In this research, some transfer learning models in combination with support vector machine (SVM) have been developed to classify levels of serum cholesterol from pictures/images of serum samples with cholesterol concentrations determined by enzymatic colorimetric methods. The transfer learning models used as a feature extractor (FE) for SVM include squeezenet, resnet18 and inceptionv3 pre-trained convolutional neural networks (PCNNs). The models produced from the use of transfer learning models as feature extractors for SVM have been proposed to classify serum cholesterol concentration (SCC) via image processing.

2. METHODOLOGY

The study recruited three hundred and forty five (345) albino rats for the experiment. At the end of the experiment, only three hundred and three rats (303) survived. The 303 rats were divided into two groups consisting of 240 rats randomly selected for lipid development through inducement and another group of 63 rats were 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 because poloxamer 407 induces lipid development in rats. The subjects in the 240 group were administered with different concentrations of poloxamer 407 solutions.

Rats were recruited for this research because as a model of human diseases, the rat offers many advantages over several animals as it provides an excellent model for cardiovascular diseases including, stroke and hypertension. Some studies in the literature have stated that, there are some genetic stocks present in rats that are ideal for the study of human diseases [22]. Mice and rats have for some decades served as preferred species for biomedical research animal models due to their physiological, anatomical, and genetic similarities to humans [23].

This research was approved by the ethics committee on animal use and care in the Department of Biochemistry, Federal University of Agriculture, Makurdi.

2.1 Serum Sample Collection

The rats were made to fast for 12 hours because most reference values for serum cholesterol measurements are established by fasting blood specimens [24]. Blood samples were collected from the heart of the rats through cardiac puncture using sterile syringe and needle in preparation for serum separation. Each serum sample was separated from blood by centrifugation at 400 rpm for 10 minutes, stored at temperatures of +2 to 5^{o}C before analysis.

2.2 Colorimetric Determination of Fasting Serum Cholesterol Concentration

Fasting serum samples involving different forms of cholesterol such as total cholesterol, triglycerides and high-density lipoprotein cholesterol were prepared for manual use as specified by Randox kits (BioSystems, Barcelona, Spain) because Randox reagents are ready-to-use liquids, they have wide range of measurements to detect abnormal lipid levels, the reagents can be used on wide range of chemistry analyzers and they also have excellent correlation to reference methods for security of accurate results. Serum samples for total cholesterol, triglycerides and high-density lipoprotein cholesterol were analyzed on an N4 ultraviolet-visible spectrophotometer shown in Fig. 1. The analysis of low-density lipoprotein cholesterol was done on a fully automated chemistry analyzer using Anamol laboratory kits, since the kits are suitable for fully automated chemistry

analyzers as they produce fast results thereby reducing the time taken for direct measurement of LDLC.

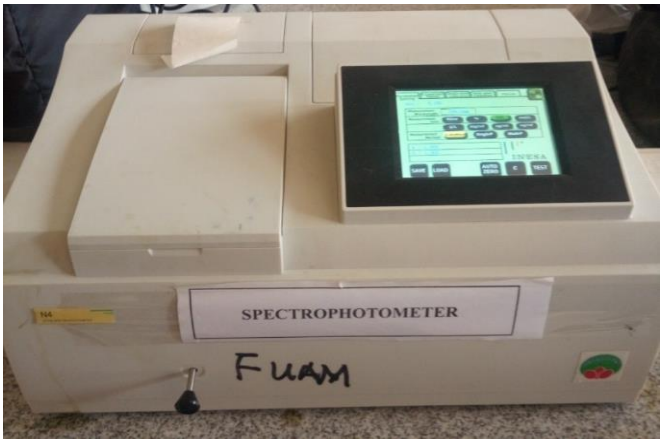


Fig. 1: N4 Ultraviolet-Visible Spectrophotometer

The quantities and proportions of how samples were prepared using Randox kits are shown in Tables 1 to 3.

Table 1: Test Serum Sample preparation for the Determination of Total Cholesterol Levels

Pipette into cuvettes:			
	Reagent blank (µL)	Standard (µL)	TC Serum Sample (µL)
Distilled water	10	-	-
Standard	-	10	-
Serum	-	-	10
Reagent	1000	1000	1000

The solutions for the determination of serum TC levels in Table 1 were mixed in quartz cuvettes of 1 cm light path for 5 minutes at 37°C. The reagent was prepared from 4-aminoantipyrine in the presence of phenol and peroxide. The absorbance of each sample solution was recorded against reagent blank at a wavelength of 500 nm and color stability of quinoneimine substance formed after the reaction was attained within 60 minutes.

