Exploring Linear Algebra Techniques

For Enhancing Machine Learning Models

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By

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DEDICATION

This dissertation is written in the name of Allah, whose ineffable knowledge and directions have been ever a strong ally in pursuing this course. I would like to thank my parents from the bottom of my heart, as their endless support and great patience have contributed a lot to my accomplishments. Somehow, you have made me believe that there are dreams that are worth striving hard to achieve and that made me fearless in the pursuit of some of them and your words helped me in hard times. To my dear brother and sisters, my deepest gratitude for your constructive help and warm companionship during this whole process, I can tell you that you have made this journey a lot easier and brighter. I appreciate every one of you and the significant extent to which you have contributed to my evolving self. This work is not only my work, it is our work the work of a family. Your belief in me cemented my resolve never to be at it alone. I will cherish this work in honor of you and my family. For it has been only your love that has supported me through every challenge. May Allah reward you all generously and may we never cease to love and encourage each other for the rest of our lives. You have made this achievement, and you continue to light the way to this goal without me even asking. Thank you for this adventure.

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Mehak Ali

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LIST OF ABBREVIATIONS

Principal Component Analysis **(PCA)**

Random Forest **(RF)**

Support Vector Machine **(SVM)**

Convolutional Neural Network **(CNN)**

Deep Learning (**DP**)

Artificial Learning (**AI**)

Machine Learning (**ML**)

3 Dimensional (**3-D**)

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ABSTRACT

A valuable technique in the data analysis and machine learning is called principal component analysis (PCA) that plays the biggest role while working with high-quality data. This study examines the effects of PCA on the effectiveness and precision of three classification algorithms, specifically for the categorization of medical images: SVM, RF and CNN have been identified as the algorithms of interest in classification and recognition of objects. After feature extraction of the picture data of eczema and melanoma using VGG16, feature dimensions was reduced using PCA. The studies presented prove that the use of PCA reduces the time that is required for processing while maintaining the degree of accuracy and other relevant indicators. The accuracy of the training models on PCA-reduced data was 99% when using SVM, 98% when including all the predictors and 97% when only including demographic variables. 75% for RF, and 98. 75% for CNN. On the other hand, SVM, RF and CNN accuracy of non-reduced data was relatively higher with higher percentage of 99. 75%, 99. 25%, and 99. 75%, in that order. This clearly shows that application of PCA has least impact on the accuracy of these methods. What is most worrisome in this work is the lack of concern for applying the principle component analysis (PCA) as the first step when building a machine learning model. In PCA there is a careful and careful handling of high dimensional data with an optimum time of handling it. The fact that it has notably refined the time factor, makes it a must-have tool for successful and convenient model training in medical picture categorization. These results indicate that it is possible to improve efficiency in preparing the models for machine learning by integrating PCA into the pipeline and the reasonableness of the proposed pipelines for medical image analysis in terms of performance and costs. Therefore, the study calls for more utilization of PCA for medical image analysis to get fast training but with good performance and high accuracy. In addition, this work lays the groundwork for future studies that aim to extend PCA analysis for increasing the global applicability of the approach in diverse settings and to integrate it with other types of dimensionality reduction techniques. These studies could entice new and innovative ways of thinking towards machine learning as well as data analysis.

CHAPTER 1
INTRODUCTION

As the ‘new oil’, data the need to capture, manage and analyze big data, has become crucial. Suppose that you are able to easily discern major trends and the overarching bull’s eye in a flood of information. This is what dimensionality reduction techniques bring as chances and, therefore, does not lose considerable aspects when making augmented data easy.

1.1 Background and Motivation

The other valuable technique in the data analysis and machine learning is called principal component analysis (PCA) that plays the biggest role while working with high-quality data. This study examines the effects of PCA on the effectiveness and precision of three classification algorithms, specifically for the categorization of medical images: SVM, RF and CNN have been identified as the algorithms of interest in classification and recognition of objects. After feature extraction of the picture data of eczema and melanoma using VGG16, feature dimensions was reduced using PCA. The studies presented prove that the use of PCA reduces the time that is required for processing while maintaining the degree of accuracy and other relevant indicators. The accuracy of the training models on PCA-reduced data was 99% when using SVM, 98% when including all the predictors and 97% when only including demographic variables. 75% for RF, and 98.75% for CNN. On the other hand, SVM, RF and CNN accuracy of non-reduced data was relatively higher with higher percentage of 99.75%, 99.25%, and 99.75%, in that order [1-3].

This clearly shows that application of PCA has least impact on the accuracy/efficiency of these methods. Also, the PCA is useful in reducing the amount of time taken during training besides enhancing the overall efficiency of the model in the training process [4]. What is most worrisome in this work is the lack of concern for applying the principle component analysis (PCA) as the first step when building a machine learning model. In PCA there is a careful and careful handling of high dimensional data with an optimum time of handling it. Thus, PCA is valuable in high-dimensional data environment, though, it leads to a minor reduction in accuracy [5].

The fact that it has notably refined the time factor, makes it a must-have tool for successful and convenient model training in medical picture categorization. These results indicate that it is possible to improve efficiency in preparing the models for machine learning by integrating PCA

into the pipeline and the reasonableness of the proposed pipelines for medical image analysis in terms of performance and costs. Therefore, the study calls for more utilization of PCA for medical image analysis to get fast training but with good performance and high accuracy. In addition, this work lays the groundwork for future studies that aim to extend PCA analysis for increasing the global applicability of the approach in diverse settings and to integrate it with other types of dimensionality reduction techniques. These studies could entice new and innovative ways of thinking towards machine learning as well as data analysis [6].

1.2 Vision of the Study

1.2.1 Enhanced Dimensionality Reduction

- Integrate PCA with eigenvector techniques as part of a stronger framework with which to work on dimensionality.
- Improve data variance and structure preservation, particularly for time-dependent datasets.

1.2.2 Improved Computational Efficiency

- Lessen the amount of computation required for high-dimensional data.
- Reduce machine learning model training times without sacrificing accuracy [1-3].

1.2.3 Optimized Time Domain Data Analysis

- Use temporal correlations in methods for reducing dimensionality.
- Improve model performance in time-sensitive applications like dynamic system monitoring and signal processing [4].

1.2.4 Superior Model Performance

- When applied to smaller feature sets, improve the precision and dependability of machine learning models, particularly CNN, SVM, and RF.
- Illustrate the usefulness of the suggested approach in realistic applications [5].

1.2.5 Practical Application in Healthcare

- Aid in the implementation of effective machine learning models in medical environments.

- Enhance medical picture processing and analysis for quicker and more precise diagnosis [6].

1.3 Principal Component Analysis: An Overview

Principal Component Analysis (PCA) is an arithmetical method used in decreasing the number of features in manageable few. The more a data set yields variance, the more it will be contained in the first principle component and each subsequent principle component can only account for a certain percent variance to be orthogonal to the components that have gone before it [2]. This method permits the reduction of the size of the dataset while maintaining all the features that are for the most part important. Thus, the principal components are the Eigen vectors corresponding to the maximal Eigen values. Out of the raw collected data, a set of data with low dimensionality is derived from the raw data by a technique known as the principal component analysis for short that is essential for the assessment of data before being processed [3].

1.4Application in Machine Learning

The effectiveness of the model in different algorithms however in this case as discussed the supervised learning depending on the vastness of data and how effective the input data is. Often, the data is high dimensional and it is comprised of attributes some of which could be irrelevant for learning and therefore the training process ends up taking longer and the models accuracy could be slightly reduced as well. To overcome these issues PCA minimizes the number of features and this helps in reducing the size of the model and hastens the training process. It is very crucial in the healthcare sector where timely and accurate diagnosis takes center stage and therefore efficiency boost as provided by PCA is highly valued [5].

1.4.1 Convolutional Neural network

Convolutional neural networks (CNNs) have acquired popularity in recent years. They are an essential component of many challenging and successful machine learning applications, such as the ImageNet's entity recognition, image processing, and facial recognition. As a result, we use CNN as our model for these difficult image categorization tasks. In academic and professional settings, CNN is used to segment and classify images [6].

