Performance Evaluation of Machine Learning Algorithms on Skin Cancer Data Set Using Principal Component Analysis and Gabor Filters

Abdul Rahaman Shaik, P. Rajesh Kumar

Abstract—**Machine Learning (ML) is an advanced branch of Artificial Intelligence (AI) focused on creating algorithms and statistical models that empower computer systems to learn from data and autonomously make informed decisions or accurate predictions, all without requiring explicit programming for every individual task. It enables computers to recognize patterns, relationships, and insights within the data and improve their performance through experience. Machine learning has had a significant impact on medical imaging in recent years, revolutionizing the field and enhancing healthcare practices. Machine Learning provides improved diagnostic accuracy, faster image analysis, reduced errors and variabilities and detection of anomalies and lesions. In this paper we applied various ML algorithms like Random Forest (RF), Support Vector Machine (SVM), K-Nearest Neighbor (KNN), Logistic Regression (LR), Naïve Bayes (NB) on HAM** (Human Against Machine) **10000 skin cancer data set. Since the data set is huge, we used dimensionality reduction and feature extracting techniques like Principal Component Analysis (PCA) and Gabor filters. The data set has 10015 images of seven classes of skin cancer. Our findings reveal that Random Forest when used with PCA produced an accuracy of 89% and when it is used with Gabor feature extraction it produced an accuracy of 84%. The SVM classifier with PCA produced an accuracy of 82% and when used with the Gabor feature extraction SVM produced an accuracy of 84%. RF produced an increased accuracy of 92% when the data samples for each class is increased.**

Index Terms—**Machine Learning, skin cancer classification, dimensionality reduction, feature extraction**

I. Introduction

IN the United States, an alarming number of over 9,500 individuals receive diagnoses of skin cancer on a daily basis. More than two people die of the disease every hour [1],[2]. The total count of people effected by skin cancer in US is more than the number of people effected by all other cancers combined [2]. Dermoscopy is a non-invasive, in-vivo technique which is used by dermatologists to evaluate skin lesions for the early detection of skin cancer. It is also known by names Dermatoscopy or skin surface microscopy. With years of experience and expertise dermatologists will be able to identify the subtle features and patterns indicative of skin cancer accurately but the possibility of human error can still affect the assessment [3],[4]. The manual inspection is also time consuming and laborious and can be affected by fatigue. Expert dermatologists may not be available across all geographical areas. All these factors may lead to misdiagnosis or delay in diagnosis. Most of these short comings are effectively addressed by using Machine Learning (ML) algorithms for skin cancer classification. ML algorithms can analyze huge amounts of dermoscopic data and learn from diverse examples. They can achieve high accuracy and sensitivity in detecting skin cancer, sometimes outperforming human experts in certain scenarios. Machine learning algorithms can process images rapidly and efficiently, providing almost instant results, making them highly suitable for quick and automated screening processes. Machine learning algorithms offer standardized and consistent evaluations, reducing inter-observer variability and providing a reliable second opinion across various medical facilities. Once trained, machine learning tools can be easily deployed and accessed remotely, allowing for broader access to skin cancer screening, even in underserved regions. Machine learning algorithms can be continuously updated and refined, improving their performance over time as more data becomes available and the technology advances.

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II. Literature Review

Several different approaches can be found in literature to classify skin lesions. In [5] a novel computerized approach for assessing skin cancer prognosis by utilizing symmetry analysis and color matching of lesion pigments is introduced. The accuracy achieved is 80%. In [6] feature extraction is done by Hue, Saturation and Value (HSV) and is associated with Random Forest for classification. The approach described in [7] adopts a sequential methodology beginning with border detection, followed by feature selection, and concluding with classification. In [8], a dual-system strategy is utilized wherein system one focuses on extracting global features such as color and texture, while system two specializes in capturing local features. These two systems work in tandem, to conduct binary classification distinguishing between melanoma and benign classes. In [9] Bag of Features (BoF) method is used in

which each image is divided into several patches of size 16x16 and wavelet decomposition is applied on these patches and for clustering K-means is used. The HAM10000 data set is widely used to train and test various machine learning (ML) models and it is developed by [10]. The comparative studies conducted by [11] show that certain models like Multilayer Perceptron (MLP) demonstrate superior performance compared to Bayesian and K-Nearest Neighbors (KNN) classifiers. Additionally, Support Vector Machines (SVM) when used with Multiple Instance Learning (MIL) approaches have shown to outperform their linear and Radial Basis Function (RBF) kernel counterparts. These findings have prompted the development of solutions that involve the amalgamation of different classifiers, aiming to achieve even better results. In [12] an intelligent segmentation is done before classification. Several studies including [12] used the ABCD rule of dermatology where A means Asymmetry, B stands for Border structure, C means Color and D means Differential Structures of the skin lesion. Feature extraction is applied on a segmented object and the extracted features are applied to SVM. In [13] Naïve Bayesian (NB) and Decision tree algorithms are applied on DermIs and DermQuest dataset [14]. Even though the results are good in [14], the data set is very small. In[15] Gabor filtering approach is used along with Collaborative Representation Classifier for image classification and achieved an accuracy between70 to 73%. In [16] an approach based on improved Gabor filter along with SVM is used for the classification of surface defects. A Melanoma detection system based on ABCD rule and Haralick texture features along with SVM as a classifier is developed in [17]. This system achieved a testing accuracy of 75% with 15 extracted features. In[18] a broad set of dermatologically distinctive features are extracted and applied to the SVM classifier and achieved an accuracy of 79%. In [19] wavelet feature extraction method is used with SVM and Naïve Bayes classifiers to classify Glaucomatous images using PCA and Gabor filters. They achieved an accuracy of 84% with SVM and 76% with Naïve Bayes. In [20] High-Level Intuitive Features (HLIF) are used. These features are designed to quantify the extent of border irregularities observed in skin lesion images captured using standard cameras. In [21] brain tumor images are classified using ensemble classifiers that produced better results than traditional classifiers. In [22] the performance analysis of various traditional classifiers is done on breast cancer ultrasound images and they achieved an accuracy of 83% with KNN. In [23] a deep convolutional neural network is used for the detection of malaria parasite. In [24] a machine learning model is used for the early detection of multi cancer types.

III. Methodology

A. Data Preparation

The data set used in our method is HAM 10000 data set [10]. It contains 10015 skin cancer images divided into 7 classes. This data set is created to facilitate research on skin cancer and help the researchers in the classification of various types of skin cancers. The data set development is led by Dr. Noel Codella at the Memorial Sloan Kettering Cancer Center (MSKCC) in collaboration with the International Skin Imaging Collaboration (ISIC). Table I shows the various classes and their abbreviations along with the count of images present for each class. From Table I we observe that the data is highly imbalanced. Fig 1. shows sample images of each class and Fig 2. shows the unbalanced distribution of data.