Table 2: Test Serum Sample preparation for the Determination of Triglycerides Levels

Pipette into cuvettes:			
	Reagent blank (µL)	Standard (µL)	TG Serum Sample (µL)
Standard	-	-	10
Serum	-	10	-
Reagent	1000	1000	1000

The solutions for the determination of serum TG levels in Table 2 were mixed in quartz cuvettes for 5 minutes at 37°C. The reagent was formed from 4-aminophenazone under the catalytic influence of peroxidase. The absorbance of each sample solution was recorded against reagent blank at a wavelength of 500 nm and color stability was attained within 60 minutes.

Table 3: Test Serum Sample preparation for the Determination of HDLC Levels

Pipette into cuvettes:			
	Reagent blank (µL)	Standard (µL)	HDLC Serum Sample (µL)
Distilled water	100	-	-
Supernatant	-	-	100
Standard Supernatant	-	100	-
Reagent	1000	1000	1000

The solutions for the determination of serum HDLC concentration in Table 3 were mixed in cuvettes and incubated for 5 minutes at 37 °C. The reagent was made up of phosphotungstic acid in the presence of magnesium chloride ions. The absorbance of the sample and absorbance of standard were recorded against the blank within 60 minutes.

Serum samples for the determination of low-density lipoprotein cholesterol were prepared with Anamol laboratory kits using direct measurements. The Anamol kits consisted of two LDL cholesterol reagents, which were ready to use liquid reagents and a calibrator. Before samples were prepared using the standard procedure, 250 µL of distilled water was added to the calibrator and mixed for a uniform solution to be obtained. All samples of low-density lipoprotein cholesterol were prepared in quartz cuvettes of 1 cm light path at wavelengths of 546 nm and 630 nm during

the first incubation and second incubation periods respectively as shown in Table 4.

Table 4: Test Serum Sample preparation for the Determination of LDLC Levels

Pipette into cuvettes:		
1st Incubation	Calibrator (µL)	LDLC Serum Sample (µL)
LDL Cholesterol Reagent, R1	600	600
Calibrator	5	-
Serum	-	5
2nd Incubation: Pipette into cuvettes		
LDL Cholesterol Reagent, R2	200	200

During the first incubation period, R1 was mixed with the serum sample and calibrator for five minutes at 37 °C. In the second incubation period, R2 was added to the serum sample and calibrator for another five minutes at 37 °C. The reaction mixtures in the flow cell were aspirated and the absorbance was recorded within 120 minutes of color stability.

2.3 Acquisition of Serum Sample Images

The back camera of techno android phone with 1440×720 screen resolution, 13 MP rear camera, and 1.3 GHz processor was used for capturing the picture/image of each serum sample of total cholesterol, triglycerides and high-density lipoprotein cholesterol with a particular concentration. The concentrations of serum total cholesterol, triglycerides, and high-density lipoprotein cholesterol were calculated using equation 1 [25].

$$\text{Conc. of serum sample} = \frac{\text{Absorbance of serum sample}}{\text{Absorbance of standard}} \times \text{Conc. of standard} \quad (1)$$

In calculating the concentrations of serum total cholesterol, the absorbance of standard was recorded as 1.211 and the concentration of standard from Randox cholesterol kits was given as 203 mg/dL. Table 5 shows some captured images of the total cholesterol serum samples, the absorbance of total cholesterol samples and their serum concentrations as calculated using equation 1.

Table 5: Serum Sample Pictures of TC with their Concentrations

Image of TC serum sample	Absorbance of TC serum sample	Concentration (mg/dL)
	0.926	155.23
	1.281	214.73
	1.471	246.58

Table 6 shows some captured images of triglyceride serum samples, the absorbance of triglyceride samples and their serum concentrations as calculated using equation 1. Here the absorbance of standard was recorded as 1.061 and the concentration of standard from Randox cholesterol kits was given as 197 mg/dL.