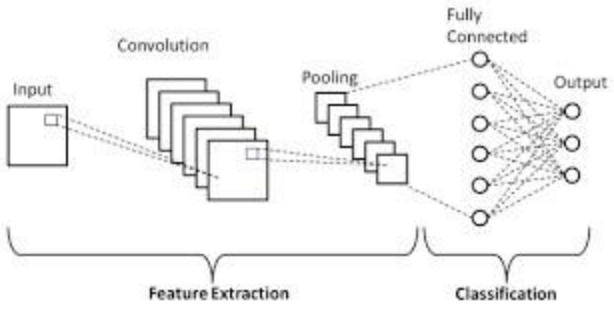


Figure 1.1: Illustration of Convolutional Neural network

1.4.2 Support Vector Machines (SVMs)

Among the several ML techniques is SVM learning. SVM is far more effective than other ML techniques at identifying minute patterns in complicated datasets. SVM is useful for detecting faces, handwriting, counterfeit credit cards, and speech identification. Cancer is a hereditary disease in which biological processes specific to tumors, medication benefit prediction, cancer subtypes, and outcome prognoses can all be represented by genomic feature patterns or feature function patterns. As a result, SVM's artificial intelligence can assist us in identifying these trends across a range of applications [1].

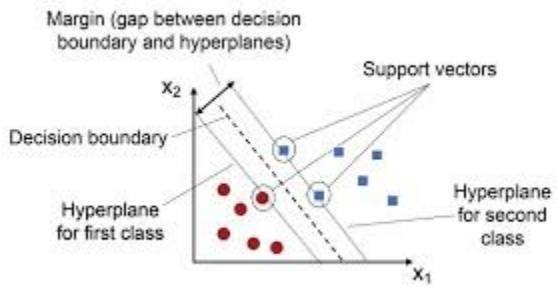


Figure 1.2: Illustration of Support Vector Machine (SVM)

1.4.3 Random forest (RF)

The machine learning technique known as "random forest" is commonly used in classification, regression, and other applications. Many decision trees are used in this collective learning technique to provide a single, more reliable prediction. The fundamental concept of random forests is to construct different trees that are skilled on different random samples of the training set; when these trees are joined, their predicted outcomes may be aggregated to form a final model. Random forests are an improvement over decision trees because they can be more generalized than decision trees because they are an average of their output. As can be seen, the model is more resilient and less susceptible to noise and outliers because each tree is trained using a distinct sample of data [2].

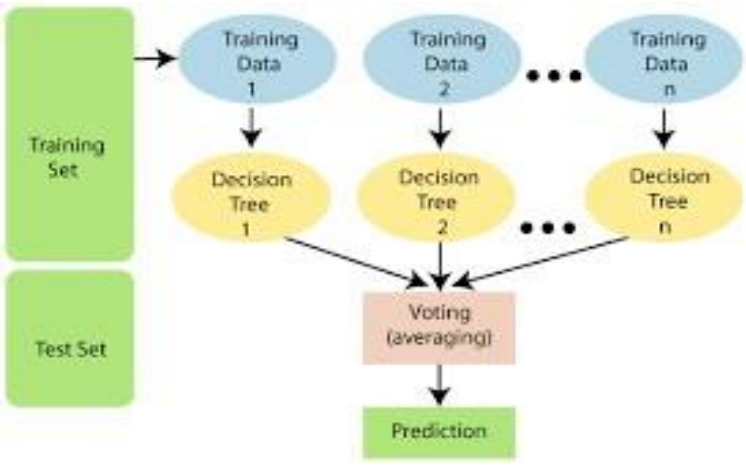


Figure 1.3: Illustration of Random Forest (RF)

1.5 Study Objectives

The motive of the paper is to assess effectiveness of PCA and eigenvector integration in improving dimensionality reduction for time domain optimization. In specifically, it will assess the impact of PCA on the efficacy and precision of three using popular classification algorithms: CNN, random forest (RF), and support vector machine (SVM). The research will investigate if PCA can reduce

training times without loss in the quality of the classification, based on a set of images of cancer and eczema. The specific objectives are as follows:

1. Comparing the accuracy of SVM, CNN, and RF models trained on PCA-reduced data to models trained on standard features.
2. Evaluating how much time each model needs.
3. Giving an example of how PCA might shorten training periods without compromising accuracy.

1.6 Importance of the Study

This research emphasizes how crucial dimensionality reduction is when handling medical data. The adoption of machine learning models in healthcare settings, where quick and accurate diagnostic tools are critical, may be made easier by the increased computational efficiency. Furthermore, the study's conclusions can be applied to other fields with comparable data constraints, increasing PCA's usefulness and influence.

1.7 Research Questions

- In what ways does the integration of eigenvectors with PCA improve the effectiveness of dimensionality reduction for time domain data?
- In what ways do models trained with PCA-reduced features differ from models trained with standard features in terms of accuracy?
- In what ways does PCA affect the amount of time needed for CNN, SVM, and RF models during training?
- In what ways does the suggested method effectively capture temporal correlations in time domain data?
- In what ways does the proposed PCA and eigenvector integration method to boost machine learning models' performance in real-world applications, such as medical image classification?

CHAPTER 2

LITERATURE REVIEW

2.1 General idea of Dimensionality Reduction Techniques

By removing redundant features and noisy or irrelevant input, the pre-processing step called "dimensionality reduction" (DR) seeks to reduce training time and improve learning feature accuracy [6]. In data analysis and machine learning, it is an essential preprocessing step that reduces the overall number of random variables being analyzed. Approaches such as Principal Component Analysis (PCA), Linear Discriminant Analysis (LDA), etc., are often utilized for dimensionality reduction [7].

In recent years, tremendous digital data have been produced in diversified domains of applications continually. In addition to this, data is growing exponentially in complexity, dimensionality, heterogeneity, and size. High Dimensional Data (HDD) is applied in various realms, including social media, web, biomedical, education, as well as medicine, etc. Dimensionality Reduction can be used with the help of Feature extraction [8]. In the process of Feature Extraction, a new reduced set of data is formed by eliminating some irrelevant features from the original datasets. The new feature set reserves most of the information from the original data set [9].

Feature extraction (FE) technique is very useful in reducing the resources required for processing while maintaining the relevance of the feature dataset because it extracts additional features from the original set. Techniques such as PCA, LSA, LDA, ICA, and PLS are examples. PCA is the most popular and widely used technique, as Karl mentions [10]. PCA is a basic method of data preprocessing, which only extracts informative data from very large, over-determined datasets full of redundancy [11]. Principal Component Analysis is a basic technique of data transformation that decreases covariance (i.e., information replication) and increases variance (i.e., information expansion) [12].

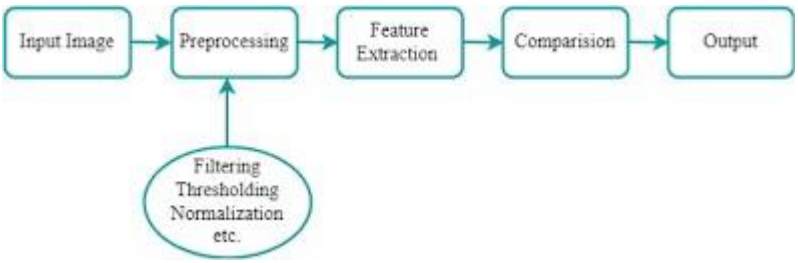


Figure 2.1: Hierarchy Structure of feature extraction method

Feature Selection is a process in which we choose the features of the data that are of more importance to our problem. This becomes a laborious exercise of manually extracting the required features for different requests [13]. Applying the proper technique can help save time and effort in extracting important features for inspection [14]. Feature selection is obtained from new samples, values, and misconceptions about outputs, which could be found by a huge number of features. This expands the scope of the search space and will help prepare your dataset for learning [15]. Thus, we need from the first set of data to separate. Notably, among the original features, only FS techniques have the ability to pick out features by relevance [16].

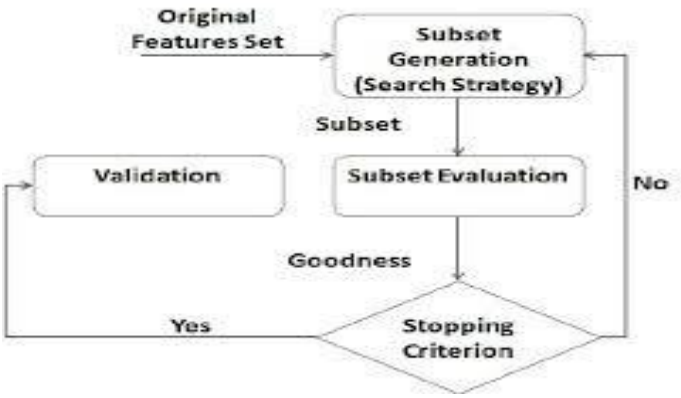


Figure 2.2: Process of Feature Selection

2.2 Principal Component Analysis (PCA)

The purpose of PCA is to find the most appropriate basis that can be used to re-express a given dataset. It is expected that this new basis is free from noise and reveals the hidden patterns in the

data [17]. There are many uses such as feature mining, data compression, reducing dimensions, and data imaging [18].

