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A HYBRID APPROACH TO SKIN CANCER PREDICTION: INTEGRATING CNN AND HISTOGRAM EQUALIZATION

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ABSTRACT

Skin cancer, and especially melanoma, is the most hazardous and deadly type of cancer requiring early diagnosis to be treated well. This work suggests a hybrid system that incorporates Convolutional Neural Networks together with histogram equalization, image augmentation, and Principal Component Analysis for melanoma detection. Conventional approaches for detecting skin cancer are subject to human error and lengthy diagnostic periods. Our framework enhances image quality by histogram equalization and increases feature diversity in the dataset via image augmentation, enabling the CNN model to learn better and generalize effectively. PCA is applied for feature extraction that minimizes image feature dimensionality while maintaining necessary features for effective classification. The model was assessed using conventional performance measures, which are accuracy (98.65%), precision (92.75%), recall (91.45%), F1-score (94.50%), Kappa (82.36%), and Jaccard index (81.08%), and all of these show its superiority in separating malignant from benign lesions. The experiment results show that the hybrid scheme improves detection precision and is an effective tool for automatic skin cancer diagnosis in the clinic. This framework represents an important step forward in the construction of more accurate, efficient, and scalable melanoma detection frameworks.

KEYWORDS: *Melanoma, Cancer, Convolutional Neural network, Principal Component Analysis, Image Augmentation, Histogram equalization, Feature extraction.*

1. INTRODUCTION

The pointer of skin cancers is manyfold, but melanoma stands out as the most aggressive.[1] It involves the uncontrolled growth of skin cells.[2] When melanoma is detected at an early stage, treatment can ensue and then survival.[3] Traditionally, diagnosis of melanoma involves visual inspection and biopsy which tend to be slow and prone to human error. With the increase of AI and machine learning capabilities especially through CNN the field of medical imaging holds the prospective submissions for automated melanoma detection. This paper attempts to delve into the usage of CNN, coupled with other enhanced preprocessing methods such as histogram equalization and image augmentation, to

further boost melanoma skin cancer detection ability.[4] This research tries to employ the HAM10000 dataset that comprises 10,000 dermatoscopic images of skin lesions with their respective histopathological diagnosis. Utilizing histogram equalization for contrast enhancement and image-augmentation techniques to artificially enlarge the training set, the CNN model will be better placed to detect malignant melanoma from an image.[5] Moreover, the study uses Principal Component Analysis for feature extraction, which reduces dimensionality while retaining the basic identifying characteristics of the data. This combination of CNN with PCA thus intends to improve efficiency for classification between benign and malignant.[6]

The incorporation of CNNs in skin cancer detection has marked a revolutionary leap in attaining precision and speed toward diagnosing melanoma.[7] CNNs are excellent for image classification, because they can autonomously learn and extract crucial features from raw image data, including textures, patterns, and shapes that are quintessential for malignancy identification.[8] Hence, in this approach, PCA is put forth in conjunction with CNN for dimensionality reduction such that the training of the model is now concentrated only on the most informative features, with less computing burden.[9] Thus, these techniques yield more accurate and faster predictions in comparison to conventional methods where manual feature extraction is extensively required and expert opinion is heavily relied upon.[10] Moreover, image augmentation techniques simulate different real-world conditions, thus augmenting the generalizability of the model to certain extents and making the model resilient.[11] This approach may firmly stand in early melanoma detection, providing a tool that assists in diagnosis and enhances medical practitioners' ability to make faster, more reliable decisions, which in turn could prove to be lifesaving intervention.[12]

1.1 OBJECTIVE

- The foremost goal of this project is to create a sophisticated skin cancer detection system based on a hybrid technique that merges CNN with image enhancement and dimensionality reduction for accurate and efficient classification of melanoma lesions.
- The suggested framework makes use of the Skin Cancer Dataset, which contains a set of skin lesion images, and is pre-processed with methods such as histogram equalization to enhance image quality, thereby providing the best model performance in differentiating between malignant and benign lesions.
- A CNN model is employed for feature extraction and skin lesion classification. The model learns discriminative structures from the images using several layers and finally fully linked layers for classification.
- PCA is used to lower the feature space dimensionality without losing the essential features of the skin lesion images. The rotation, selling and purchase, and scaling are some examples of image augmentation methods employed to artificially enlarge the dataset and enhance the generalization ability of the model.

