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Skin Cancer Classification Based on Deep Learning Transfer Learning Algorithm and Data Augmentation

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Abstract— The skin is the largest organ in the human body. It also has several different layers, the epidermis (upper) and the dermis (lower). Skin cancer appears in three types of cells: squamous cells, basal cells, and melanocytes. Melanocytes make melanin and are found in the lower part of the epidermis. Melanin is the pigment that gives color to the skin. When the skin is exposed to sunlight, the melanocytes secrete more pigment and making the skin darker. Skin cancer is diagnosed by several methods such as clinical examination, skin tissue analysis, and dermatology. Early warning of skin cancer can help facilitate treatment and is a challenging task even for expert dermatologists in its early stages. Recent studies have found that deep learning and transfer learning are very useful for melanoma classification as well as medical diagnosis. This paper proposes an efficient method to classify melanoma using deep learning. The proposed model uses the ISIC dataset and can run on other databases. We screened the results for accuracy, sensitivity, and specificity. It will be helpful for dermatologists to classify the image as melanoma or benign, with ease, speed, and high accuracy, and does not require the high capabilities of the deep learning machine used.

Keywords— Classification, deep learning, dermoscopic images, models, skin cancer.

I. INTRODUCTION

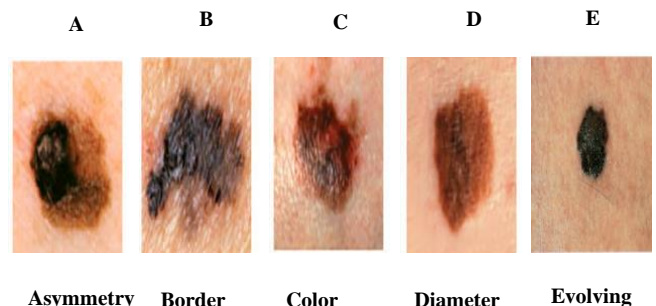
Cancer is a disease in which cells of the body get out of control. Cancer is known as skin cancer when it begins in the skin. Currently, the detection, diagnosis, and grading of skin cancer are very important. Basal cell carcinoma and squamous cell carcinoma are the two most common types of skin cancer. They begin in the basal and squamous layers of the skin [1]. Treatment for both can be generic, but they can be disfiguring and expensive. Melanoma, the third most common type of skin cancer, begins in melanocytes. Of all types of skin cancer, skin cancer causes the most deaths because it tends to spread to other parts of the body, including vital organs. Most cases of skin cancer are caused by excessive exposure to ultraviolet rays from the sun and sunlamps. Ultraviolet rays can damage skin cells. In the short term, this damage causes sunburn. Over time, UV rays build up, leading to changes in skin texture, premature skin aging, and sometimes, skin cancer. Dermoscopic is used to diagnose early stage skin cancer. Skin cancer is difficult to identify owing its similarity. The classification of melanomas using endoscopic images can be considered a problem for image classification. The traditional

technique of classifying pictures may represent salient features that are provided to the class for training. These features can be the texture, color, or shape of color images; however, in the case of melanoma, extracting features and classifying the image base based on these features is a difficult task. This has drawn the attention of researchers to the use of deep neural networks (CNNs) for extracting these features.

Many researchers have worked on the segmentation, detection, and classification of skin cancer using different classification, image processing, machine learning, computer vision, and deep learning techniques. Younis et al proposed a classification of skin cancer dermoscopy images using transfer learning [17]. Anas, Mohd, Kailash Gupta, and Shafeeq Ahmad proposed a skin cancer classification using K-means clustering [18]. Ruthra, V., and P. Sumathy introduced Color and Texture based Feature Extraction for Classifying Skin Cancer using Support Vector Machine and Convolutional Neural Network [19]. Minango, Pablo, et al. showed a new tool in research on tilted melanoma classification based on three very deep neural networks [20]

II. PROBLEM FORMULATION

Simple image processing techniques are used to classify skin tissues based on the extracted features [2]. CNNs work well and automatically extract features. Symptoms and signs of melanoma can be recognized using ABCDE (asymmetry, border, color, diameter and development) as shown in Fig.1. Asymmetric melanoma has an irregular shape and cannot be divided into two halves. Borderline melanoma has jagged and irregular edge [3]. Melanoma is usually a combination of two or three colors. Diameter: Melanomas are generally more than



Asymmetry Border Color Diameter Evolving
FIGURE 1. The ABCDEs rule of melanoma.