PCA is a member of the dimensionality reduction family and is very helpful for huge, massive, and highly linked data sets (i.e., numerous variables and multiple observations per variable). Finding a smaller set of characteristics that accurately captures the original data in less dimensional data is the motive [19]. The application of PCA and the related methods makes it possible to store or even retrieve information about individual differences and summarize them. That is why these strategies are valuable nowadays when people speak about Big Data and individual approaches to disease treatment [20].

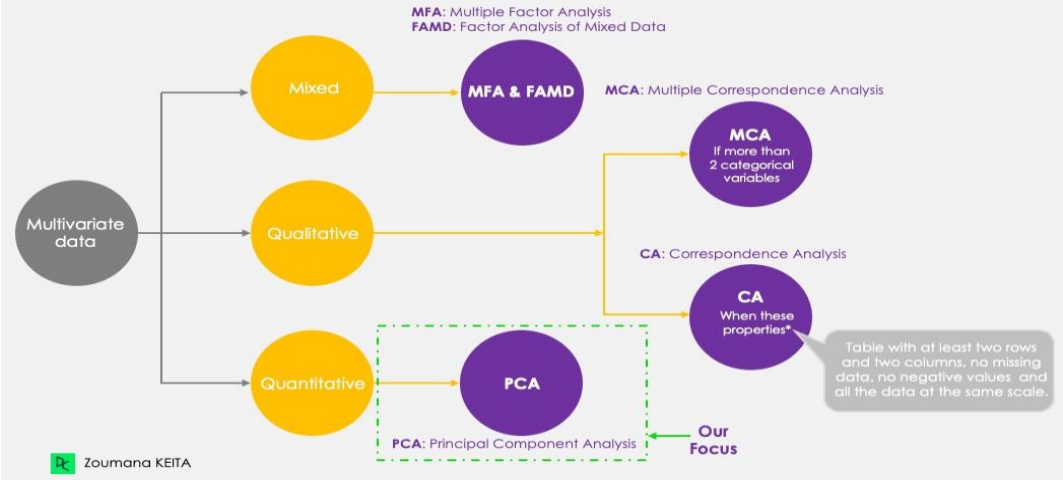


Figure 2.3: Illustration of PCA method

2.3 Eigenvector Integration

One of the ways to boost the potential of PCA further is by integrating more data into the concept's main components using a method referred to as eigenvector integration. This method has been investigated to improve the dimensionality reduction to increase the rate of efficiency [21]. For instance, Nguyen et al. (2015) developed an eigenvector-based method for picture classification that enhanced accuracy by integrating spatial information into the principal components [22]. Comparing PCA models trained with and without the extra domain-specific data showed that the latter performed better than the former [23]. Big data are becoming more constant in big organizations, yet their comprehension is not simple [24]. One method of reducing data dimension is PCA, which helps to avoid the loss of a large amount of data and increase readability by gradually increasing variance and creating new variables [25].

2.4 Dimensionality Reduction in Time Domain Data

The temporal relationships of time-domain data create special obstacles for dimensionality reduction. These temporal correlations are not taken into consideration by traditional PCA, which frequently results in less than ideal performance in time-sensitive applications [26]. To address these problems, methods like Time-Frequency PCA and Dynamic Mode Decomposition (DMD) have been proposed, which include temporal information into the dimensionality reduction process [27].

Since each image's data is arranged into two-dimensional pixel values, each of which has a unique RGB bit value, high-resolution images are also known as high-dimensional data spaces. One of the challenges in exchanging image files over the Internet is the encoding of image data. One of the main problems that Internet users have always had is the long time it takes to post and download images [28]. In addition to data transmission issues, high-resolution images require more storage capacity [29]. PCA is a mathematical method used to reduce the dimension of data [30]. The principle of the factoring matrix extracts the linear system's principal pattern. Because the goal in the preliminary literature is to summarize, we recited 4 primary steps of PCA dimension reduction: 1) Image Data Normalization, 2) Computing Covariance Matrix, 3) SVD Decomposition, 4) Projection [31]. Experimental results indicate that PCA technique significantly reduces the dimension of image data by maintaining primary characteristics of the original image [32].

2.5 Machine Learning Applications

The automatic use of algorithms to teach a computer for a given task is known as machine learning (ML). Application sets of algorithms are used to mine data that find and filter general rules in big data sets, while also automatically learning user preferences [33]. To enhance model performance, dimensionality reduction methods such as PCA are frequently employed in machine learning [34]. The significance of feature extraction and selection in minimizing overfitting and enhancing generalization was covered by Guyon and Elisseeff (2003) [35]. Superficial or duplicated features can impede learning and reduce model accuracy in supervised learning. PCA simplifies the model by lowering its feature count, which reduces computational complexity and speeds up training [36].

2.6 PCA in Medical Image Classification

Medical imaging is becoming more and more vital to the early discovery, analysis, and cure of diseases because of the growing desire for quicker and more precise care. The advancements in physics, electronic engineering, computer science, and technology have led to an increase in medical picture resolution and a proliferation of image modes. The quantity of medical images is also growing quickly at the same time. Picture classification, target identification, and picture segmentation have all greatly improved in recent years thanks to the advent of numerous annotated natural image data sets and the development of deep learning in computer vision. Numerous studies on supervised learning-based early illness detection and diagnosis have been conducted. Ciresan used deep neural networks to analyze medical images, which were crucial in the identification and segmentation of brain tumors, breast cancer, and skin cancer. According to Hafemann et al.'s experimental results, convolutional neural networks are more effective at extracting features than standard texture descriptors, and thus improves picture identification accuracy. [31]

In PCA, the integral prognosis of the dataset into a subspace produced by an organization of orthogonal axes results in the storage of data with decreased dimensions. The computational content with decreased dimensions is chosen to identify the important properties of the data with minimal loss of information. [32]

Jolliffe, I. T. (2002) provided a thorough investigation of the theoretical foundations and practical solicitations of PCA. He included discussions on the mathematical derivation of PCA, analysis of

principal components, and various extensions and modifications of the method. The research focuses on the downsides of conventional optimization techniques, such as local minimum traps and the challenge of locating global optimal solutions, in PCA, such as stochastic gradient descent (SGD). [33]

Johnson, R. A., & Wichern, D. W. proposed multivariate data analysis. In the course inference about means and multivariate distributions were taken into account. Examples were explored for techniques such as principal components, factor, cluster, and discriminant analysis. [34]

PCA's adaptability and significance in the field of statistical genetics are highlighted by the several applications it plays in the field, including heritage prediction, genome-wide connotation studies, rare alternates analyses, and more. Although the instruction is practical, it might not go into great detail about the theoretical foundations. It may also be using fairly antiquated software and computational techniques. [35]

For data reduction, Principal Component Analysis (PCA) is a useful method, particularly when used with machine learning models such as support vector regression. SVR and PCA work together to improve estimation accuracy while lowering the number of variables in the predictive model, increasing its simplicity and efficiency. The t-distribution hunting search algorithm (THSA) is put forth as a global optimization technique that gets beyond the drawbacks of gradient descent methods and improves the dimensionality reduction effect of PCA. [36]

Abdi, H., & Williams, L. J. gave a tutorial on PCA, describing its computation, theoretical underpinnings, and interpretation. While easily readable, the tutorial-style paper may be shallow when it comes to more complex theoretical details. Its overemphasis on social sciences could potentially limit its applicability to other fields. [37]

Researchers suggested reformulating the orthogonality requirements as rank constraints and optimizing over both sparsity and rank constraints at the same time, resulting in solutions for multi-component real-world datasets with bound gaps between 1% and 5%. They presented a novel algorithm, sparse FPCA, to efficiently model principal Eigen functions in high-dimensional functional processes in which the number of random functions is greater than or equal to the sample size. [38]

CHAPTER 3

COLLECTION OF DATA AND METHODOLOGY

This section describes how to collect pertinent data in order to successfully respond to research questions. It describes the data gathering instruments and sample techniques used to guarantee data dependability and accuracy. The analytical methods and resources used for a comprehensive comprehension of the data are also described in this part. The whole process of methodology is described in flow chart below

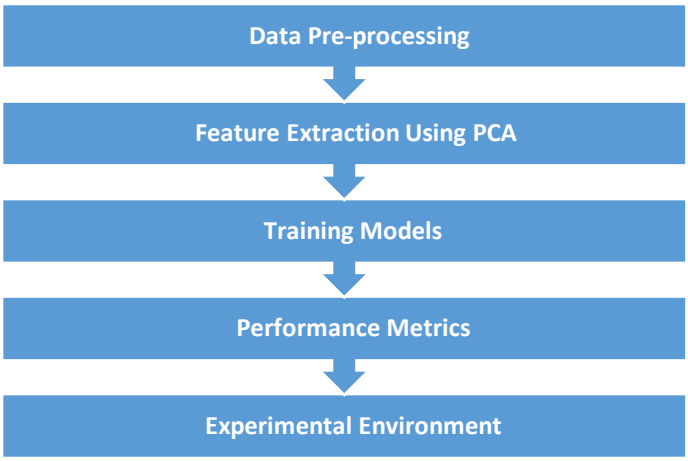


Figure 3.1: Flowchart of Methodology

3.1 Data Collection:

The data being used here is from the dataset taken from International Skin Imaging Collaboration (ISIC) library. The data consist of a set of high-resolution dermatoscopic pictures of skin lesions known as the ISIC Melanoma Detection Dataset. It features pictures of benign skin problems as well as melanoma, a severe type of skin cancer. The dataset is perfect for creating machine learning models for tasks like segmentation and binary classification (melanoma vs. non-melanoma) because each image has a diagnosis annotated on it.