Table 6: Serum Sample Pictures of TG with their Concentrations

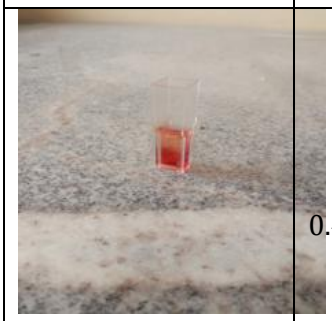
Image of TG serum sample	Absorbance of TG serum sample	Concentration (mg/dL)
	0.433	80.40
	1.063	197.37
	1.178	218.72

Table 7 shows some captured images of high-density lipoprotein cholesterol serum samples, the absorbance of samples and high-density lipoprotein cholesterol serum concentrations as calculated by equation 1. Here, the absorbance of standard was recorded as 0.023 and the concentration of standard from Randox cholesterol kits was given as 50 mg/dL.

Table 7: Serum Sample Pictures of HDLC with their Concentrations

Image of HDLC serum sample	Absorbance of HDLC serum sample	Concentration (mg/dL)
	0.037	80.43
	0.026	56.52
	0.008	17.39

The techno android phone was also used to capture pictures/images of serum samples of LDLC concentrations recorded on the fully automated chemistry analyzer as shown by few representative samples in Table 8.

Table 8: Serum Sample Pictures of LDLC with their Concentrations

Image of LDLC serum sample	Concentration (mg/dL)
	40.19
	138.77
	171.00

2.4 Block Diagram of the Proposed Method

The workflow for the classification of cholesterol levels in serum through image processing is shown in Fig. 2.

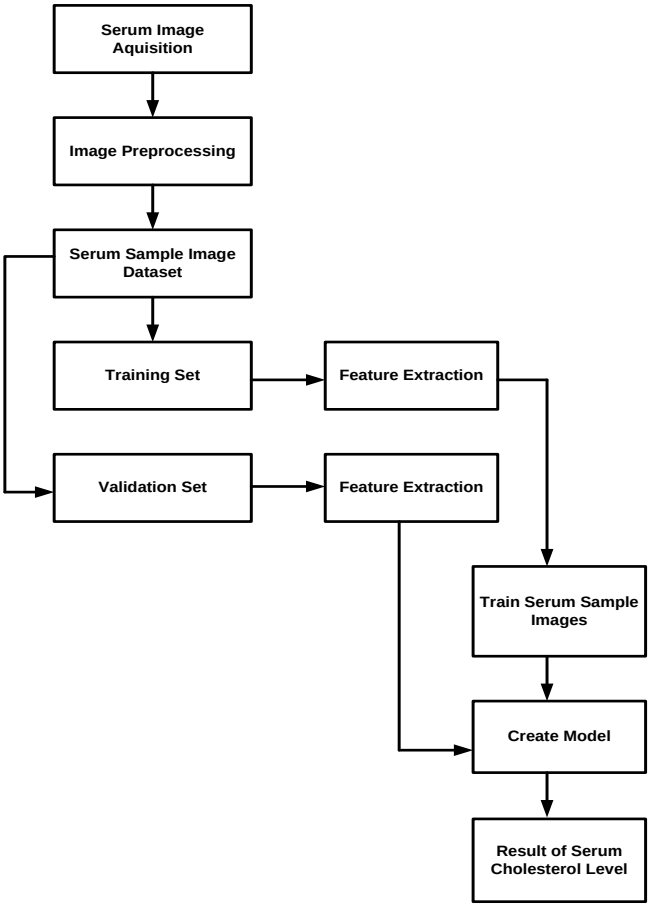


Fig. 2: Block Diagram for the Classification of Different Forms of Serum Cholesterol Levels

2.5 Preprocessing of Serum Sample Images

The first preprocessing technique applied to the acquired images was scaling. The camera of techno android phone used to acquire serum images produced high image resolutions. The resolution of each serum sample image was reduced to 227×227, 224×224 and 299×29 as required by the input sizes of SqueezeNet, ResNet18 and Inceptionv3 PCNNs respectively. In each case, transfer learning was applied to each network to create a model which was used to extract features for the SVM algorithm. Data augmentation was applied to the dataset to prevent the CNNs used in this work from memorizing training data. Random affine geometric transformations such as serum sample image resizing, rotation, reflection and translation were applied. Random reflection of images in the dataset was done in the left and right directions by reflecting each image horizontally with 50% probability.

2.6 Dataset of Serum Sample Images

The captured serum sample pictures or images were grouped based on the calculated or measured serum

cholesterol concentrations. The grouped images were classified according to the United States National Cholesterol Education Program (NCEP) Expert Report Panel, [26] as summarized in Tables 9 to 12 and the description of the classes that contained the serum sample images in the dataset is given in Table 13.