TABLE I. THE NUMBER OF IMAGES IN EACH CLASS PRESENT IN THE HAM10000 DATA SET

S.No	CLASS NAME	Class Abbreviation	Count of Images Per Class
1	Melanocytic Nevi	NV	6705
2	Melanoma	MEL	1113
3	Benign Keratosis like Lesions	BKL	1099
4	Basal Cell Carcinoma	BCC	514
5	Acnetic Keratosis and Intraepithelial Carcinoma	AKIEC	327
6	Vascular Lesions	VASC	142
7	Dermatofibroma	DF	115

An imbalanced data results in biased training where the model learns to recognize the classes with more images and fails to recognize minority classes. This results in overall reduced accuracy, reduced generalization and increased false negatives and false positives. Therefore, it is very important to balance the data. As we can see from Table I that Melanocytic Nevi class has 6705 images while dermatofibroma has only 115 images. We use sampling method for balancing the data set. Each class images are up sampled or down sampled to 2000 images per class.

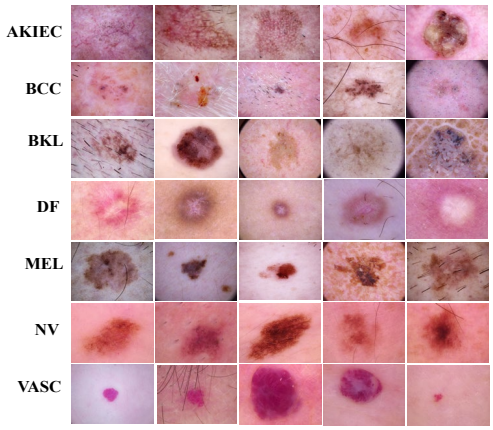

Fig. 1. Sample images of each class in HAM10000 data set

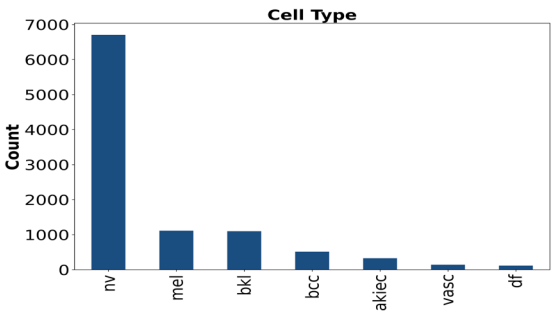

Fig. 2. Data distribution of different classes in HAM10000 data set

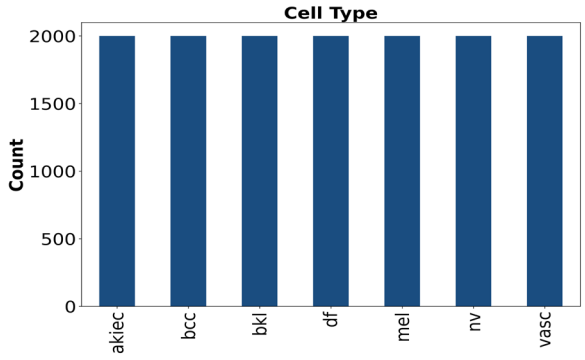

Fig. 3. Data distribution after balancing

After balancing the data, we have now 2000 images for each class which means a total of 14000 images. Fig 3. shows the data distribution post balancing.

The HAM10000 [10] data set images come with a size of 600x450. If we apply these images directly to a classifier it consumes lot of time and computational complexity will very high and system may run out of memory, therefore its necessary to resize the data and we shall resize such that we will not be losing important information and at the same time we are reducing the computational complexity and memory requirements of the system will be relaxed. Fig 4. shows the images with original size and images after resizing.

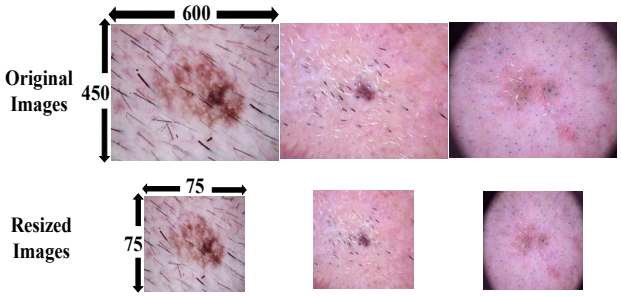

Fig. 4. Original and Resized images

B. Dimensionality Reduction and Feature Extraction

We implement Principal Component Analysis (PCA) to reduce dimensions and feature extraction is done by Gabor filters. These methods are applied independently.

a.) Principal Component Analysis (PCA)

Principal Component Analysis (PCA) stands as a highly utilized method in data analysis known for its efficacy in dimensionality reduction. Its primary goal is to transform a dataset into a new coordinate system, where the data's variance is maximized along the principal axes (the new coordinates). This process allows you to find the most prominent patterns and reduce the data's dimensionality while retaining as much relevant information as possible.

Given a dataset with n data points and m features, let X be an n x m matrix where the rows and columns indicate data points, and features respectively. To perform PCA, the mean is deducted from data and then result is divided by the standard deviation for each feature: The mean of each feature is obtained as

$$\mu_j = \frac{1}{n}\sum_{i=1}^{n} x_{ij} \quad (1)$$

The standard deviation of each feature is measured as

$$\sigma_j = \sqrt{\frac{1}{n}\sum_{i=1}^{n}(x_{ij} - \mu_j)^2} \quad (2)$$

The standardized data is then obtained by using

$$SX = \frac{X-\mu}{\sigma} \quad (3)$$

Now we can find the co-variance matrix of the standardized data. The co-variance between two features (j,k) can be found as follows,

$$C = cov(j,k) = \frac{1}{n-1}\sum_{i=1}^{n}(SX_{ij} - \mu_j)(SX_{ik} - \mu_j) \quad (4)$$

$C = cov(j,k)$ will be an mxn matrix where the element at (j,k) represents the co-variance between the features at j and k. Performing eigen decomposition on matrix C yields eigen values and eigenvectors. These eigenvectors correspond to the principal components, while the eigen values quantify the variance that each principal component accounts for.

The eigen decomposition of C is given by $C = V\Lambda V^T$ where V is an m x m matrix, and each column of V represents an eigenvector. Λ is a diagonal matrix containing the eigen values in descending order.