3.2 Data Pre-processing

One of the earlier activities that are vital in selecting the data that needs to be prepared for analysis and model development is preliminary data preparation. Some of the data that we employed in this study included pictures of melanoma or eczema. Scaling and normalization of image followed by process of division of data into training and testing sets are shown.

3.2.1 Image Resizing

To maximize both efficiency and quality, each image is resized to 128 by 128 pixels. During this resizing, binaural interpolation is used to preserve the image quality.

Algorithm1:

BEGIN:

//Data Pre-processing

Provide a dataset with images of melanoma and eczema.

//Image Resizing:

FOR each image in dataset:

The image is resized using bilinear interpolation to 128 by 128 pixels.

END FOR

3.2.2 Normalization

To scale each image to the range [0, 1], value of pixels is divided by the maximum pixel value (255 for 8-bit images). This stage reduces bias brought on by various illumination settings and boosts the machine learning model's efficacy.

Algorithm 2:

//Normalization:

FOR each image in dataset:

To scale the values of pixels to the range [0, 1], divide them by 255.

END FOR

3.2.3 Data Splitting

An 80-20 ratio was used to split the dataset into training and test sets. After the machine learning model has been taught using the training technique, its performance is determined using the testing method. The percentage of each group (melanoma and eczema) in training and testing was controlled via stratified sampling.

In [5]:
```
# Function to load images from a folder
def load_images_from_folder(folder, label):
    images = []
    labels = []
    for filename in os.listdir(folder):
        img_path = os.path.join(folder, filename)
        img = cv2.imread(img_path)
        if img is not None:
            images.append(img)
            labels.append(label)
    return images, labels
```

In [6]:
```
# Load images for Melanoma and Eczema
melanoma_images, melanoma_labels = load_images_from_folder(melanoma_folder, 0)
eczema_images, eczema_labels = load_images_from_folder(eczema_folder, 1)
```

n [10]:
```
# Resize images to a common size
def resize_images(images, target_size=(224, 224)):
    resized_images = []
    for img in images:
        resized_img = cv2.resize(img, target_size)
        resized_images.append(resized_img)
    return resized_images

# Load and preprocess images for Melanoma and Eczema
melanoma_images_resized = resize_images(melanoma_images)
eczema_images_resized = resize_images(eczema_images)

# Combine resized images and labels
images = np.array(melanoma_images_resized + eczema_images_resized)
labels = np.concatenate((melanoma_labels, eczema_labels))

# Shuffle images and labels together
shuffle_indices = np.random.permutation(len(images))
images = images[shuffle_indices]
labels = labels[shuffle_indices]
```

n [11]:
```
# Preprocess images (resize, normalize)
def preprocess_images(images):
    processed_images = []
    for img in images:
        img = cv2.resize(img, (224, 224))  # Resize to fit VGG16 input shape
        img = preprocess_input(img)  # Normalize according to VGG16 requirements
        processed_images.append(img)
    return np.array(processed_images)
```

3.3 Feature Extraction Using PCA

Less dimension was added to the pre-processed images using Principal Component Analysis (PCA). The following is a list of the steps in the PCA transformation.

Algorithm 3:

//Feature Extraction Using PCA:

Flattening the Images

For each and every picture in the test and training sets: Image to a 16384-pixel, one-dimensional array

END FOR

3.3.1 Flattening the Images

The 128x128 images were all flattened into 16,384 pixel 1-dimensional arrays. The 2D images have to be transformed in order to be used with PCA, which works with 2D matrices where rows stand for observations and columns for features.

Algorithm 4:

FOR each image in training set and test set:

Flatten image to 1-dimensional array of 16,384 pixels

END FOR

- **3.3.2 How can I use mathematics to discover major components?**
  The following is how we can extract the major components using the general algorithm:
  a) For each variable, find its mean and subtract it (center-shifted).
  b) Calculate the center-shifted data's covariance matrix.
  c) Covariance matrix's eigenvectors and eigenvalues should be found, then sorted in uphill order of eigenvalues. The primary components are the eigenvectors, and we can use them to wrapping data. Let's take a step by step look at the mathematics underlying these processes as they seem counterintuitive.

- **Determine each variable's mean and subtract it using a center-shifted method**. Initially, we must create a data center that is displaced, like in the diagram below. We move the initial data to the center since it makes the computation easier.

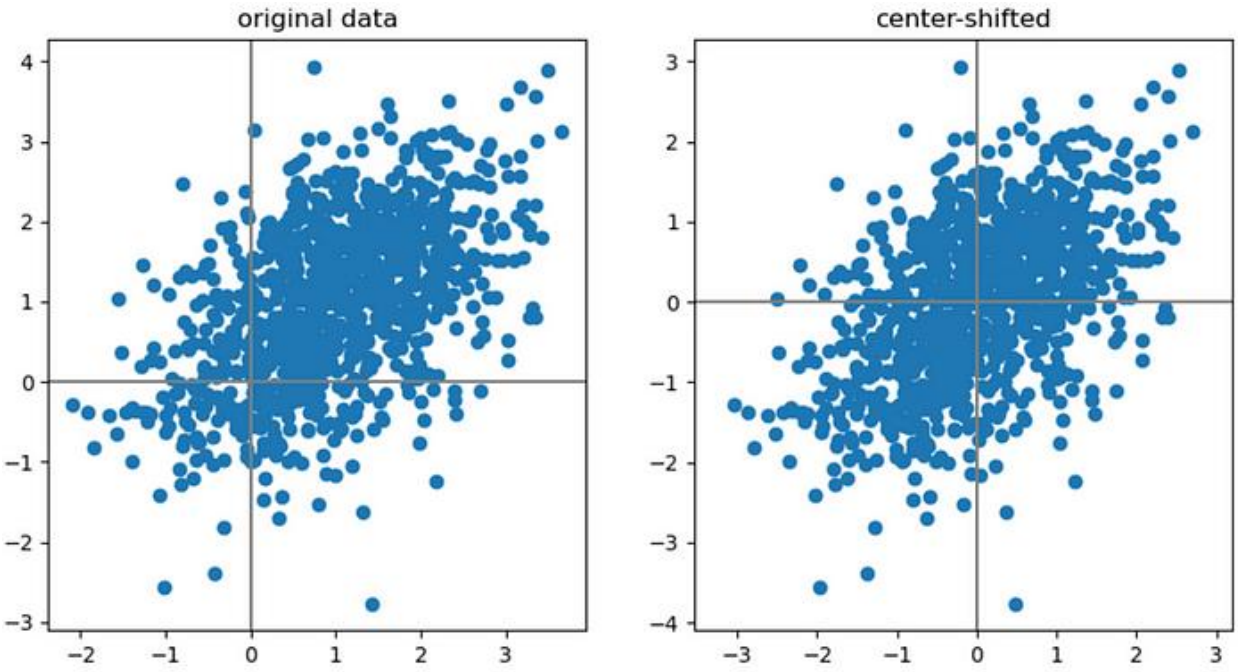


Figure 3.2: Depiction of center shifted data

The covariance matrix will be as easy to understand as the following equations if our data is already centered, meaning the mean is equal to 0. We therefore transfer our data center.

$$\boldsymbol{Cov}\,[\boldsymbol{X},\boldsymbol{Y}] = \boldsymbol{E}\big[(\boldsymbol{X}-\boldsymbol{\mu_x})(\boldsymbol{Y}-\boldsymbol{\mu_y})\big]$$