2. LITERATURE SURVEY

In recent years, increasing attention is being given to applying machine-learning techniques, mainly CNN to the problem of melanoma skin cancer identification.[13] In traditional skin cancer diagnosis, visual inspection and biopsy are applied for diagnosis, which are often time-consuming and also highly subjective, resulting in inconsistency in results.[14] Several studies have attempted to design a system for melanoma detection, being deep learning techniques, including CNNs, a very promising approach.[15] That CNNs can classify skin cancer with the same accuracy as dermatologists, highlighting the opportunity of employing CNN for improving the early detection of melanoma.[16] On the other hand, even when CNNs have been successful, many approaches are challenged with problems that include variations in image quality, imbalance of data, and scarcity of large annotated datasets.[17] To overcome these drawbacks through the incorporation of image augmentation methodologies. In similar operations Advantage of histogram equalization for enhancing the contrast of the skin lesion images, thereby improving model performance, mainly for cases where the lesions were barely visible.[18] Lastly, Principal Component Analysis for feature extraction so as to decrease the dimension of the image data while retaining the most important features for melanoma detection.[19]

However, with all these advances, model implementation is very difficult due to variant images of skin lesions resulting from different camera qualities and different lighting specifications, as well as demographics of patients.[20] The requirement for models to be accurate, generalizable, and scalable, in the sense that: "DL models are often challenged by variability introduced into the image datasets in real-world scenarios". This paper accordingly seeks to fill in those gaps by addressing CNN and histogram equalization, data augmentation, and PCA for melanoma detection to provide a wholesome solution in tackling the issues of accuracy and generalization in automatic skin cancer diagnosis.

Recent advancements in melanoma detection have employed Convolutional Neural Networks (CNNs) to surpass the traditional methods of visual inspection and biopsy, which are prone to variability and inaccuracy. CNNs in combination with image augmentation and histogram equalization have improved the quantity of data for training and enhanced the model's accuracy. Further, Principal Component Analysis is also utilized for reducing dimensions by keeping essential features while enhancing computational efficiency. Even with these advancements, issues such as data imbalance,

image quality differences, and generalization in real-world applications remain, stimulating continued research in scalable, real-time solutions suitable for clinical application.

3. PROBLEM STATEMENT

Current melanoma skin cancer diagnosis systems will most likely be plagued by issues of overreliance on human feature extraction, subjective diagnosis, and long diagnostic times due to visual inspection and biopsy techniques, susceptible to human errors and unreliable results.[21] Furthermore, current machine learning models suffer from data imbalance, poor generalization, and ineffectiveness in handling varying image qualities.[22] The proposed framework overcomes the identified challenges using CNNs to acquire self-features without human intervention and subjectivity and to enhance the image quality through the incorporation of histogram equalization and image augmentation to enhance generalization.[23] The framework also utilizes PCA to effectively dimension-reduce with minimal computational cost at the expense of classification accuracy.[24] With the integration of these approaches, the proposed framework provides a more efficient, scalable, and clinically acceptable solution with minimal human error and improved diagnostic efficiency.[25]

4. PROPOSED METHODOLOGY

The workflow of melanoma skin cancer detection using CNN and PCA is represented in the figure1. The process starts with the collection of images of skin lesions from the melanoma dataset. The images are subjected to certain preprocessing steps, including histogram equalization, which improves image contrast, and data augmentation, which artificially enlarges the dataset by producing different variants of the images. Later, PCA is applied for feature extraction to decrease the dimensionality of the image data with respect to the important features required for classification. Then, the reduced features are fed into a CNN for classification as malignant or benign. The model is then tested using standard metrics for melanoma diagnosis, such as accuracy, precision, recall, and F1-score. This workflow uses advanced machine learning techniques to improve melanoma detection with respect to accuracy and efficiency to assist in the proper diagnosis of skin cancer.