After obtaining the eigen values and eigenvectors, it is essential to select the leading k principal components that retain the majority of variance inherent in the data. The total variance of the data is the sum of all eigen values.

$$TV = Total\_Variance = \sum_{i=1}^{m} \lambda_i \quad (5)$$

We can calculate the ratio of variance elucidated by each principal component is expressed as:

$$PV = Proportion\_Variance = \frac{\lambda_i}{TV} \quad (6)$$

Choose the top k eigenvectors corresponding to the k highest eigen values to form the projection matrix P.
Finally, we project the standardized data onto the selected principal components using the projection matrix P.

$$PCA_{Result} = SX \times P \quad (7)$$

The resulting matrix PCA_Result will have reduced dimensions, and it represents the transformed dataset based on the selected principal components. Fig 5. shows the evaluation process with PCA.

b.) Gabor Filters (GABOR)

Gabor filters find extensive application in the realms of computer vision and image processing, notably for the purposes of feature extraction and dimensionality reduction. These filters are based on the concept of Gabor functions, which are a family of complex sinusoidal functions modulated by a Gaussian envelope. The filters are designed to resemble the response of human visual system cells, particularly those found in the primary visual cortex. Mathematically a 2D Gabor filter can be defined as

$$g(x,y) = \frac{1}{2\pi\sigma_x\sigma_y}\exp\left(-\frac{x'^2}{2\sigma_x{}^2} - \frac{y'^2}{2\sigma_y{}^2}\right)\cos(2\pi f_x x' + \varphi) \quad (8)$$

Where

- x, y are the spatial coordinates of the image
- σ_x *and* σ_y control the spread of the Gaussian envelope along the x and y directions, respectively,
- f_x is the frequency of the cosine function (spatial frequency of the sinusoid),
- φ is the phase offset,
- $x' = x\,cos\theta + y\,sin\theta$ *and* $y' = -x\,sin\theta + y\,cos\theta$ are the coordinates of the rotated image, with θ representing the orientation of the filter

The application of Gabor filters involves convolving the image with the Gabor function. The result of the convolution highlights different patterns in the image, such as edges, textures, and blobs, depending on the parameters of the Gabor filter

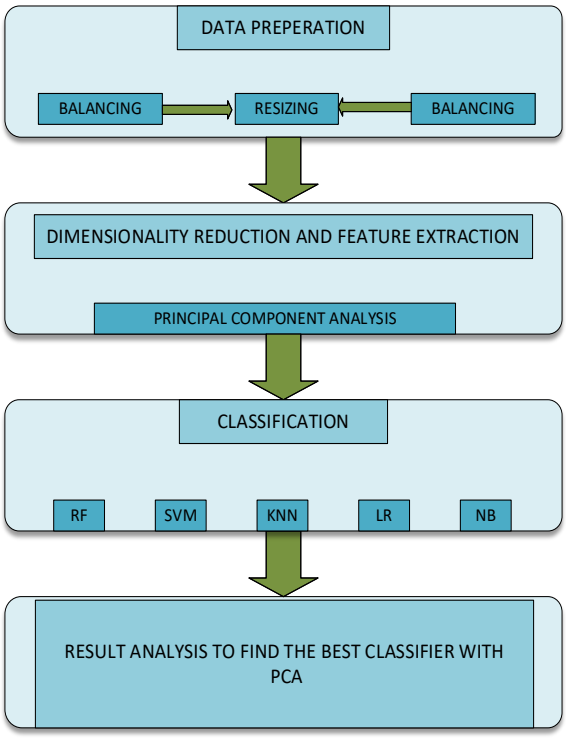

Fig. 5. Performance evaluation process with PCA

C. Selection of Classifier

From the literature review we observe that the most successful classifiers for medical image processing are Random Forest (RF), Support Vector Machine (SVM), K-Nearest Neighborhood (KNN), Logistic Regression (LR) and Naïve Bayes (NB). The prepared data is first subjected to PCA and the output of PCA is applied to the above said classifiers. The flow chart shown in the Fig 5. explains the evaluation process.

We used python with tensor flow for carrying out the above process and ran our code on Kaggle. With PCA for dimensionality reduction we got highest accuracy of 89% when Random Forest is used as a classifier. We used an iterative method to find the number of components that are needed to perform Principal Component Analysis. We repeated the same procedure using Gabor filter as a dimensionality reduction and feature extraction tool. Fig 6. shows the evaluation process using Gabor filter for feature extraction.

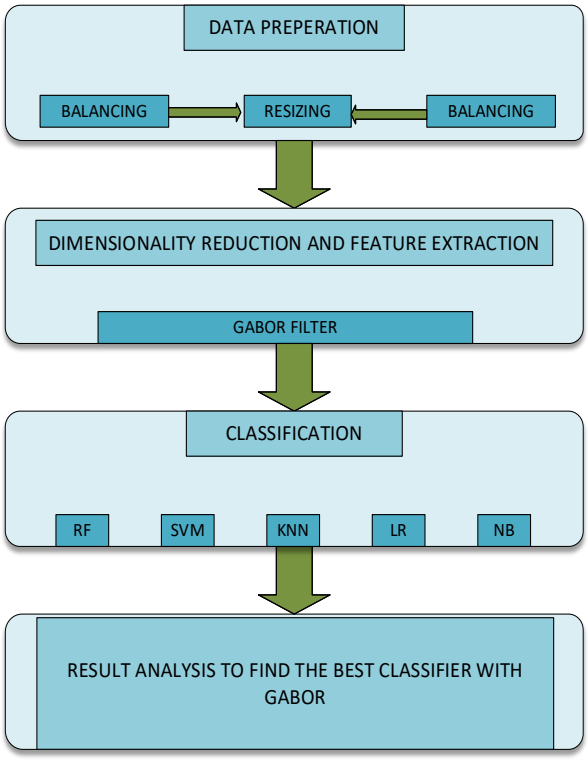

Fig. 6. Performance evaluation process with GABOR

IV. Results and Discussion

The data is divided into 80:20 ratio for training and testing. We used confusion matrix and classification report to estimate and compare various performance metrics of the classifiers. Fig 7 to Fig 11 shows the confusion matrices and classification reports of all the classifiers when used with PCA.

A confusion matrix serves as a tabular representation used in classification tasks to concisely summarize a machine learning model's performance evaluation. It provides a breakdown of actual and predicted classes for a dataset, allowing visualization of a classification algorithm's effectiveness. This tool is especially valuable in multi-class classification scenarios, involving more than two classes. By offering insights into the model's performance, a confusion matrix becomes crucial for understanding its accuracy and error patterns.

A fundamental tool in machine learning and statistics, the confusion matrix aids in assessing classification model performance. It comprehensively demonstrates a model's effectiveness in categorizing instances. This matrix is particularly beneficial when tackling imbalanced class situations, ensuring a comprehensive understanding of model behavior.