6 mm in diameter and differ from normal moles. Enlargement or development: Moles that change in shape and size after a while usually become melanoma. Figure 1 illustrates the ABCDE rule for melanoma. However, a limitation of CNNs is that they require very large amounts of data to train. To overcome this problem, a learning method is used. A simple approach to deep learning, called transfer learning, uses the raw weights of pre-trained networks trained on multiple other datasets. Anabik et al. and Pereira et al. used different transfer learning models- ResNet50, DenseNet, MobileNet, and Fine- and ensemble-tuned these models to increase the accuracy and robustness of the cation-fi categorized, but the results were not up to the mark. In this study, we proposed a melanoma grading method to classify endoscopic melanoma images using the

VGG16 model with modifications in the last two layers of this model to benign or malignant.

III. PROPOSED METHODOLOGY

The proposed approach was used to classify melanomas using deep learning. Early diagnosis of skin cancer using machine-assisted therapy provides physicians with significant assistance. We implemented our model using Keras and TensorFlow libraries, which use deep learning techniques with a five-layer convolutional neural network algorithm, convolutional layer, pooling layer, fully connected layer, and leak activation. The convolutional layer is the first layer used to extract various features from input images. In this layer, the mathematical operation of the convolution between the input image and a filter of a certain size $M \times M$, is performed. By moving the filter over the input image, the raster product is taken between the filter and the parts of the input image with respect to the filter size ($M \times M$), and the output is a feature map that provides information about the image, such as corners and edges. This feature map is fed to other layers so that many other features of the input image can be learned. A convolutional layer is followed by a grouping layer to reduce the size of the convoluted feature map and reduce computational costs. This is accomplished by reducing the connections between the layers and working independently on each feature map. The FC layer consists of weights and biases next to the neurons and is used to connect the neurons between two different layers. These layers were placed before the output layer. A dropout layer was used, where few neurons were dropped from the neural network during the training process, which reduced the size of the model. When passing the 0.3 dropout ratio, 30% of the nodes were randomly dropped from the neural network. In our model, the activation function is. They were used to determine and approximate any type of continuous and complex relationship between the network variables. In simple words, deciding which information from the form should be fired in the forward direction and which should not be fired at the end of the grid. We used a sigmoid activation function so that our model was precisely optimized because we used a classification of two classes. The main goals are to perform the following operations:

- Input data.
- Preprocessing.
- Feature Extraction.

- Data Augmentation.
- Convolutional neural network (CNN Model).
- Classification.

This forms a basic step in the detection of abnormal skin cancers, as shown in Fig.2.

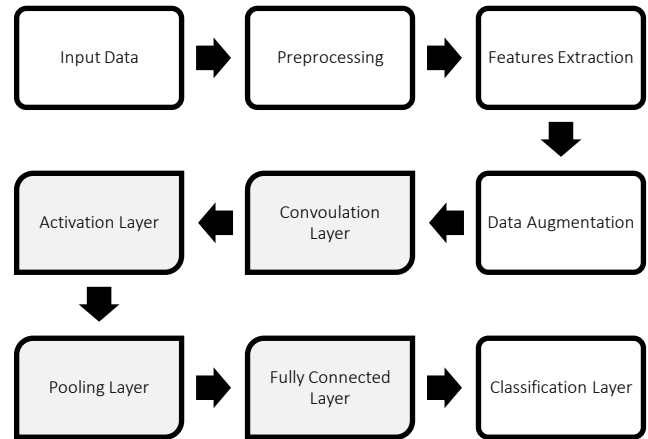


FIGURE 2. Proposed Architecture of CNN.

The study of medical imaging applications plays an important role in this field. The dataset was received from the International Skin Imaging Collaboration (ISIC) website, which contains 3267 images divided into training and testing: the training folder contains 1440 benign images and 1197 malignant images, and the testing folder contains 360 benign (the negative class) and 300 malignant (the positive class) images [5]. Fig.3 shows the distribution of the images used.