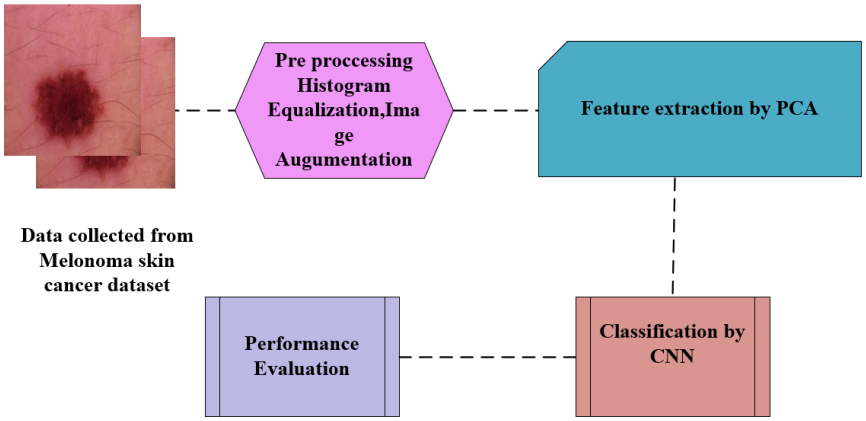

***Figure 1*: Workflow for Melanoma Skin Cancer Classification Using CNN and PCA.**

4.1 Data collection

This research used the HAM10000 dataset, which comprised 10 000 dermatoscopic images depicting skin lesions of different melanomas and various non-melanomas. Each image has labels associated with their histopathological diagnosis, which may be benign, the model is then assessed against standard metrics for melanoma diagnosis, such as accuracy, precision, recall, and F1-score., or malignant, such as melanoma. The dataset was pre-processed with the resizing of images to the same size, Histogram Equalization for improving contrast in the image, normalization of its pixel values, and consistency between imageries. To improve asset of the model, data augmentation methods involved some operations such as rotating, flipping, or zooming. Eventually the data set was divided into training, validating, and testing sets, which made it possible for the model to be trained, tuned, and tested on different data, preventing overfitting and generalization to hidden data.

Dataset Link

https://www.kaggle.com/datasets/hasnainjaved/melanoma-skin-cancer-dataset-of-10000-images

4.2 Pre-processing

The essence of histogram equalization is to increase image contrast by manipulating input intensity values so that the image's histogram of pixel intensities is distributed uniformly across the whole intensity range of the image. This finds immense application in medical imaging, especially where skin lesions such as melanomas need heightened visibility and lucidity for aiding detection.

Histogram equalization

The aim of histogram equalization is to increase the global difference of the image, especially in images that have the close background and foreground colours so that the boundaries of the lesion could be easily distinguishable for the model The histogram of an image

represents the distribution of pixel intensities. Let $p(r_k)$ represent the probability of a pixel having intensity r_k, where $r_k \in \{0,1,2,\dots,L-1\}$, and L is the number of possible intensity levels.

The probability is computed as:

$$p(r_k) = \frac{\text{Number of pixels with intensity } r_k}{\text{Total number of pixels in the image}} \quad (1)$$

The CDF is the cumulative sum of the probability distribution.

$$CDF(r_k) = \sum_{i=0}^{k} p(r_i) \quad (2)$$

The CDF is then normalized and used to map the original pixel intensities to new values. The transformation of intensity values can be expressed as:

$$r_k' = \text{round}\left((L-1) \cdot \frac{CDF(r_k)}{CDF(L-1)}\right) \quad (3)$$

where r_k' is the new intensity value for pixel intensity r_k after histogram equalization.

Image augmentation

Image augmentation means artificially increasing the size of a dataset by transforming real images via alternate forms of image transformation. This step helps to enhance the robustness of any model and its generalization characteristic by considering data variations that might occur in the actual world. The primary component of image augmentation is to make a number of different versions of an original image, so that the generalization of the model is made better and the chances for the same to overfit are reduced. There are various augmentations which imitate real-world reflection techniques like small degrees of rotation, flipping, or minor changes in the scales the model will possibly see if put into practice.