The confusion matrix is typically structured in a grid layout, with rows representing the correct labels and columns indicating the guessed labels. This arrangement allows for a clear visualization of the model's classification performance across different categories

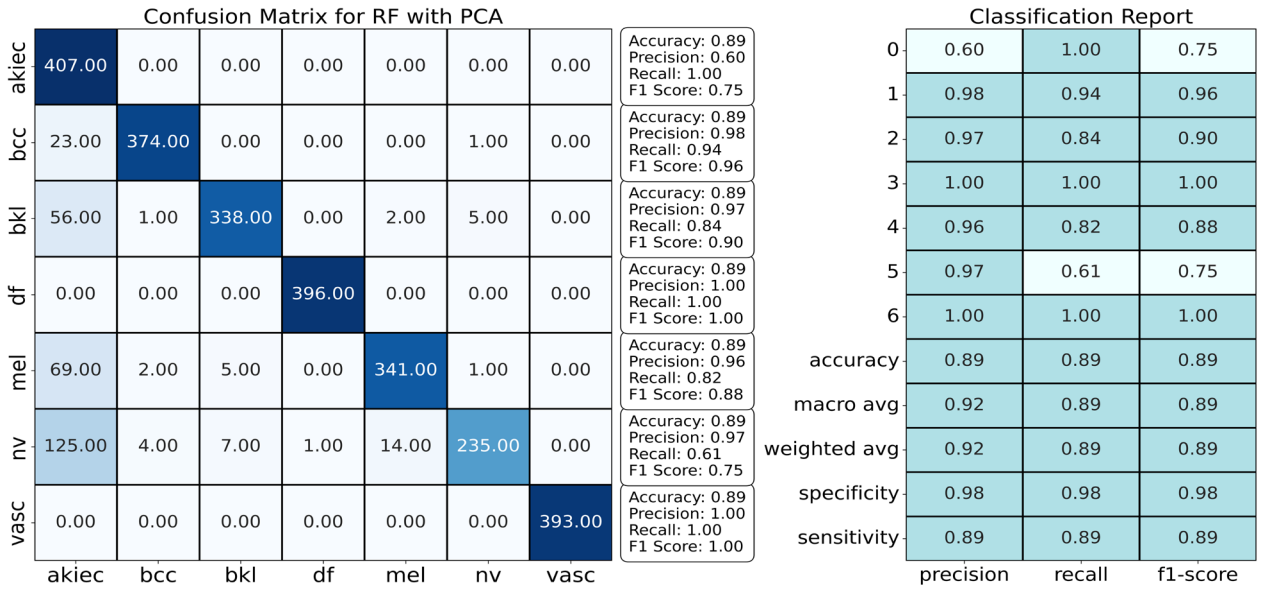

Fig. 7. Confusion Matrix and Classification Report for RF with PCA

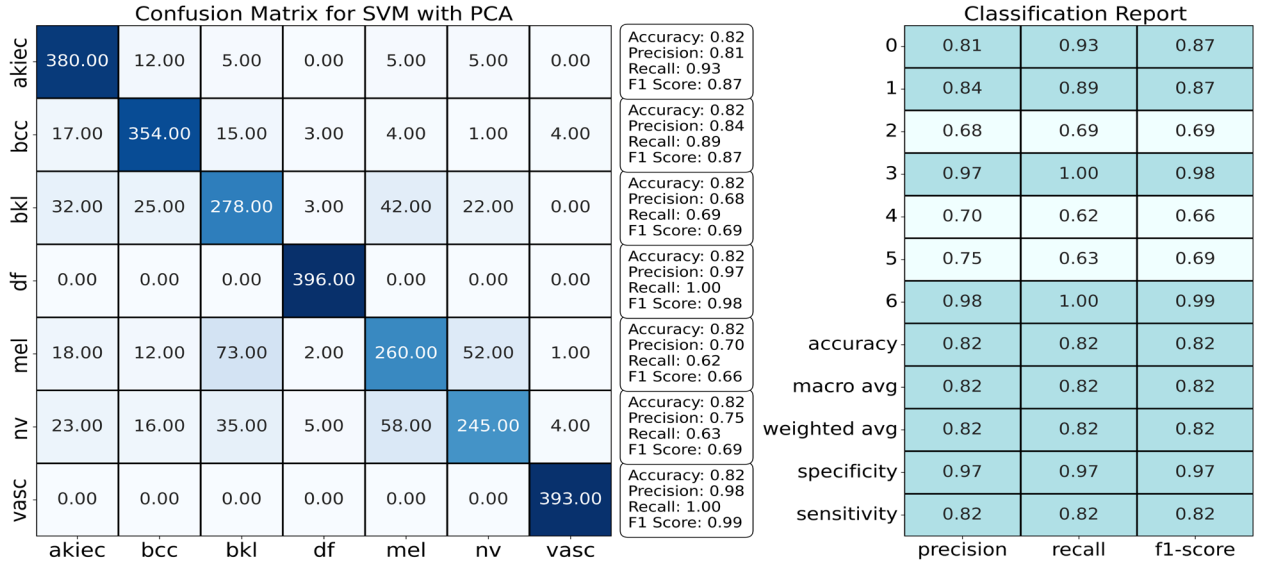

Fig. 8. Confusion Matrix and Classification Report for SVM with PCA

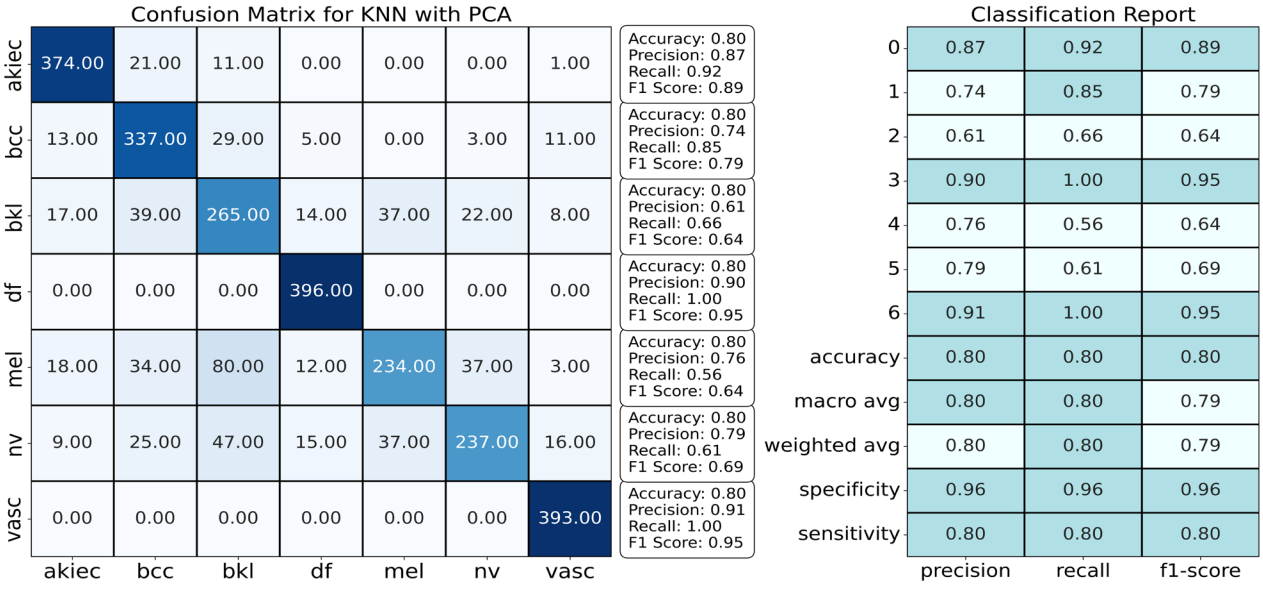

Fig. 9. Confusion Matrix and Classification Report for KNN with PCA

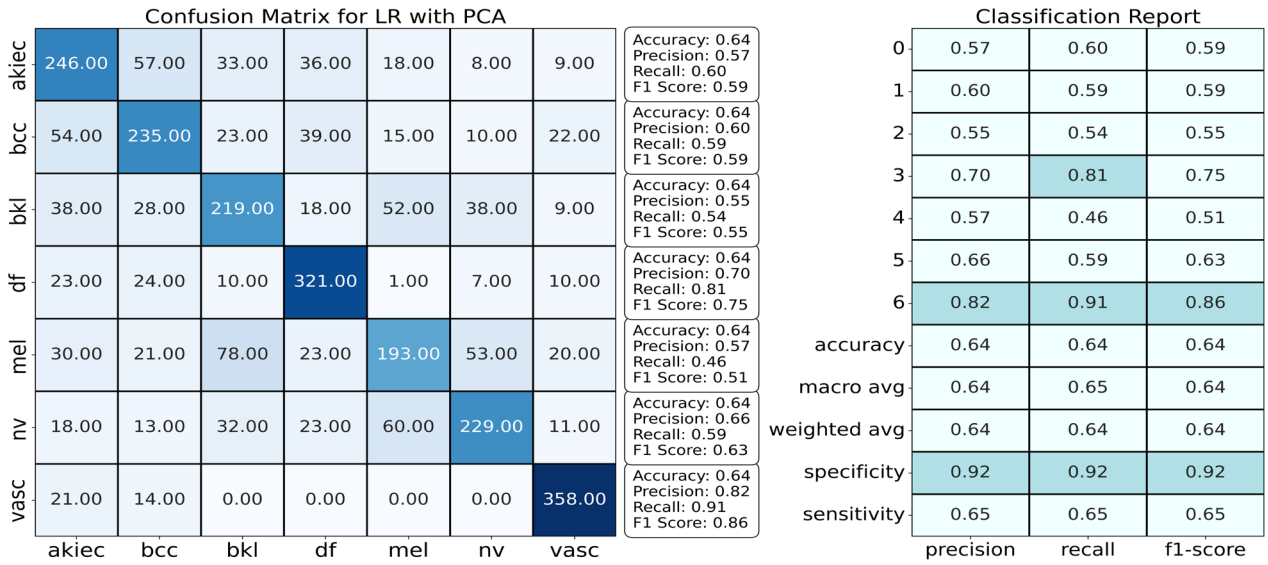

Fig. 10. Confusion Matrix and Classification Report for LR with PCA

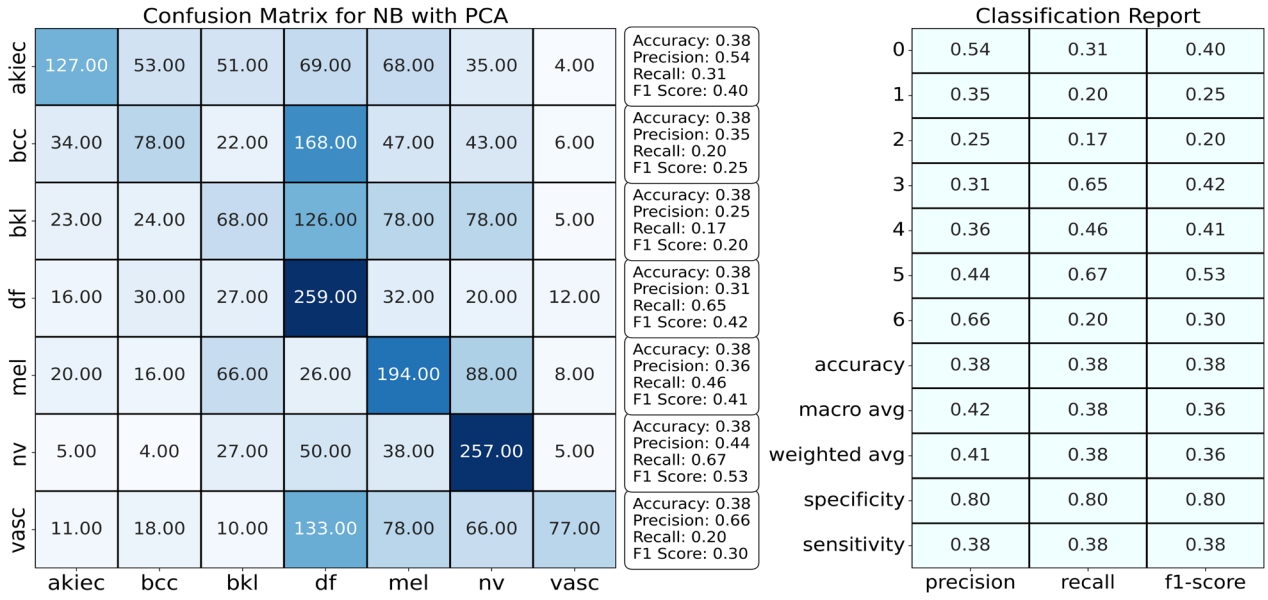

Fig. 11. Confusion Matrix and Classification Report for NB with PCA

Notably, upon inspecting the matrix, it becomes evident that the Random Forest (RF) model when coupled with Principal Component Analysis (PCA) has produced the most favorable confusion matrix in contrast to alternative approaches.

In a confusion matrix, the predicted classifications made by a model are compared with the actual classifications (ground truth) to determine how many instances were classified correctly and how many were misclassified.

Here's a breakdown of the terms used in a confusion matrix:

- True Positive (T_P): This count represents instances correctly predicted as part of the positive class. In other words, these are the situations where the model accurately identifies positive cases.
- True Negative (T_N): This value indicates instances accurately predicted as part of the negative class.
- False Positive (F_P): This figure reflects instances wrongly predicted as part of the positive class when they actually belong to the negative class.(Type I error).
- False Negative (F_N): This number signifies instances mistakenly classified as part of the negative class when they are actually part of the positive class. (Type II error).