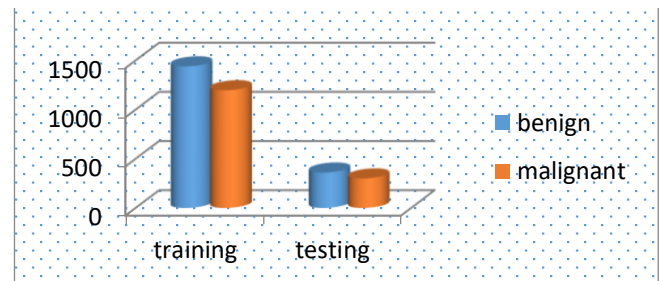


FIGURE 3. Class distributions of the images in skin lesion dataset.

B. Preprocessing

The preprocessing of skin images refers to enhancement intensity and contrast manipulation, normalization, noise reduction, filtering, etc. Thus, the major goal of the preprocessing step is to enhance the image parameters such as quality, clarity, etc.... By removing the unwanted parts of the image, quality stage done [4]. In the proposed system, all images were normalized and resized. For example, if the x- and y-axis are scaled with scaling factors p and q, the transformation matrix is shown in (1):

$$\begin{bmatrix} x' \\ y' \\ 1 \end{bmatrix} = \begin{bmatrix} p & 0 & 0 \\ 0 & q & 0 \\ 0 & 0 & 1 \end{bmatrix} \cdot \begin{bmatrix} x \\ y \\ 1 \end{bmatrix} \quad (1)$$

First, we require an angle θ that represents the degree to which we rotate our image. When we perform rotation in linear algebra, we always rotate along the center of the coordinate system. Now, we need to define the rotation matrix M.

$$M = \begin{bmatrix} \cos\theta & -\sin\theta & 1 \\ \sin\theta & \cos\theta & 0 \\ 0 & 0 & 1 \end{bmatrix} \quad (2)$$

Transformation matrix is:

$$\begin{bmatrix} x' \\ y' \\ 1 \end{bmatrix} = \begin{bmatrix} \cos\theta & -\sin\theta & 1 \\ \sin\theta & \cos\theta & 0 \\ 0 & 0 & 1 \end{bmatrix} \cdot \begin{bmatrix} x \\ y \\ 1 \end{bmatrix} \quad (3)$$

Where (x, y) pixels are the coordinates in the original image, and (x', y') are the corresponding pixel coordinates in the transformed image. Used the Keras image processing API to load all skin photos in the training dataset and then reshaped them to 224×224 square photos that were suitable for the vgg16 model. Labels were determined for each photo. A tuple of photos and labels was saved.

C. Feature Extraction

Feature extraction is considered to play the most important role in the entire classification process. The extraction of relevant features from a given input dataset for detection and classification is called feature extraction. Our proposed system uses ABCD method that is the standard for any dermatological applications which need to consider in skin cancer situation, they are Asymmetry, Border irregularity, Color and Diameter Fig.1. The feature extraction layer existing at the beginning of the architecture is composed of several layers, each of which consists of neurons connected to the local area (local region) of the previous layer [4]. We used a convolutional neural network for skin image feature extraction.

D. Data Augmentation

Data augmentation is used to multiply the variation in images from the dataset by rotating the image, increasing or decreasing the image's length and width, zooming in the image, and flipping the image horizontally. An example of this data augmentation is shown in Fig.5. We augmented the training set while the validation set remained unchanged. The deep convolutional models used in this study required a large number of images for training to achieve better performance without over fitting. However, the number of images in our dataset was insufficient. Data augmentation was used to increase the number of training images and the variation among the images. This also supports the enhancement of prognosis performance and decreases the over fitting problem as an augmentation function; we used rotation, flipping, shearing, and zooming [6]. The random rotation angle was $0-30^\circ$. We made a small change to the input photos of skin cancer that are useful for our problem, such as small shifts and horizontal flips. These augmentations can be specified as arguments for the Image Data Generator used for the training dataset but not for the testing dataset. In this case, photos in the training dataset were augmented with small (10%) random horizontal and vertical shifts as shown in Fig.4 and random horizontal flips that created a mirror image of a photo. Photographs in both the training and test steps will have their pixel values scaled in the same manner.