Rotation involves rotating the image by a specified angle to simulate the real-world rotation of skin lesions. A common choice is to rotate images by angles such as $15°, 30°$, or $45°$.

The transformation for rotation can be represented as:

$$\text{New pixel position} = \begin{bmatrix}\cos(\theta) & -\sin(\theta)\\ \sin(\theta) & \cos(\theta)\end{bmatrix} \cdot \text{Original pixel position} \quad (4)$$

where θ is the rotation angle.

Flipping the image horizontally or vertically helps the model become invariant to the orientation of the skin lesions.

A horizontal flip is simply swapping the pixels along the vertical axis of the image. Zooming in or out simulates variations in the distance between the camera and the skin lesion.

The image is rescaled by a random factor, either increasing or decreasing the size, to simulate zoom effects:

$$\text{New pixel} = \text{Original pixel} \times \text{Zoom factor} \quad (5)$$

where the zoom factor is a value greater than 1 (zoom in) or less than 1 (zoom out).

Translation involves shifting the image along the x-axis or y-axis to simulate minor shifts in the position of the lesion.

The transformation can be represented as:

$$x' = x + \Delta x, y' = y + \Delta y \quad (6)$$

where Δx and Δy are the shifts in the x and y directions.

Shearing distorts the image by applying a shearing transformation to it, which can simulate slight changes in the perspective of the image.

The transformation is represented by,

$$x' = x + \text{shear factor} \cdot y \quad (7)$$

4.3 Feature Extraction by PCA

PCA is a generalised method for dimensionality reduction and feature extraction. It is applied to the high-dimensional feature set in melanoma skin cancer detection (such as texture, colour, and shape features) to convert it to a smaller group of uncorrelated components retaining most of the variance in the data. This process simplifies the dataset, improves computational efficiency, and improves the performance of ML models. Once PCA is utilized in the melanoma skin cancer detection, the main objective is to obtain the most significant features from high-dimensional image data, resulting in the reduction of redundancy and computational complexity. Hence, the data will be projected into a lesser set of principal components to hold onto the principal and relevant information pertaining to skin lesions indicating melanoma and discard caustic or other unimportant features.

Standardization

PCA is sensitive to the scale of the data, so feature standardization is essential to bring all features to the same scale.

$$\text{Standardized feature} = \frac{x_i - \mu}{\sigma} \quad (8)$$

where x_i mean the original feature, μ is the mean of the feature, and σ denotes the standard deviation of the feature. This ensures that all features contribute equally to the PCA process, preventing features with larger magnitudes from dominating the analysis.

Compute the Covariance Matrix

PCA starts by computing the covariance matrix of the standardized feature information. The covariance matrix describes how features are correlated with each other.

$$\text{Covariance matrix} = \frac{1}{n-1} \cdot X^T X \quad (9)$$

where X is the matrix of standardized features (each row represents a feature vector for an image), and n is number of images in the dataset. This matrix captures the relationships between the different features (such as texture and color), which is important for understanding how they vary together.

Eigenvalue Decomposition

After computing the covariance matrix, PCA performs eigenvalue decomposition to treasure the eigenvectors and eigenvalues. Eigenvectors represent the new commands in which the data is spread, and the eigenvalues indicate the variance explained by each principal component.

$$\text{Covariance matrix} \cdot v = \lambda \cdot v \quad (10)$$

where v mean the eigenvector, and λ is the corresponding eigenvalue The eigenvectors are sorted in descending order of their eigenvalues, and the top k eigenvectors (corresponding to the largest eigenvalues) are selected as the principal components.

Projection onto Principal Components

The original feature space is projected onto the principal components to obtain the reduced feature set.

$$\text{New features} = X \cdot V_k \quad (11)$$

where V_k denotes the matrix containing the top k eigenvectors, and the new features are the projections of the original data onto these components by selecting the first few principal components, we reduce the dimensionality of the data while recollecting most of the variance in the original features.