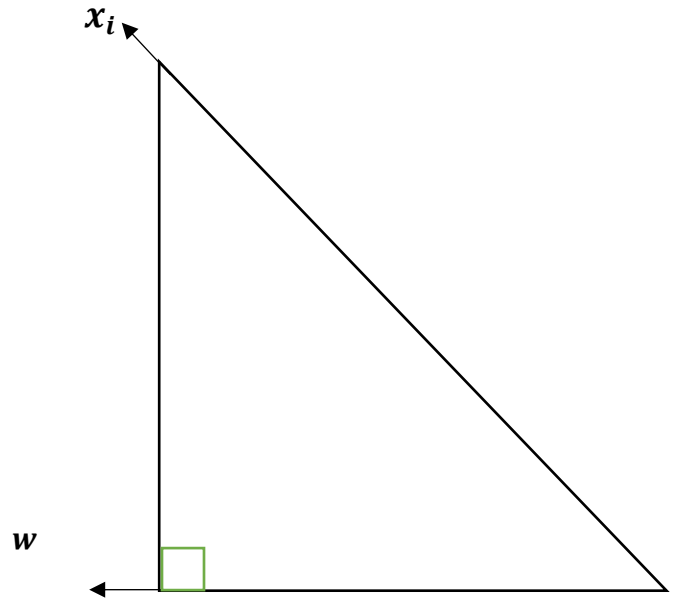
Substitute $\boldsymbol{Cov}\,[\boldsymbol{X},\boldsymbol{Y}] = \boldsymbol{E}[\boldsymbol{XY}]$

$\boldsymbol{\mu_x = 0}\,, \boldsymbol{\mu_y = 0}$

- **Covariance Matrix Calculation**

Another quantity that needs to be computed is the covariance matrix of the data. Wait, where does this covariance matrix come from? I'll write down the mathematical argument for why the covariance matrix is needed.

First, we are looking for a one-dimensional projection. We want to project our p-dimensional vectors onto a line, which is a one-dimensional space. Suppose we have that the line has a unit vector $\boldsymbol{w}$, along it. Then we can write the projection of a data vector $\boldsymbol{x}$i, onto the line to be the length of the projection vector which will be given by the dot multiplication of $\boldsymbol{x}$i and $\boldsymbol{w}$ a scalar.



Cos $\boldsymbol{\theta}=\frac{x_i.w}{\|x_i\|\|w\|}$

The length: $\|xi\| \cos\theta = \frac{x_i.w}{\|xi\|\|yi\|} = x_i$ .w

Figure3.3: Projection of p-dimensional vectors on a line

This projected vector can therefore be denoted in p-dimensional space as a projection vector $\boldsymbol{w}$ dot multiplication of $\boldsymbol{x}$i and $\boldsymbol{w}$. Since we center-shifted the data, we can use the means of the vectors $\boldsymbol{x}$i to determine that the projection will be zero.

$$\frac{1}{n}\sum_{i=1}^{n}\boldsymbol{x_i} = 0 \tag{1}$$

$$\frac{1}{n}\sum_{i=1}^{n}(\boldsymbol{x_i}\cdot\boldsymbol{w})\boldsymbol{w} = ((\frac{1}{n}\sum_{i=1}^{n}\boldsymbol{x_i})\cdot\boldsymbol{w})\boldsymbol{w} = 0 \tag{2}$$

Since the projected vectors are not equal to the original vectors, we have some errors when we compress our data from p to one dimension. There are some residuals as seen from the image if we try to make two-dimension data to the single line (the red line in the image).

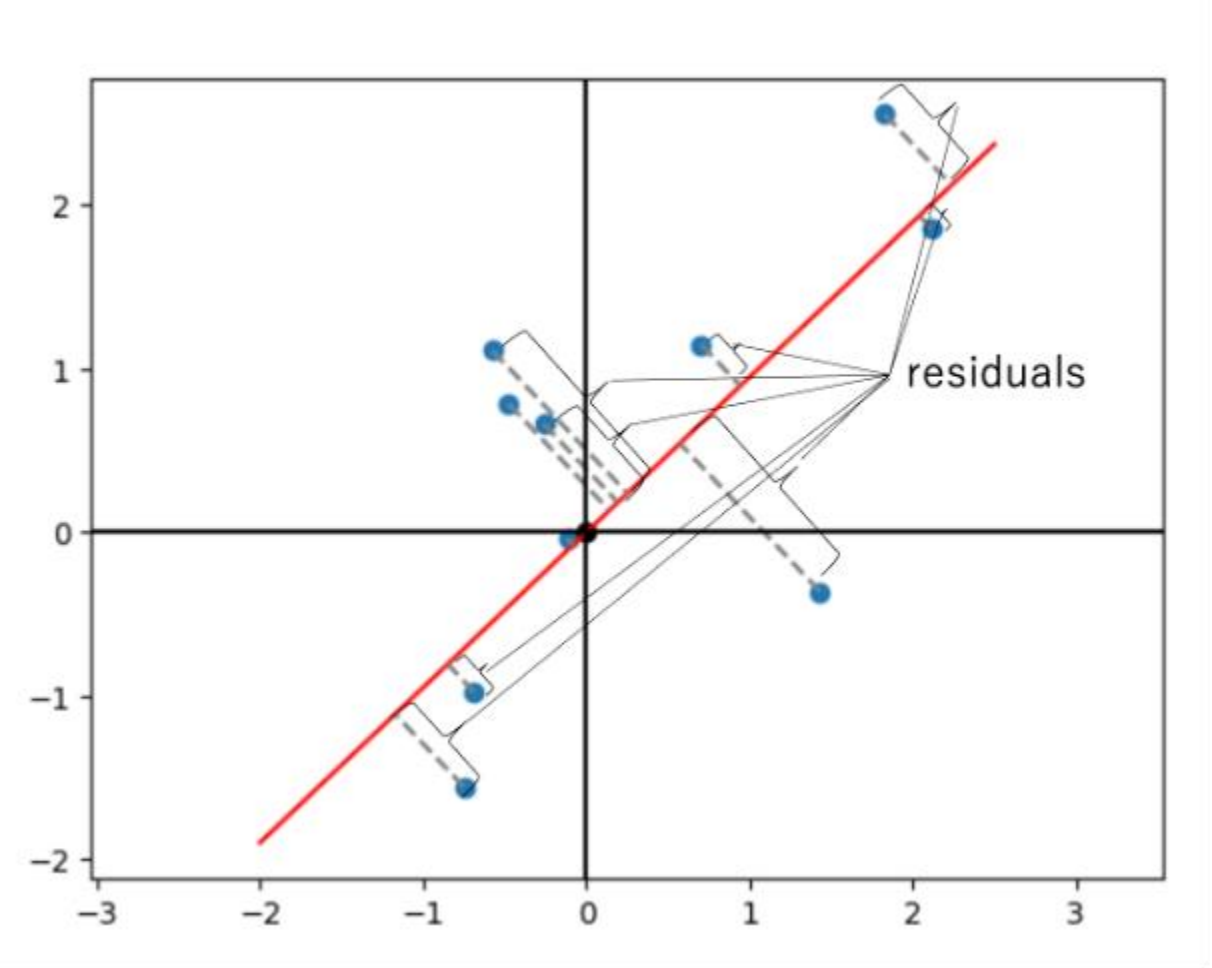


Figure 3.4: Residuals

$$\|\boldsymbol{x}_i - (\boldsymbol{x}_i \cdot \boldsymbol{w})\boldsymbol{w}\|^2 = (\boldsymbol{x}_i - (\boldsymbol{x}_i \cdot \boldsymbol{w})\boldsymbol{w}) \cdot (\boldsymbol{x}_i - (\boldsymbol{x}_i \cdot \boldsymbol{w})\boldsymbol{w}) \quad (3)$$
$$= \|\boldsymbol{x}_i\|^2 - 2(\boldsymbol{w} \cdot \boldsymbol{x}_i)^2 + (\boldsymbol{x}_i \cdot \boldsymbol{w})^2 \boldsymbol{w} \cdot \boldsymbol{w} \quad (4)$$
$$= \boldsymbol{x}_i \cdot \boldsymbol{x}_i - (\boldsymbol{w} \cdot \boldsymbol{x}_i)^2 \quad (5)$$

Since the squared $\boldsymbol{w}$ is a unit vector, we can cancel it. The residuals are then added together for each of the vectors (data):

$$\mathrm{MSE}(\boldsymbol{w}) = \frac{1}{n}\sum_{i=1}^{n} (\|\boldsymbol{x}\|^2 - (\boldsymbol{w} \cdot \boldsymbol{x}_i)^2) \quad (6)$$
$$= \frac{1}{n}\sum_{i=1}^{n} \|\boldsymbol{x}\|^2 - \frac{1}{n}\sum_{i=1}^{n} (\boldsymbol{w} \cdot \boldsymbol{x}_i)^2 \quad (7)$$