FIGURE 4. Vertical shift image augmentation.

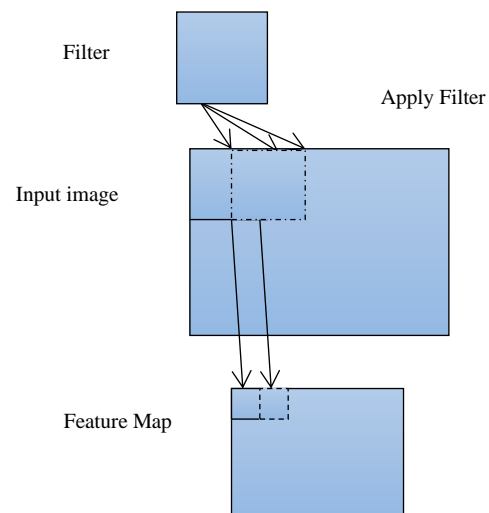
E. CNN Model

Machine learning technology uses multiple layers to extract important features from an image, identify patterns, and classify them. Deep learning uses artificial neural networks to solve problems using large datasets for easy supervised machine learning. When more layers are added, the machine-learning model handles the tagged image data better. In deep learning, a computer can learn to classify images, texts, or sounds [3]. In deep learning, a computer with a large amount of data is trained, and the pixel value of an image is then modified into an internal vector feature from which the new data can be categorized using the same approach. Deep neural networks have succeeded in supervised learning, reinforcement learning, hybrid learning, and unsupervised learning [7]. The first step in training a deep belief network is to learn the features using the first layer. This was followed by activating the trained features from the previous layer in the next layer. This was performed until the final layer was obtained. Deep learning has been used to analyze medical images worldwide. Some of the challenges in the accurate classification of skin lesions using deep learning are the availability of high-quality data, which is a major requirement for good classification results.

A convolutional neural network (CNN) is a powerful technique for extracting useful features from image data. We can develop a basic convolutional neural network model for the ISIC (International Skin Imaging Collaboration) melanoma dataset. The application of convolutional operations to image data is a common technique used in computer vision because it has many different advantages. In recent years, some network architectures have demonstrated outstanding results in image classification problems using deep neural networks. These architectures are used for various applications worldwide using a technology called transfer learning. The weights of an already-trained model for a given task are used for some new task types required for classification [6]. There are some common architectures, such as VGG16 and VGG19. Four types of layers are used: convolutional layer, pooling layer, fully connected layer, and activation function. These concepts are discussed in the following sections [8].

1) Convolutional layer

The convolution process uses the image input by using the filter and passing it on the image pixels to extract the features to create the output function as a feature map for this image, thus reducing the storage space in which each image is stored. The convolution layer performs convolution operations on the output of the previous layer as the input to the current layer [3].



Convolution operations in general can be written with the formula below:

$$y(t) = (x * w) \quad (4)$$

The equation $y(t)$ gives results in the form of a feature map as a single output with the first argument used as the input expressed as x and the second argument used is the kernel or filter, which is stated as w . Because the input used is an image that has two dimensions, it can be expressed as t as a pixel and replaced with arguments i and j . Therefore, convolution operations with more than one-dimension input can be written as follows:

$$y(i, j) = (k * I)(i, j) = \sum_n \sum_m (i - m)(j - n) k(m, n) \quad (5)$$

Two-Dimensional Input Filter Applied to Create a Feature Map as in Fig.5

2) Activation function

In a neural network, the activation function converts the weighted sum of the inputs into the output of a node or a node in a layer of the network. We defined the activation function as the output of that node, given an input or set of inputs that determines the output value owing to some roles. In this study, the activation functions used were binary sigmoidal functions that perform input editing between 0 and 1. It is positive in nature. It is always bounded, which means that its output cannot be less than 0 and more than 1. It also strictly increases in nature, which means that a higher input would be the output. It can be defined as