Table 9: Reference Values of Serum TC Concentration

Serum sample	Value (mg/dl)
Normal	< 200
Borderline-high	200-239
High	≥240

Table 10: Reference Values of Serum TG Concentration

Serum sample	Value (mg/dl)
Normal	< 150
Borderline-high	150-199
High	200-499

Table -11: Reference Values of Serum HDLC Concentration

Serum sample	Value (mg/dl)
Low	40
Borderline-low	41-59
Normal	≥60

Table -12: Reference Values of Serum LDLC Concentration

Serum sample	Value (mg/dl)
Normal	≤100
Borderline-high	130-159
High	≥160

Table 13: Description of Classes in the Serum Image Dataset

Name of class	Description of image class	No. of images
HDL BORDERLINE LOW	Serum sample images whose serum HDL levels are moderately low	75
HDL LOW	Serum sample images whose serum HDL levels are low	75
HDL NORMAL	Serum sample images whose serum HDL levels are normal	75
LDL BORDERLINE HIGH	Serum sample images whose serum LDL levels are moderately high	75
LDL HIGH	Serum sample images whose serum LDL levels are high	75
LDL NORMAL	Serum sample images whose serum LDL levels are normal	75
TC BORDERLINE HIGH	Serum sample images whose serum TC levels are moderately high	75
TC HIGH	Serum sample images whose serum TC levels are high	75
TC NORMAL	Serum sample images whose serum TC levels are normal	75
TG BORDERLINE HIGH	Serum sample images whose serum TG levels are moderately high	75
TG HIGH	Serum sample images whose serum TG levels are high	75
TG NORMAL	Serum sample images whose serum TG levels are normal	75

3. Training Algorithms

The experimental work was conducted to train and evaluate the performance of deep learning algorithms with SVM in the classification of serum levels of total cholesterol, triglyceride, high-density lipoprotein and low-density lipoprotein cholesterols in albino rats based on image processing. These learning algorithms include transfer learning using Squeezenet with SVM (TLS-SVM), transfer learning using ResNet18 with SVM (TLR18-SVM) and transfer learning using Inceptionv3 with SVM (TLIv3-SVM). In these

algorithms, transfer learning was used with Squeezenet, Resnet18 and Inceptionv3 pre-trained CNNs to create models which were used as feature extractors for the SVM algorithm. The learnable and final classification layers of SqueezeNet, Resnet18 and Inceptionv3 PCNNs were replaced with new layers to adapt to the new input images for cholesterol classification. To use the pre-trained networks for transfer learning, a new classification layer with an input of 12 classes from the serum sample image dataset was introduced in each network to replace the final classification layer in the pre-trained network with original one thousand (1000) classes previously trained on the ImageNet dataset. The deeper layers of these transfer learning models which could learn rich features extracted from the serum sample images were used to train the support vector machine. An image data augmenter was used to configure a set of preprocessing options for image augmentation such as random reflection and translation. The transfer learning models used as feature extractor for the SVM classifier were trained using stochastic gradient descent with momentum. The training of the networks also used a mini batch with 11observations at every epoch and the maximum number of epoch was set at 7 with an initial learning rate of 2×10^{-4}. The features extracted by the transfer learning networks were used to train the multiclass error-correcting output codes SVM classifier using the fit classification class, *fitcecoc ()*.

4. Evaluation of Trained Models

The serum image dataset had twelve (12) classes and each class contained seventy-five (75) images as shown in Table 13. In training each algorithm, the images in the dataset were split into 80% of training set and 20% of validation set. Confusion matrix plot (CMP) was used to validate the accuracy of all the trained models using the 20% validation data. This means that about 15 images, which were not part of the training data in each class of the dataset was reserved for validation. The 15 images in each class of the serum dataset were used to evaluate the accuracy of the models in the classification of serum cholesterol concentration.

On the CMP shown in Fig. 3 to Fig. 5, the rows correspond to the predicted class representing the output class and the columns correspond to the true class for the target class. The diagonal cells correspond to serum images that are correctly classified whereas the off-diagonal cells correspond to wrongly classified serum sample images. Both the number of serum images and the percentage of the total number of images in the validation set are shown in each cell. The column on the far right of the plot shows the percentages of all the sample images predicted to belong to each class that are correctly and wrongly classified. The metrics that show the percentages of all serum sample images predicted to belong to each class that are correctly and wrongly classified are often called the precision or positive predictive value and false discovery rate, respectively. The row at the bottom of the plot shows the percentages of all the examples of the validation data belonging to each correctly and wrongly classified class. These metrics are often called the recall or true positive rate and false negative rate, respectively. The cell in the bottom right of the plot shows the overall accuracy of the network on the validation data.