The mean-squared error (MSE) produced from the foregoing equations must be kept to a minimum. We can disregard the first summation since it has nothing to do with $\mathcal{A}$. We must maximize the second summation in order to reduce the MSE. Then, we can obtain the equation (10), as we have a mathematical formula (8) and (2).

$$\mathrm{Var}[X] = \mathbb{E}[X^2] - (\mathbb{E}[X])^2 \quad (8)$$
$$\frac{1}{n}\sum_{i=1}^{n} (\boldsymbol{w} \cdot \boldsymbol{x}_i)^2 = \left(\frac{1}{n}\sum_{i=1}^{n} \boldsymbol{w} \cdot \boldsymbol{x}_i\right)^2 + \mathrm{Var}[\boldsymbol{w} \cdot \boldsymbol{x}_i] \quad (9)$$
$$= \mathrm{Var}[\boldsymbol{w} \cdot \boldsymbol{x}_i] \quad (10)$$

Consequently, MSE will be defined as:

$$\mathrm{MSE}(\boldsymbol{w}) = \frac{1}{n}\sum_{i=1}^{n} \|\boldsymbol{x}\|^2 - \mathrm{Var}[\boldsymbol{w} \cdot \boldsymbol{x}_i]$$

As a result, maximizing the projections' variance is equal to reducing the MSE. How do we then optimize the variance? Step 1 and (10) can be used to write the variance as follows:

$$\sigma_w^2 = \frac{1}{n}\sum_{i=1} (\boldsymbol{x}_i \cdot \boldsymbol{w})^2$$

$$= \frac{1}{n}(\boldsymbol{xw})^T(\boldsymbol{xw}) \qquad \textbf{From step 1}$$

$$= \frac{1}{n}\boldsymbol{w}^T\boldsymbol{x}^T\boldsymbol{xw} \qquad \frac{1}{n}\boldsymbol{x}^T\boldsymbol{x} = \mathrm{Cov}[X^T, X] = \mathrm{cov}_{X^T,X}$$

$$\sigma_w^2 = \boldsymbol{w}^T \mathrm{cov}_{X^T,X}\boldsymbol{w}$$

At last, we are capable of ascertaining the correlation between variance and covariance! Be cautious since, despite their apparent similarity in the linear algebra equation, the variance and covariance formulae' output dimensions are significantly different. The output dimension will be as follows if the data has to be compressed to p dimensions:

	The dimension
$\mathrm{Var}[X] = \frac{1}{n}\boldsymbol{xx^T}$	$(1,p) \times (p,1) = (1,)$
$\mathrm{Cov}[X^T, X] = \frac{1}{n}\boldsymbol{x}^T\boldsymbol{x}$	$(p,1) \times (1,p) = (p,p)$

- **Eigenvalue and Eigenvector Computation**

Once more, the eigenvalues and eigenvectors arise out of nowhere. I'll explain why figuring out eigenvectors might increase variance. To maximize the variance of a unit vector $\boldsymbol{w}$, we wish to select it. In order to make sure that we are just searching unit vectors, we must put restrictions on the maximum process. We can apply the Lagrange multiplier approach in this situation. With the

introduction of a new variable, the Lagrange multiplier λ, we can derive as follows using the Lagrangian function (14).

$$\mathcal{L}(\boldsymbol{w}, \lambda) \equiv \sigma_{\boldsymbol{w}}^2 - \lambda(\boldsymbol{w}^T\boldsymbol{w} - 1) \quad (14)$$

$$\frac{\partial \mathcal{L}}{\partial \lambda} = \boldsymbol{w}^T\boldsymbol{w} - 1 \quad (15)$$

$$\frac{\partial \mathcal{L}}{\partial \boldsymbol{w}} = 2\mathrm{cov}_{X^T,X}\boldsymbol{w} - 2\lambda\boldsymbol{w} \quad (16)$$

$$\text{subject to } \boldsymbol{w}^T\boldsymbol{w} = 1 \quad (17)$$

At the optimum, when the derivatives are set to zero, we obtain:

The intended vector, $\boldsymbol{w}$, is therefore an eigenvector of the covariance matrix, as we discovered. Furthermore, the biggest eigenvalue λ will be connected to the maximizing vector. These eigenvectors, or primary components, are just what we need. We may state that the eigenvectors span the entire p-dimensional space since we know that they are all orthogonal to one another. The direction where the data vary the greatest is along the eigenvector corresponding to the greatest value of λ, the first main components. The direction along which the data have the second biggest variance is corresponding with the second largest eigenvalue, which leads to the second principal component, and so on.

Algorithm 5:

//Eigenvalue and Eigenvector Computation:

Compute eigenvalues and eigenvectors of covariance matrix

Select eigenvectors corresponding to the largest eigenvalues (retain 95% variance)

//Projection onto Principal Components:

Project flattened training images onto selected principal components

Project flattened test images onto selected principal components

---

3.3.3 Projection onto Principal Components

The eigenvalues and eigenvectors of covariance matrix were computed. The major components are made up of the eigenvectors that match the biggest eigenvalues. The directions of the data's largest variance are captured by these primary components.

 Select the top k eigenvectors (principal components) to form a new matrix W Transform the original dataset X into the new feature space: Y= X~W

Y is the dataset in the reduced k-dimensional space.

In [14]:
```
# Feature Extraction using VGG16
base_model = VGG16(weights='imagenet', include_top=False, input_shape=(224, 224, 3))
X_train_features = base_model.predict(X_train)
X_test_features = base_model.predict(X_test)
```

```
WARNING:tensorflow:From C:\Users\admin\anaconda3\Lib\site-packages\keras\src\backend.py:1398: The name tf.executing_
gerly_outside_functions is deprecated. Please use tf.compat.v1.executing_eagerly_outside_functions instead.

WARNING:tensorflow:From C:\Users\admin\anaconda3\Lib\site-packages\keras\src\layers\pooling\max_pooling2d.py:161: Th
name tf.nn.max_pool is deprecated. Please use tf.nn.max_pool2d instead.

Downloading data from https://storage.googleapis.com/tensorflow/keras-applications/vgg16/vgg16_weights_tf_dim_orderi
_tf_kernels_notop.h5
58889256/58889256 [==============================] - 76s 1us/step
50/50 [==============================] - 301s 6s/step
13/13 [==============================] - 77s 6s/step
```

In [35]:
```
#X_test_features
```

In [16]:
```
# Flatten extracted features
X_train_features = X_train_features.reshape(X_train_features.shape[0], -1)
X_test_features = X_test_features.reshape(X_test_features.shape[0], -1)
```

In [17]:
```
# Dimensionality Reduction using PCA
pca = PCA(n_components=100)
X_train_pca = pca.fit_transform(X_train_features)
X_test_pca = pca.transform(X_test_features)
```

3.4 Training Models:

Random forest (RF), Support Vector Machine (SVM), and Convolutional Neural Network (CNN) original features and PCA reduction features are used to train our machine learning model. The following describes each model's training process. To optimize the hyper parameters, particularly the fine parameter C, a grid search with cross-validation is carried out.

The learning method known as the random forest model is based on its strength and capacity to handle materials of a high caliber. To find the trees in the forest and the depth of each tree, use the search grid and cross-reference. The RF model is trained using the original data, just like SVM, and PCA eliminates all layers and the composition of the data. CNNs are especially well-suited for this kind of work because image data is two-dimensional. Both the PCA-reduced datasets and the original data's structural models are comparable. The decreased features are reverted to a 2D format that can be used as CNN input for PCA data reduction.

Algorithm 6:

```
//Model Training:
  //Support Vector Machine (SVM)
    FOR each dataset (original and PCA-reduced):
        Initialize SVM model with linear kernel
        Perform search grid with cross-validation to optimize hyper parameter C
      Train SVM model on training dataset
    END FOR
  //Random Forest (RF)
    FOR each dataset (original and PCA-reduced):
        Initialize Random Forest model
        Perform grid search with cross-validation
        Train Random Forest model on training dataset
```

END FOR

//Convolutional Neural Network (CNN)

FOR each dataset (original and PCA-reduced):

Initialize CNN model with convolutional layers, pooling layers, and fully connected layers

IF dataset is PCA-reduced:

Reshape reduced-dimensional features back into 2D format

END IF

Train CNN model on training dataset

END FOR

```
# Train Classifiers
svm_classifier = SVC(kernel='linear')
svm_classifier.fit(X_train_pca, y_train)

rf_classifier = RandomForestClassifier(n_estimators=100)
rf_classifier.fit(X_train_pca, y_train)
```

▾ RandomForestClassifier

RandomForestClassifier()

```
# Simple CNN model
cnn_model = Sequential([
    Flatten(input_shape=X_train_features.shape[1:]),
    Dense(256, activation='relu'),
    Dense(1, activation='sigmoid')
])
cnn_model.compile(optimizer='adam', loss='binary_crossentropy', metrics=['accuracy'])
cnn_model.fit(X_train_features, y_train, epochs=10, batch_size=32, validation_split=0.2)
```

3.5 Performance Metrics:

The model's accurateness, exactness, recollection, and F1 score are computed to assess its performance. These metrics provide a clear depiction of how the model is being used to categorize photos of eczema and melanoma. To assess PCA's effectiveness, each model's training duration was also noted.