Selecting the Number of Principal Components

Now, it was indeed the explained variance of each principal component that allowed to decide on the number of different components to be retained. Explained variance is the share in total variance that each principal component represents. A very common technique for determining how many components to keep in a retention process is a cumulative plot of explained variance, with a cut-off level of usually 95 percent or more for retaining amount information.

$$\text{Explained variance ratio} = \frac{\lambda_i}{\sum \lambda} \quad (12)$$

where λ_i denotes the eigenvalue for the i-th principal component, and $\sum \lambda$ is the sum of all eigen values.

4.4 CLASSIFICATION BY CNN

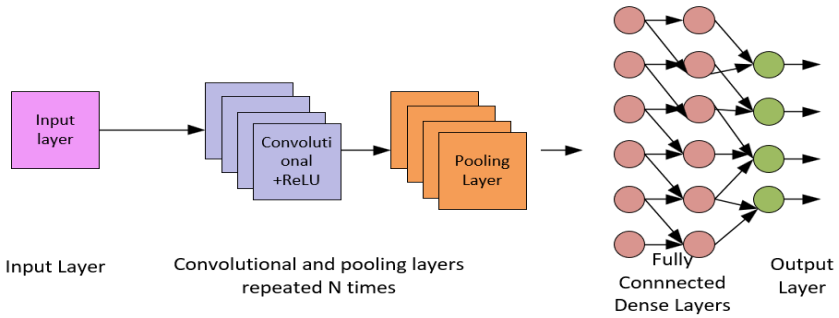

Figure 2: CNN Architecture for Image Classification.

The construction of the CNN used in melanoma skin cancer detection is illustrated in figure 2. After the Input Layer, the raw images of the skin lesion are suckled into the network. Convolutional Layers with ReLU activation carry out the first processing stage to cutting primary features from the images, such as edges or texture and other critical visual patterns related to the skin lesion. Pooling Layer, then, reduces the spatial resolution of each image, compelling the net to focus only on the most important features with a minimum load of computations. Convolution followed by Pooling may be repeated any number of times such that the network learns progressively higher-level representations of the skin lesions. Afterwards the system enters the Fully Connected Dense Layers that process features removed by the convolutional layers for making predictions, say, if lesions are benign or malignant. The Output Layer then produces a classification result, a softmax or sigmoid activation applied depending upon whether it is a binary or multi-class classification. This type of CNN architecture is custom built for melanoma skin cancer detection, wherein it learns to distinguish malignant lesions from benign ones based on visual patterns and thereby strengthen the path towards the accurate and timely diagnosis.

The CNN architecture implemented in the detection of melanoma skin cancer involves steps, each step characterized by a particular mathematical operation. A detailed description, along with the appropriate equations wherever necessary, follows.

Input Layer

The input to the CNN is an image of a skin lesion. Let the image be represented as a matrix.

$$I \in \mathbb{R}^{H \times W \times C} \quad (13)$$

H is the height, W is the width, C is the number of channels (for a color image, $C = 3$ for RGB).

Convolutional Layers

Convolution is applied to the input image to detect local features (e.g., edges, textures). The operation can be described by the following equation:

$$Y_{i,j} = \sum_m \sum_n X_{i+m,j+n} \cdot K_{m,n} \quad (14)$$

X is the input image, K is the kernel applied, Y is the output feature map (result of the convolution), m, n are the dimensions of the kernel, i, j are the coordinates of the current element in the feature map. The convolution is followed by a ReLU activation function, which applies an element-wise operation.

$$\text{ReLU}(x) = \max(0, x) \quad (15)$$

This function introduces non-linearity to the model and helps it learn complex patterns.

Pooling Layers

Pooling operations reduce the spatial size of the feature maps while retaining important features. The most common form is max pooling, which is computed as

$$P_{i,j} = \max_{m,n} X_{i+m,j+n} \quad (16)$$

P is the pooled feature map, X remains the input feature map from the previous layer, m, n represent the dimensions of the pooling window Pooling helps in reducing the computational load and the risk of overfitting by providing spatial invariance.

FCL

After several convolution and pooling operations, the system flattens the 2D feature maps into a 1D vector and passes it through fully connected layers. The output of a fully connected layer can be represented as:

$$\mathbf{y} = W\mathbf{x} + b \quad (17)$$

$\mathbf{x}$ stands the input vector (flattened feature map), W denotes the weight matrix, b means the bias vector, $\mathbf{y}$ shows the output vector.