The metrics that can be used to estimate the performance of a classification network are:

- Accuracy: This metric gauge the portion of instances that the model has accurately classified in relation to the total instances evaluated. It offers a broad assessment of the model's overall correctness.
- Precision: Precision involves the proportion of instances that the model has correctly predicted as positive compared to the total instances it has labelled as positive.
- Recall (Sensitivity): Recall quantifies the fraction of positive instances the model has successfully identified among all actual positive instances,

- measuring the model's ability to capture positives.
- F1 Score: F1 Score provides balancing between accurate prediction and capturing true positives, by using their harmonic mean.

$$Accuracy = \frac{T_P+T_N}{T_P+T_N+F_P+F_N} \quad (9)$$

$$Precision = \frac{T_P}{T_P+F_P} \quad (10)$$

$$Recall = \frac{T_P}{T_P+F_N} \quad (11)$$

$$F1-score = \frac{2*T_P}{2*T_P+T_N+F_P+F_N} \quad (12)$$

A classification report is a table or textual representation that presents performance metrics for each class in a classification problem. It's often used to evaluate the effectiveness of ML models, specifically in scenarios where you have multiple classes (more than two) to predict.

A classification report is a concise way to assess a model's performance on a per-class basis, which is crucial for understanding how well the model is doing across different categories. It's particularly valuable when you want to identify if the model is performing well for some classes but not others, which can guide improvements or adjustments in your model and training process. Fig 7. to Fig 11. include classification reports of all the classifiers.

The information obtained from the classification reports is also embedded in the confusion matrix figures in Fig 7.to Fig 11. The RF is giving the maximum accuracy of 89% with recall almost equal to 1 for the class labels 0,3,6 and recall of 0.94, 0.84, 0.82 and 0.61 for labels 1,2,4,7 respectively. The f1-score is 1 for labels 3,6 and it is 0.75,0.96,0.90,0.88,0.75 for labels 0,2,4,5,7 respectively. The next best performance is given by SVM with accuracy 82% followed by KNN with accuracy 80% followed by LR and NB with accuracies 64% and 38% respectively. The summary of results is given in Table II. The parameters specificity and sensitivity are also measured and summarized in the Table II. RF with PCA obtained a sensitivity of 89% and a specificity of 98%.

A similar approach is followed with GABOR feature extraction. The features that are extracted using GABOR are used as inputs to the classifiers. Fig 12. To Fig 16. show the confusion matrix and classification reports of RF, SVM, KNN, LR and NB with GABOR. The summary of the results from these graphs is tabulated in Table III.

From Table III, we can observe that RF produced best results again. The accuracy of Random Forest with Gabor filter is 84% while precision is 92%, recall and f1-score both are 84%. RF with GABOR obtained a sensitivity of 84% while the specificity is 97%.

TABLE II. COMPARISON OF PERFORMANCE METRICS AMONG VARIOUS CLASSIFIERS WITH PCA

Method	Accuracy (%)	Precision (%)	Recall	F-1 Score	AUC (%)	STD (%)	Sensitivity (%)	Specificity (%)
RF+PCA	**89**	**92**	**89**	**89**	**94**	**9**	**89**	**98**
SVM+PCA	82	82	82	82	90	9	82	97
KNN+PCA	80	80	80	79	88	9	80	96
LR+PCA	64	64	65	64	79	8	65	92
NB+PCA	38	42	38	36	64	7	38	80