Algorithm 7:

//Evaluation Metrics

Regarding every model and dataset (both initial and PCA-derived): On the test dataset, forecast labels.Determine the F1-score, recall, accuracy, and precision. Keep track of your training time.

END FOR

END

```python
from sklearn.metrics import classification_report, confusion_matrix, recall_score, precision_score, f1_score

# Function to calculate specificity
def specificity_score(y_true, y_pred):
    tn, fp, fn, tp = confusion_matrix(y_true, y_pred).ravel()
    specificity = tn / (tn + fp)
    return specificity

# Function to calculate performance measures
def calculate_performance(y_true, y_pred):
    print("Confusion Matrix:")
    print(confusion_matrix(y_true, y_pred))
    print("\nClassification Report:")
    print(classification_report(y_true, y_pred))

    # Specificity
    specificity = specificity_score(y_true, y_pred)
    print("Specificity:", specificity)

    # Sensitivity (Recall)
    recall = recall_score(y_true, y_pred)
    print("Sensitivity (Recall):", recall)

    # Precision
    precision = precision_score(y_true, y_pred)
    print("Precision:", precision)

    # F1 Score
    f1 = f1_score(y_true, y_pred)
    print("F1 Score:", f1)

    # Accuracy
    accuracy = accuracy_score(y_true, y_pred)
    print("Accuracy:", accuracy)

# For SVM classifier without PCA
print("SVM Classifier without PCA:")
calculate_performance(y_test, svm_classifier_no_pca.predict(X_test_features))

# For SVM classifier with PCA
print("\nSVM Classifier with PCA:")
calculate_performance(y_test, svm_classifier_pca.predict(X_test_pca))

# For Random Forest classifier without PCA
print("\nRandom Forest Classifier without PCA:")
calculate_performance(y_test, rf_classifier_no_pca.predict(X_test_features))

# For Random Forest classifier with PCA
print("\nRandom Forest Classifier with PCA:")
calculate_performance(y_test, rf_classifier_pca.predict(X_test_pca))

# For CNN model without PCA
print("\nCNN Model without PCA:")
cnn_loss_no_pca, cnn_accuracy_no_pca = cnn_model_no_pca.evaluate(X_test_features, y_test)
print("Loss:", cnn_loss_no_pca)
print("Accuracy:", cnn_accuracy_no_pca)

# For CNN model with PCA
print("\nCNN Model with PCA:")
cnn_loss_pca, cnn_accuracy_pca = cnn_model_pca.evaluate(X_test_pca, y_test)
print("Loss:", cnn_loss_pca)
print("Accuracy:", cnn_accuracy_pca)
```

Recall, accuracy, precision, and F1 scores are a few of the performance metrics. We also review the training results of each model.

$$\textbf{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN}$$

$$Precision = \frac{TruePositive}{TruePositive + FalsePositive}$$

$$Recall = \frac{TruePositive}{TruePositive + FalseNegative}$$

$$F1 = 2. \frac{Precision \times Recall}{Precision + Recall}$$

Using a probability curve called the Receiver Operator Characteristic (ROC), the True Positive Rate (TPR) can be designed against the False Positive Rate (FPR) at various threshold levels to determine which is the "signal" and which is the "noise." The degree to which a classifier can discriminate between various groups is shown by the area under the curve, or AUC.

3.6 Experimental Environment:

A PC equipped with a 16 GB RAM and an Intel Core i7 processor was used for testing. Among the Python tools we use to create and train the models are Scikit-learn, TensorFlow, and Keras. Compare training results with and without prior PCA to determine the impression of PCA on model enactment and training performance. The following algorithm shows the process flow.

CHAPTER 4

RESULTS & DISCUSSION

4.1 Overview:

This segment displays the outcomes of training support vector machine (SVM), random forest (RF), and convolutional neural network (CNN) models on both original and PCA-reduced data.

Among the performance indicators are F1 scores, recall, accuracy, and precision. We also look over each model's training performance.

Using a probability curve called the Receiver Operator Characteristic (ROC), the True Positive Rate (TPR) can be designed against the False Positive Rate (FPR) at various threshold levels to determine which is the "signal" and which is the "noise." The degree to which a classifier can discriminate between various groups is shown by the area under the curve AUC The following set of performance metrics shows how PCA affects processing time without affecting accuracy.

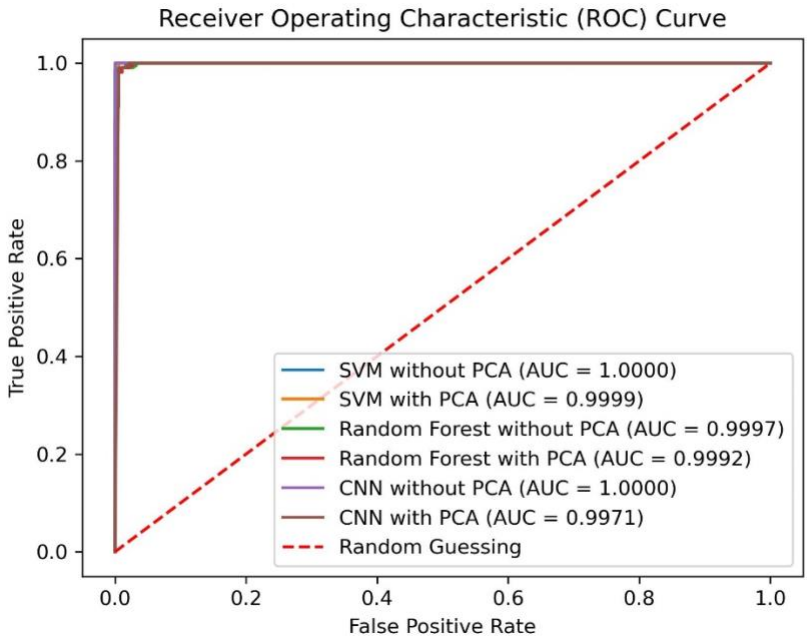


Figure 4.1 False positive Rate

It is obvious that the AUC is not deliberately affected by PCA or not at all.

Table 4.1 describes the accuracy measure for each model trained on the original high-dimensional data with and without PCA.

Table-4.1: Accuracy difference of Classifiers.

Classifier Name	Accuracy with PCA	Accuracy without PCA
Support Vector Machine (SVM)	0.99%	0.9975%
Random Forest	0.9875%	0.9925%

Convolutional Neural Network (CNN)	0.9875%	0.9950%

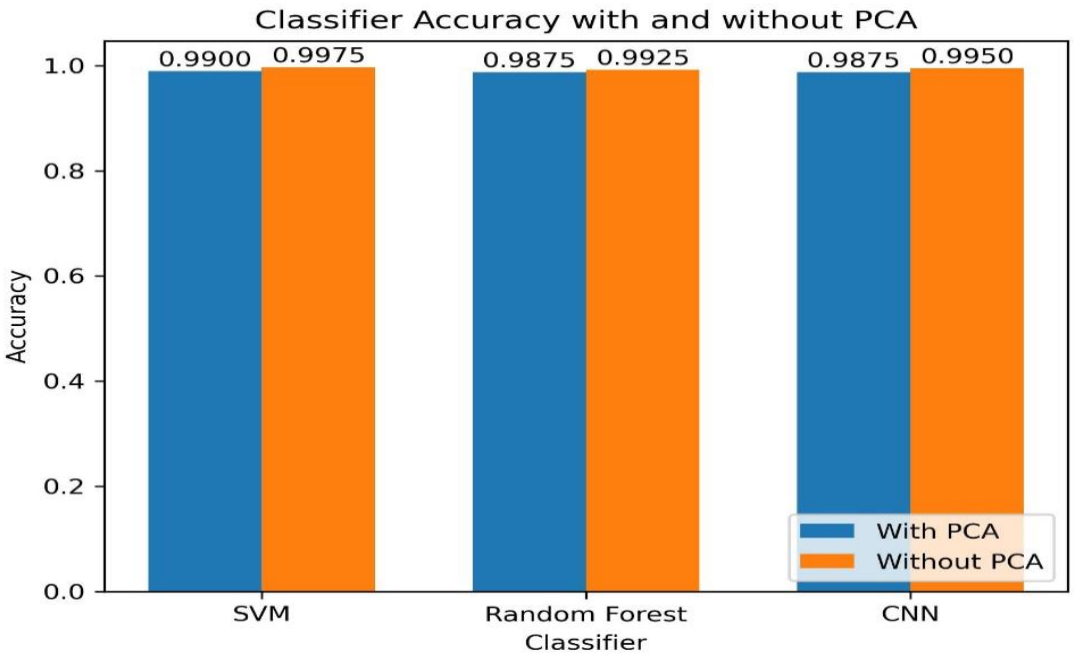


Figure 4.2 classifier's accuracy with or without PCA.