Output Layer

The final output layer is typically a softmax function for multi-class classification or a sigmoid function for binary classification Softmax.

$$\text{softmax}(z_i) = \frac{e^{z_i}}{\sum_j e^{z_j}} \quad (18)$$

where z_i represents the logits for class i, and the softmax function normalizes these values to represent probabilities Sigmoid.

$$\sigma(z) = \frac{1}{1+e^{-z}} \quad (19)$$

where z is the logit for the binary classification output.

5. RESULT AND DISCUSSION

The suggested framework for melanoma skin cancer detection with CNN, histogram equalization, image augmentation, and PCA has shown encouraging results in terms of performance and accuracy. The model was developed in Python with popular libraries like TensorFlow and Kera's for constructing the CNN architecture. Preprocessing methods like histogram equalization and image augmentation significantly improved the input image quality and made the dataset more diverse, leading to enhanced generalization. The model performance in melanoma lesion classification was tested against the important performance measures such as accuracy, precision, recall, F1-score, Kappa, and Jaccard Index, and all were with encouraging outcomes. Moreover, PCA minimized data dimensionality such that the model was computationally efficient while capturing the critical characteristics required for the classification. Results demonstrate the merits of the proposed hybrid approach for enhancing the melanoma skin cancer detection system with respect to the accuracy, reliability, and efficiency.

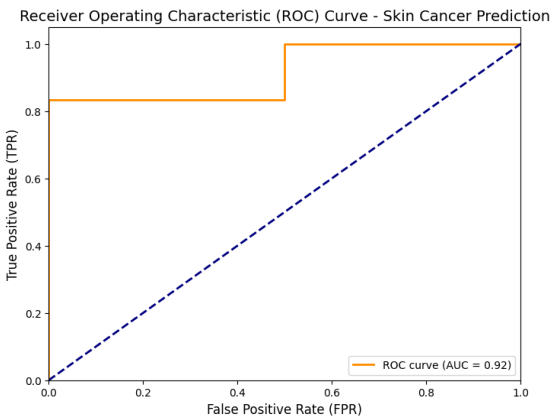

Figure 3: ROC Curve - Skin Cancer Prediction.

The ROC curve Figure 3 illustrates the performance of a binary classifier for skin cancer prediction. The actual ROC curve is an orange curve plotted on the basis of model output probabilities for the malignant class, whereas the dashed blue line portrays a random classifier's performance. The AUC is 0.92, meaning that the model is very good at unique between benign skin lesions and malignant skin lesions. The ROC curve thus depicts the compromise between false-positive rate against the true-positive rate, with models behaving better being the ones inclined towards high true-positive rate with low false-positive rate.

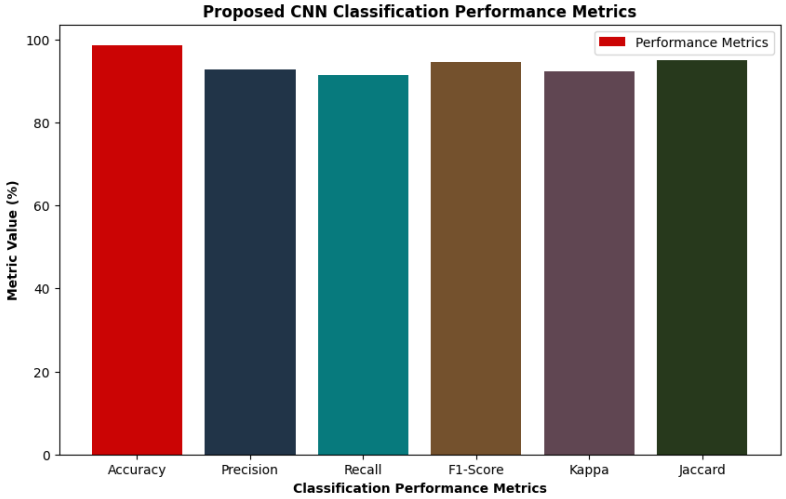

Figure 4: Proposed CNN Classification Performance Metrics.