5. Results

Transfer learning was applied to squeezenet, resnet18 and inceptionv3 networks, which were trained on the subset of serum image dataset to create models that were used as feature extractors for the support vector machine algorithm. Transfer learning was adopted because it does not involve training of data from scratch but from a model trained on another model to learn features of the new input data [27]. In this research, the starting point was the training of squeezenet, resnet18 and inceptionv3 networks on serum sample image dataset. The serum image dataset was the new input data and the ImageNet challenge dataset of natural images was the original dataset that was used to train the PCNNs. The dataset contained nine hundred (900) images that belonged to 12 classes with each class comprising 75 images as shown in Table 13. The dataset was divided into two parts, consisting of a total of 720 images for training and 180 sample images for validation. Each class contributed 60 images for training and 15 images for validation. The accuracy of each trained model is shown in the bottom right cell of the model's confusion matrix as shown in Fig. 3 to Fig. 5 and the summary of the accuracies for the models are shown in Table 14.

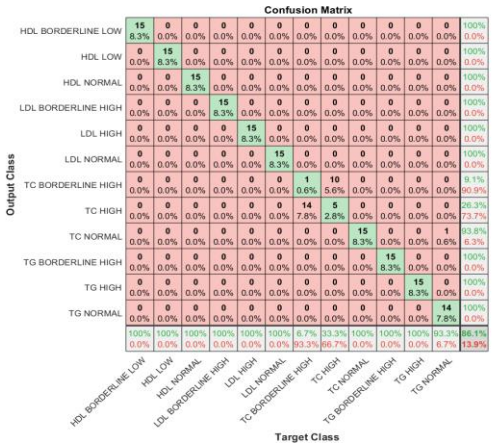


Fig. 3: Confusion Matrix Plot of TLS-SVM Model

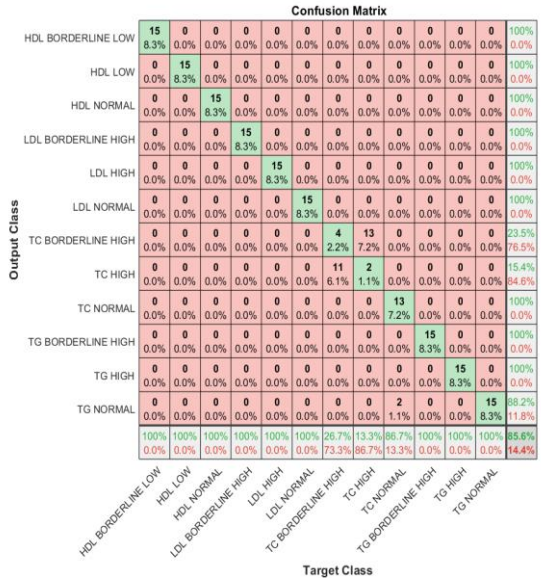


Fig. 4: Confusion Matrix Plot of TLR18-SVM Model

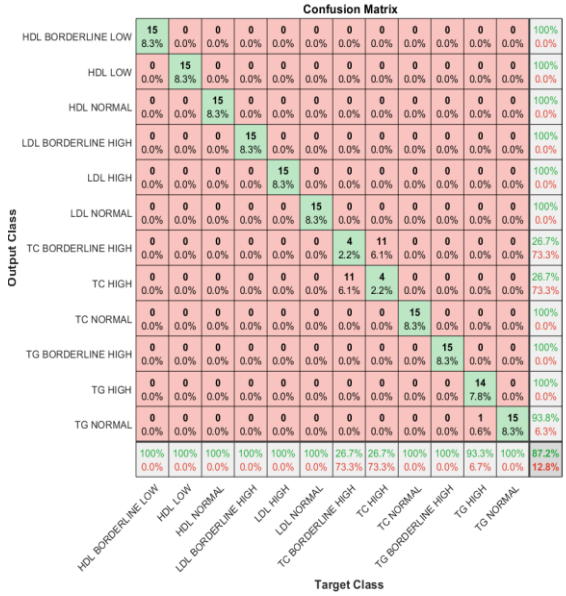


Fig. 5: Confusion Matrix Plot of TLIv3-SVM Model

Table 14: Accuracies of Trained Models

S/No.	Trained model	Accuracy
1	TLS-SVM	86.10%
2	TLR18-SVM	85.60%
3	TLIv3-SVM	87.20%