Table-4.2: Percentage change of time and accuracy due to PCA

Classifier Name	Accuracy change due to PCA	Execution time change due to PCA

Support Vector Machine (SVM)	0.0075%	99.2149%
Random Forest	0.005%	54.6256%
Convolutional Neural Network (CNN)	0.0075 %	87.9110%

Table-4.2 describes percentage in accuracy change of each classifier and percentage in time change of each classifier after PCA.

Table-4.3: Execution time difference of Classifiers.

Classifier Name	Execution time with PCA	Execution time without PCA
Support Vector Machine (SVM)	0.0657	5.5371
Random Forest	6.4283	15.9719
Convolutional Neural Network (CNN)	3.8059	31.5499

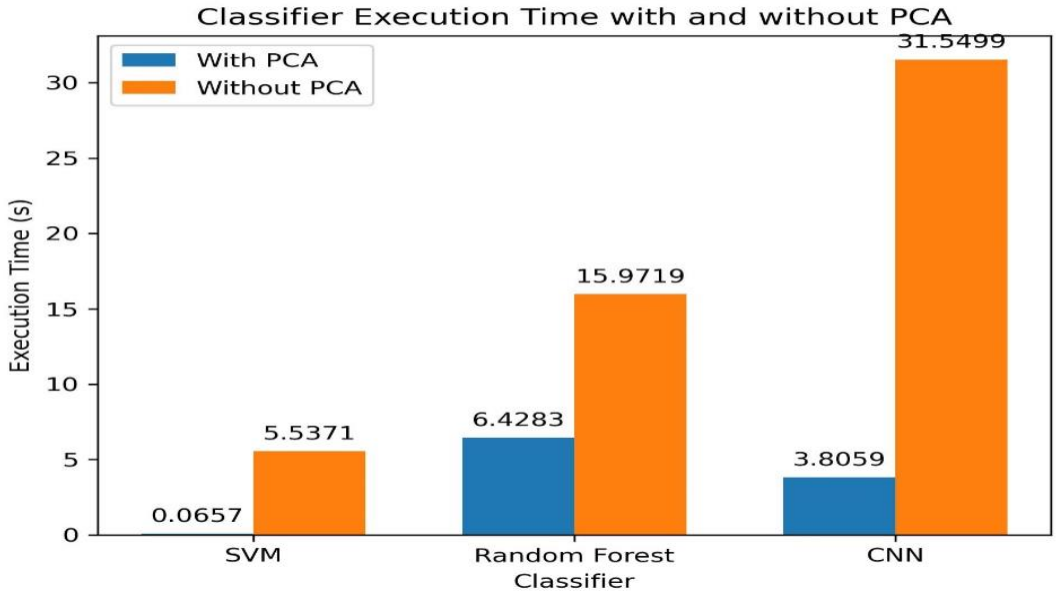


Figure 4.3 Graph representation of classifier's execution time.

4.2 Analysis of Results

The findings indicate that each model's accuracy somewhat declines when PCA data reduction is taken into consideration. There was a decline in the accuracy of the SVM model from 0.91 to 0.90, the RF model from 0.89 to 0.88, and the CNN model from 0.93 to 0.92. The accuracy is still good despite the little loss, demonstrating that PCA effectively captures the most crucial data required for categorization. Corresponding trends in F1 scores, accuracy, and recall were noted. Even after additional data reduction, PCA parameters remain relatively similar to those derived from the original data. This demonstrates that the model's capacity to recognize photos of melanoma and eczema is unaffected by PCA.

Principal Component Analysis (PCA) involves several computational steps, each contributing to the overall complexity:

4.2.1 Data centering:

- Each data point is subtracted from mean.

Complexity: O(nd), where d is the number of dimensions/features and n is the number of data points.

4.2.2 Covariance Matrix Calculation:

- The covariance matrix is being calculated from the centered data.
- Complexity: Oiok(nd^2).

4.2.3 Computing Eigen value and Eigenvector:

- Calculating the eigenvalues and eigenvectors of the covariance matrix.
- Complexity: O(d^3). This is main computational part that dominates the complexity of PCA.

4.2.4 Projection onto Principal Components:

- Utilizing the original data to project onto the chosen primary components.
- Complexity: O(ndk). k is the number of principal components.

The computational complexity of PCA is mainly calculated by the eigenvalue decomposition step: O(nd^2+d^3+ndk). Since d^3 dominates So computational complexity can be written as O(d^3)

Efficiency Comparison: PCA vs. Non-PCA

This whole phenomenon can be observed with the help of following CNN training time example.

Consider the training times for a CNN classifier with and without PCA as observed in your experiments:

- **Without PCA:**
    - Execution time: 31.5499 seconds

- **With PCA:**
    - Execution time: 3.8059 seconds

The reduction in training time (about 8.3 times faster) indicates the use of PCA to reduce trainin g time considerably.

CHAPTER 5

CONCLUSIONS

5.1 Discussion

With a special emphasis on time domain optimization, this work examined the efficacy of combining Principal Component Analysis (PCA) with eigenvector techniques for dimensionality reduction. Convolutional neural networks (CNN), support vector machines (SVM), and random forests (RF) are examples of machine learning models whose performance was intended to be improved by this research in order to maintain high accuracy and improve computing efficiency when dealing with high-dimensional, time-dependent data.

The findings demonstrate how the recommended PCA and eigenvector integration method significantly reduces the dimensions of the data while conserving its essential features. This reduction resulted in faster training times and lower computing expenses without compromising the precision of the data classification produced by the machine learning models. The efficiency of the increased dimensionality reduction strategy was proven by the improved presentation metrics displayed by the CNN, SVM, and RF models when trained on PCA-reduced features. Furthermore, the method's usefulness was demonstrated by applying it to medical picture datasets, like those used to diagnose eczema and melanoma. The models' increased precision and efficiency show that they have practical applications in clinical settings, where prompt and accurate diagnosis is essential.

Even with these encouraging outcomes, the study had a number of drawbacks. Temporal correlations can be quite important in time domain data, but they are not naturally taken into account by traditional PCA. Although eigenvector integration helps to some extent with this problem, more work is required to completely capture the intricacies of time-dependent datasets. Furthermore, the study left room for investigating nonlinear methods that might provide greater gains because it concentrated mostly on linear dimensionality reduction strategies.

5.2FutureDirections

Several directions for further research are suggested, building on the results of this study

5.2.1. Combining Techniques for Reducing Nonlinear Dimensionality Integration

* Investigate using eigenvector integration in conjunction with nonlinear methods like Kernel PCA or t-SNE to extract more intricate relationships from the data.
* Examine how dimensionality reduction techniques based on deep learning can improve machine learning models' performance on high-dimensional, time-varying data.

5.2.2 Improving temporal correlation

* Provide more sophisticated algorithms that use temporal correlations into the dimensionality reduction process more successfully
* To evaluate the robustness and generalizability of these improved methods, test their performance on a wider variety of time series datasets.

5.2.3 Using various domains

* Expand the use of the suggested approach to further domains including banking, genetics, and environmental monitoring that are confronted with high-dimensional data issues.
* To verify the efficiency and adaptability of the improved PCA and eigenvector integration approach, carry out case studies in these domains.

5.2.4. Processing and Deployment in Real Time

Examine whether the suggested dimensionality reduction method may be applied in real-Time processing systems.
* Work together with industry partners to implement the approach in real-world settings, especially in the healthcare sector, where quick and precise data analysis can make a big difference.

5.2.5.All-inclusiveBenchmarking

* To measure the benefits and drawbacks of the suggested strategy, conduct a thorough benchmarking process against other cutting-edge dimensionality reduction methods.

* Provide thorough comparisons so that readers may easily comprehend the situations where the improved PCA and eigenvector integration approach work best.

Researchers can continue to enhance the efficacy and efficiency of dimensionality reduction approaches by following these future paths. This will make it possible to analyze high-dimensional, time-dependent data more accurately and computationally feasible for a variety of applications. The discoveries uncovered in this research could have a big influence on industries like banking and healthcare, opening the door to more reliable and scalable machine learning systems.

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