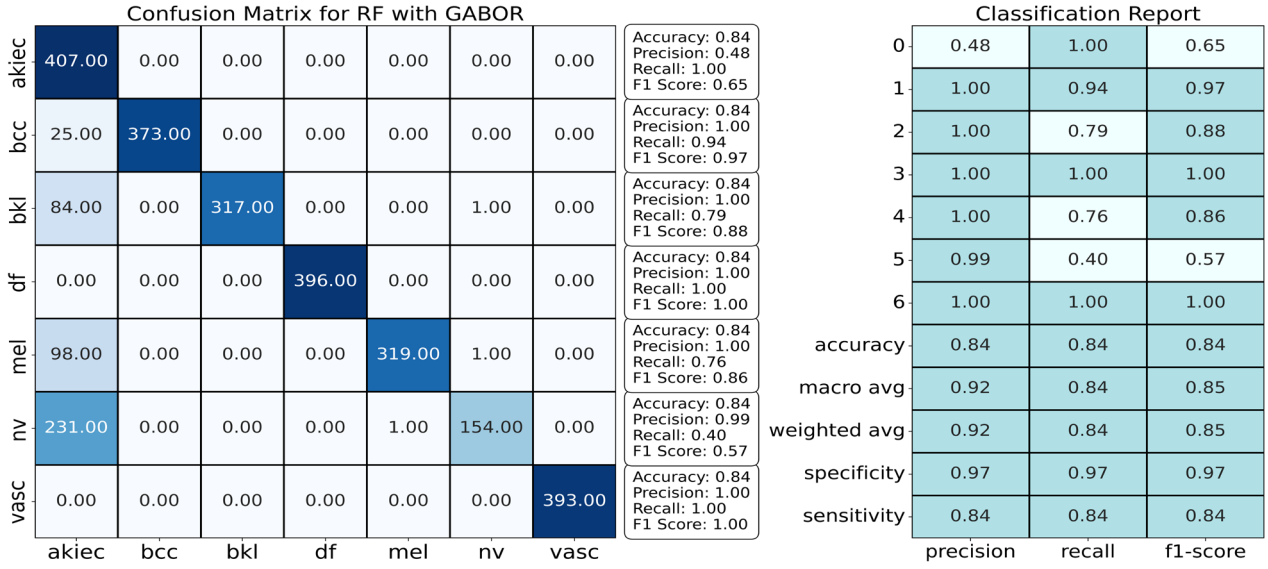

Fig. 12. Confusion Matrix and Classification Report for RF with GABOR

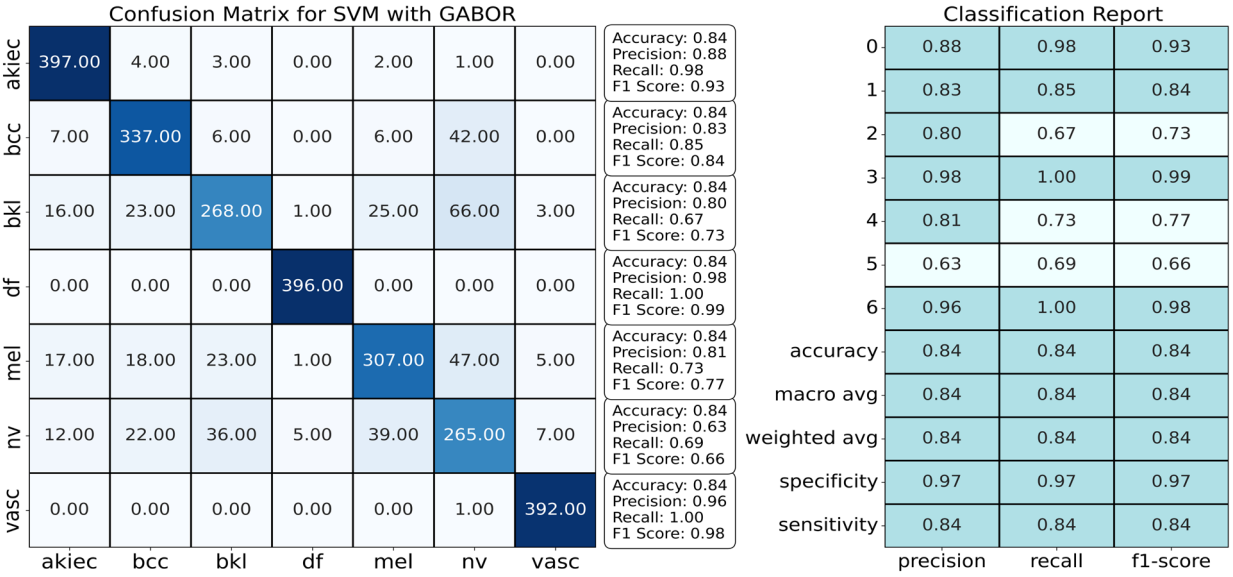

Fig. 13. Confusion Matrix and Classification Report for SVM with GABOR

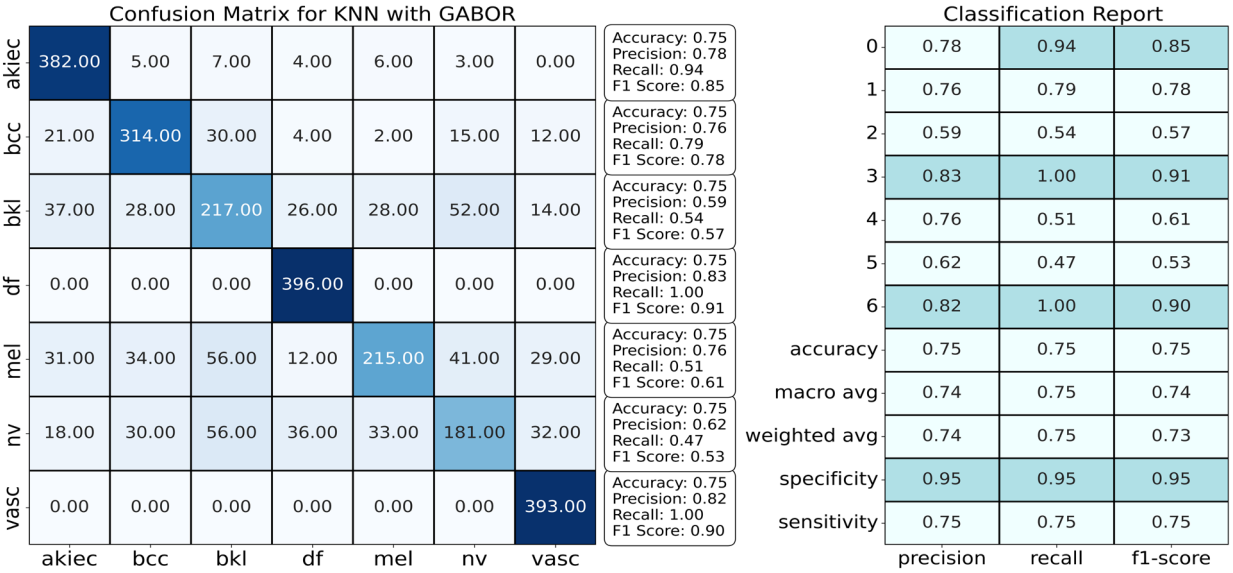

Fig. 14. Confusion Matrix and Classification Report for KNN with GABOR

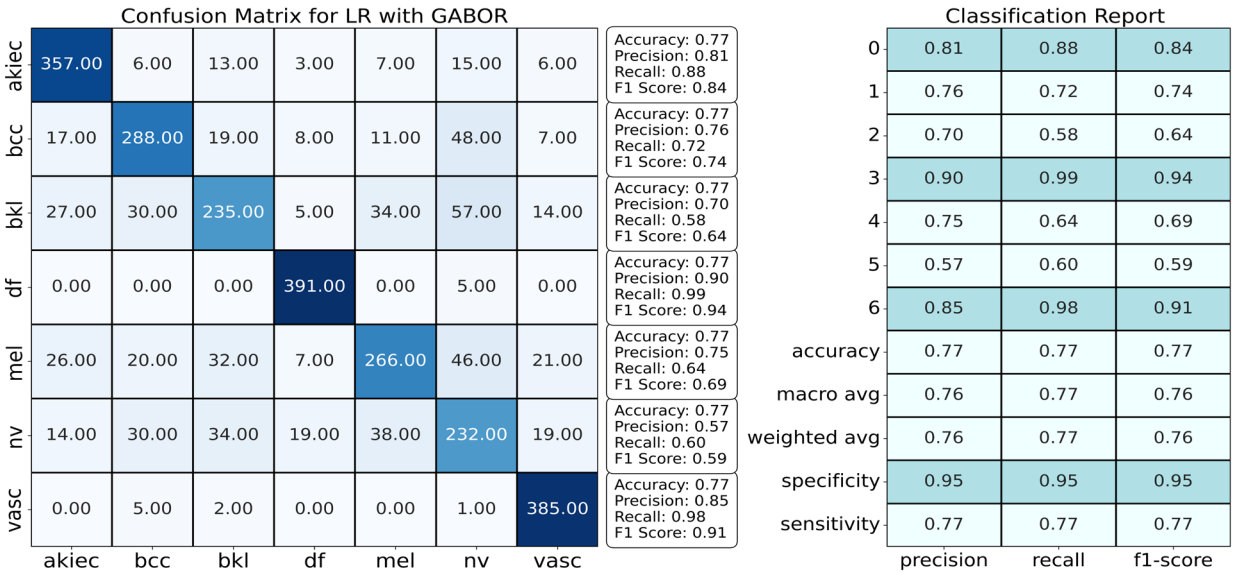

Fig. 15. Confusion Matrix and Classification Report for LR with GABOR

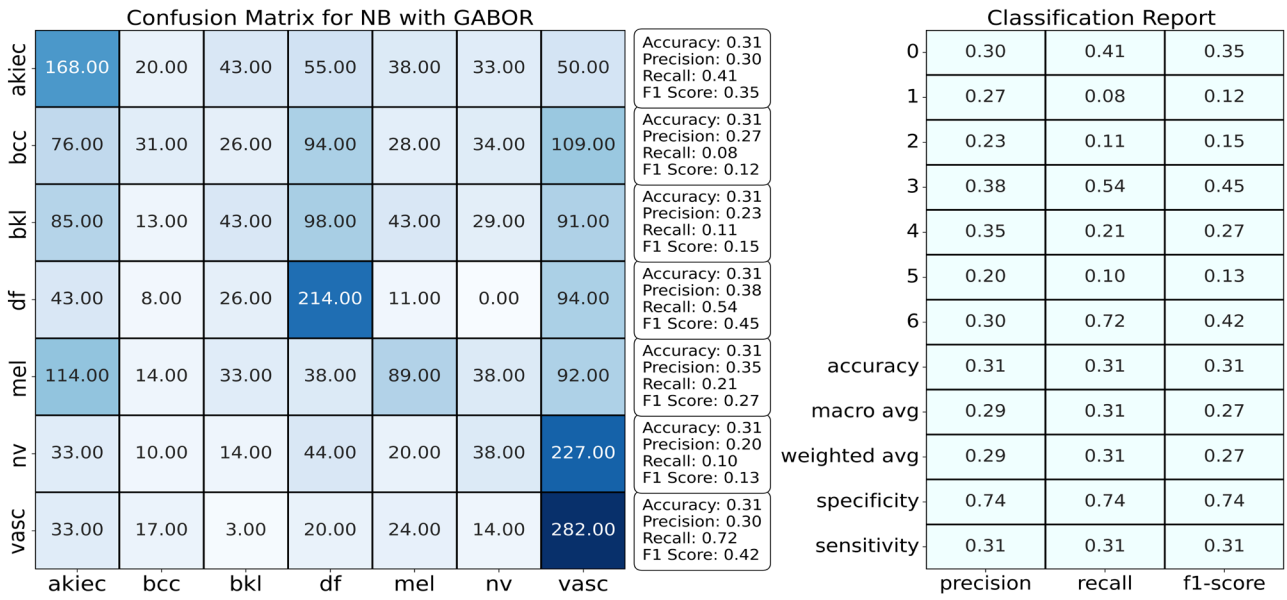

Fig. 16. Confusion Matrix and Classification Report for NB with GABOR

TABLE III. COMPARISON OF PERFORMANCE METRICS AMONG VARIOUS CLASSIFIERS WITH GABOR

Method	Accuracy (%)	Precision (%)	Recall	F-1 Score	AUC (%)	STD (%)	Sensitivity (%)	Specificity (%)
RF +GABOR	**84**	**92**	**84**	**84**	**100**	**10**	**84**	**97**
SVM+GABOR	84	84	84	84	98	8	84	97
KNN+GABOR	75	74	75	74	95	11	75	95
LR+GABOR	77	76	77	76	92	9	77	95
NB+GABOR	31	29	31	27	63	8	31	74

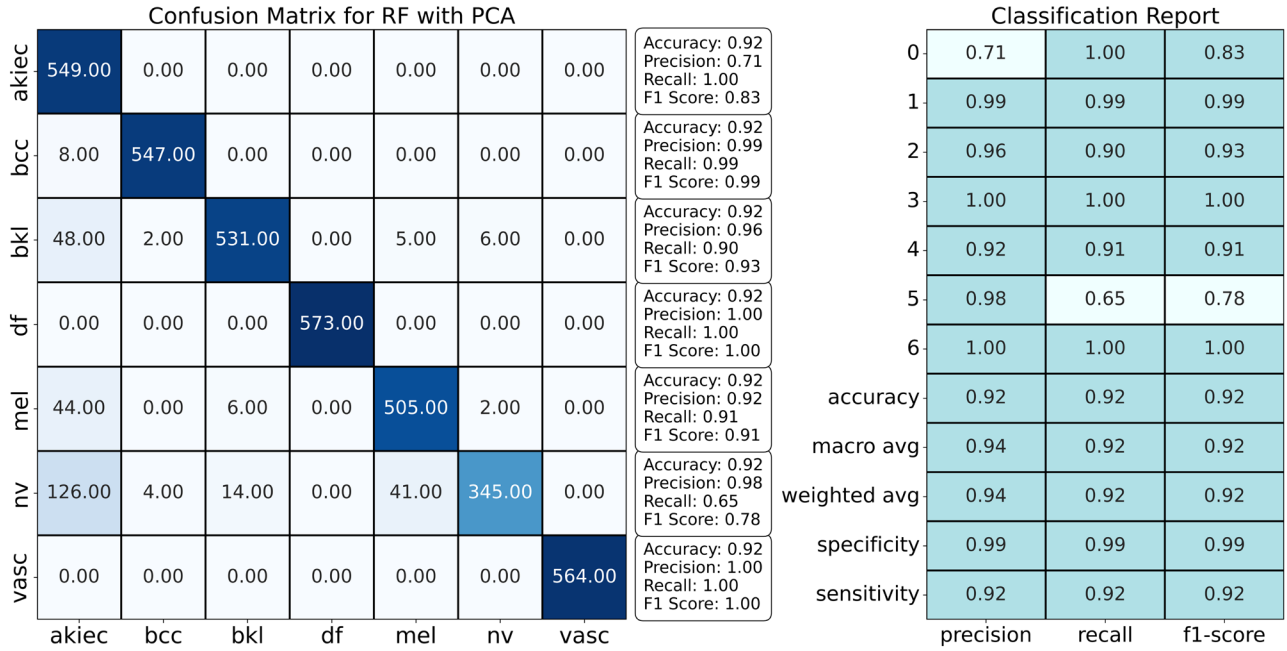

Fig. 17. Confusion Matrix and Classification Report for RF with PCA with 2800 Samples

TABLE IV. COMPARATIVE RESULTS

Published Works	Classifier	Accuracy (%)	Sensitivity (%)	Specificity (%)
[9]	BoF	82.21	86.00	72.21
[12]	SVM	91.84	91.30	91.87
[18]	SVM	79.00	72.00	90.00
[20]	SVM	87.38	90.76	82.76
This Work	**RF with PCA**	**92.00**	**92.00**	**99.00**

From the results in Table II and Table III, we conclude that Random Forest algorithm performed best with both Principal Component Analysis and Gabor feature extraction but with Principal Component Analysis it produced best results. We can further increase the accuracy of Random Forest with PCA by increasing the number of samples per class. In the results of Table II and Table III we chose 2000 samples per class. When we increased the number of samples per class to 2800, we achieved an Accuracy of 92%, Sensitivity of 92% and Specificity of 99% with Random Forest using PCA. The confusion matrix and classification report with the new sample size is shown in the Fig. 17.

The results are compared with some of the published works and are shown in the Table IV.

V. CONCLUSION AND FUTURE WORK

Random Forest in combination with PCA gave the best results compared to other classifiers. The highest accuracy obtained is 92 % on HAM10000 dataset. The accuracy of RF+PCA is good and better than some of the published works. The Machine learning algorithms need feature extraction techniques like Gabor or PCA or Wavelet filters etc in order to reduce dimensionality and hence reduce the computational complexity. In our future work we want to explore deep learning techniques with Convolutional Neural Networks in order to improve the accuracy.

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