6. Discussion of Results

In this study, an image based method was proposed for the classification of serum cholesterol levels based on NCEP Expert Report, 2011. By exploiting transfer learning with some pre-trained CNNs as FEs for SVM, the trained models demonstrated the ability to classify serum cholesterol levels correctly. Confusion matrix plot was used to validate the training accuracy of each network using the validation set from the serum image dataset. The validation set in each class contained 15 images. On the confusion matrix of TLS-SVM model shown in Fig. 3, the model predicted and classified the serum cholesterol levels of different forms of cholesterols with 100 % accuracy as shown in HDL BORDERLINE LOW, HDL LOW, HDL NORMAL, LDL BORDERLINE HIGH, LDL HIGH, LDL NORMAL, TC NORMAL, TG BORDERLINE HIGH and TG HIGH classes. However, the TLS-SVM model was able to predict moderately or borderline high levels of serum total cholesterol with 9.1% accuracy and to correctly classify moderately high levels of serum total cholesterol with an accuracy of 6.70 % as can be seen in TC BORDERLINE HIGH class. The model also predicted high levels of serum total cholesterol with 26.30% accuracy but correctly classified high concentrations of serum total cholesterol with an accuracy of 33.30% as illustrated by the TC HIGH class.

The TLR18-SVM model predicted and classified serum cholesterol concentrations of different forms of cholesterol with an accuracy of 100% as can be seen in HDL BORDERLINE LOW, HDL LOW, HDL NORMAL, LDL BORDERLINE HIGH, LDL HIGH, LDL NORMAL, TC NORMAL, TG BORDERLINE HIGH and TG HIGH classes of the confusion matrix shown in Fig. 4. The TLR18-SVM model predicted moderately high levels of serum total cholesterol with 23.50% accuracy but correctly classified moderately high levels of serum total cholesterol as shown in TC BORDERLINE HIGH class with an accuracy of 26.70%. The TLR18-SVM model also predicted high concentrations of serum total cholesterol with 15.4 % accuracy but correctly classified high levels of serum total cholesterol as seen in TC HIGH class with an accuracy of 13.30%.

On the CMP of TLIv3-SVM model shown in Fig. 5, the model classified the serum cholesterol levels of different forms of cholesterol correctly with an accuracy of 100% as shown in all classes except for moderately high serum total cholesterol levels as shown in TC BORDERLINE HIGH class, high serum total cholesterol levels as seen in TC HIGH class and high serum triglycerides levels as seen in TG HIGH class. The TLIv3-SVM model classified moderately high levels of serum total cholesterol as seen in the TC BORDERLINE HIGH class and high levels of serum total cholesterol as seen in TC HIGH class with the same accuracy of 26.70 %. However, the model predicted high concentration of serum triglycerides with 100% accuracy but correctly classified high levels of serum triglycerides with an accuracy of 93.30 % as seen in TG HIGH class.

7. Conclusion

In this paper, an image based method using some deep learning models with support vector machine was proposed to detect and classify different forms of serum cholesterol levels. Given the limitation of using imaging technologies in the detection of serum cholesterol levels, there were no available image datasets for the determination of serum cholesterol concentrations and as a result, a techno android phone was used to capture the pictures of the serum samples with known cholesterol concentrations determined from enzymatic colorimetric analysis on a spectrophotometer and fully automated chemistry analyzer. The captured images of the samples were used to create the dataset which was used to train the networks employed in this study. A subset of the serum image dataset was trained on squeezenet, resnet18 and inceptionv3 PCNNs using transfer learning which produced models that were used to extract features of serum sample images for the SVM algorithm to produce TLS-SVM, TLR18-SVM and TLIv3-SVM models when trained on the entire dataset. The TLIv3-SVM model produced the highest classification accuracy of 87.20% followed by TLS-SVM model with 86.10 % accuracy which shows that learning models are capable of predicting different forms of serum cholesterol levels accurately using image processing. This research shows that image processing with learning algorithms could provide better accuracy, reduce the time taken for serum cholesterol measurements and enhance the efficiency of serum cholesterol level diagnosis in tele-medicine. Further research is needed to investigate the poor accuracy of the networks on some few classes in the dataset so that the overall accuracy of the networks or models could be improved for clinical diagnosis.

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