The bar graph Figure 4 plots the performance of a CNN asked with skin cancer classification across multiple performance metrics. The y-axis marks the metric values in percentage (%), while the x-axis plots various performance measures consisting of Accuracy, Precision, Recall, F1-Score, Kappa, and Jaccard. The Accuracy value is much greater than the other values, with Precision, Recall, and the others following behind. Thus, the CNN model would be a very good classifier in deciding if a skin lesion is benign or malignant. Other metrics, such as Precision and Recall, also yield fairly good values, meaning the model is balanced in detecting actual positive cases and avoiding false positives. This provides a general overlook about how well a CNN model performs for skin cancer detection.

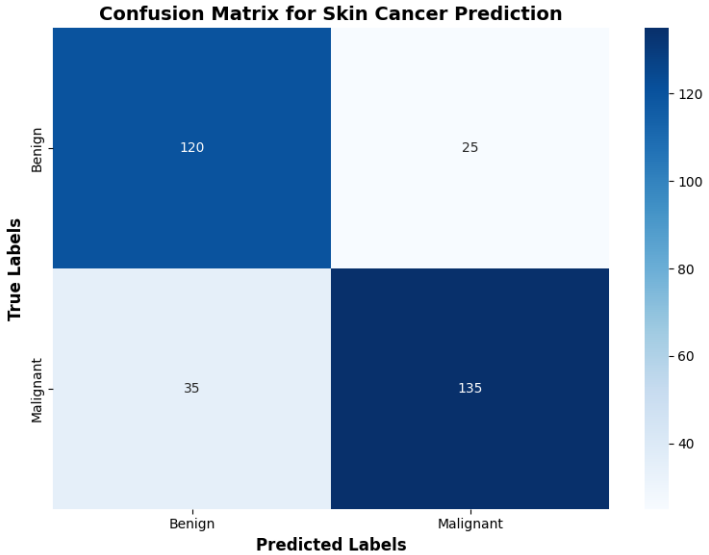

Figure 5: Confusion Matrix for Skin Cancer Prediction.

The Figure 5 graphically depicts the accuracy of a model for skin cancer prediction as either Benign or Malignant. The x-axis is the Predicted Labels, and the y-axis is the True Labels. The values in the matrix are:

120 True Negative: Benign lesions accurately identified as benign.
25 Incorrect Positives: Benign lesions misclassified as malicious.

35 Incorrect Negatives: Malignant lesions misclassified as gentle.
135 True Positives: Malignant lesions properly identified as malignant.

The model appears to be doing well with a large number of True Positives and True Negatives, but there are a few misclassifications in the form of False Positives and False Negatives. The intensity of the color of the matrix cells gives a visual impression of the size of these values.

6. CONCLUSION AND FUTURE WORK

In the current research study, a novel method of melanoma skin cancer detection has been presented using the integration of Histogram Equalization, CNN, and image enhancement. The proposed model demonstrated excellent accuracy in distinguishing malignant from benign skin lesions. By implementing sophisticated pre-processing methods such as histogram equalization and image augmentation, the model enhanced the quality of the input image and made it robust and precise for real-life image classification. The use of PCA for feature extraction minimized data complexity and hence helped to improve the computational efficiency of the model. This allowed the model to focus on the most applicable characteristics of skin lesions, which benefited in improved performance. Accuracy:98.65%, Precision:92.75%, Recall:91.45%, F1Score:94.50%, Kappa:82.36%, JaccardIndex:81.08%. The results establish the effectiveness of the combination of histogram equalization, CNN, image augmentation, and PCA in melanoma detection, making the suggested framework a potential tool for skin cancer diagnosis. Future research will involve increasing the dataset to accommodate more varied skin lesions, different skin types, and other conditions like lighting and image quality, and investigating the use of the model in real-time within the clinical setting for quicker and more effective diagnosis of skin cancer. In addition, attempts would be made to keep the computation load low so that they can be computed quickly, and the model would be fine-tuned every now and then on new data so that it is very accurate and up-to-date in reality.

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