$$F(x) = \text{sigm}(x) = \frac{1}{1 + \exp(-x)} \quad (6)$$

We also use the rectified linear unit (ReLU) activation function, which is the positive part of its argument, that from equation 7:

$$F(x) = x^+ = \max(0, x) \quad (7)$$

3) Pooling layer

The pooling layer is another building block of the CNN. It is executed after each convolutional layer. The aggregation process involves moving a 2D filter over each channel of the feature map as it summarizes the features within the area covered by the filter to reduce the dimensions of the feature maps [9]. This reduces the number of tasks that need to be learned and the number of operations performed in the network. The pooling layer types are max pooling (the maximum element from the area of the feature map enveloped by the filter) and average pooling (the average of the elements present in the region of the feature map covered by the filter).

4) Fully connected layer

The fully connected layer is a layer in which all activation neurons from the previous layer are connected to all neurons in the next layer and the aim is to transform data dimensions so that data can be classified linearly. Fully connected layers in neural networks are those where all the inputs from one layer are connected to every activation unit of the next layer. In the most popular machine learning models, the last few layers are fully connected layers that compile the data extracted by previous layers to form the final output. This is the second most time-consuming layer to the convolution layer. We can divide the entire neural network classification into two parts: feature extraction (extracting features from the data to make the classification) and classification (classifying the data into various classes) [10].

F. Classification

The CNN algorithm was used to categorize skin lesion images into melanoma or benign lesions. It comprises a sequence of several convolutional layers with filters, pooling layers, and a fully connected layer. The convolution layer is the initial layer that extracts the features from an image. The pooling layer minimized the size of the activation map. The max pooling layer preserved the largest value in the activation map. Pooled activation maps are flattened to form a feature vector that is applied to the fully connected layer [21].

CNN can classify skin lesions in two ways. In the first case, a CNN is used as the feature extractor of the images, and classification is performed by another classifier. For the other case, a CNN is used to perform end-to-end learning, which can be further split into learning from scratch or learning from a pre-trained model. To train the CNN from scratch, a large number of images are required to process the over fitting problem. Because the number of skin lesion images required for training is insufficient, training the CNN from scratch is less workable. Training from a pre-trained model is the best approach, and is generally referred to as transfer learning (TL). TL helps the model learn well even with less data and introduces a generalization property to the trained model [11]. A useful model for transfer learning is one of the VGG models, such as VGG-16 with 16 layers that at the time it was developed, achieved top results on the ImageNet photo classification challenge. The model comprises two main parts: the feature extractor part of the model, which is composed of VGG blocks, and the classifier part of the model, which is composed of fully connected layers and the output layer. We can use the feature extraction part of the model and add a new classifier part that is tailored to the skin cancer dataset. We can hold the weights of all the convolutional layers fixed during training and only train new fully connected layers that will learn to interpret the features extracted from the model and make a binary classification [11].

IV. NUMERICAL RESULTS

Our model uses Keras and TensorFlow libraries. Keras is a deep learning API written in Python that runs on top of the machine learning platform TensorFlow. It was developed with a focus on enabling rapid experimentation. Being able to go from idea to result as fast as possible is the key to doing good research. TensorFlow is an open-source software library developed by the Google Brain team to support smart computing to support the search and learning of their products.

Computing using tensor flow can be executed with a variety of systems, ranging from mobile devices such as cellphones and tablets to hundreds of large-scale distributed systems of machines and thousands of computing devices such as GPU cards [12]. The model used was VGG16.

The convolution neural net (CNN) architecture was used to win (ImageNet) competition in 2014. This is excellent vision model architecture to date. The most unique feature of VGG16 is that instead of having many hyper-parameters, they focused on having convolution layers of 3×3 filters with a stride of 1 and always used the same padding and max -pool layer of a 2×2 filter of stride 2. It follows this arrangement of convolution and max pool layers consistently throughout the architecture. Finally, it has 2 FC (fully connected layers (FC) followed by a softmax function for the output. Sixteen in VGG16 refers to 16 layers that have weights [13]. This is a large network of approximately 138 million (approx.) parameters.

Five evaluation metrics were applied to assess the performance of the proposed method [14]. These metrics were sensitivity (*SEN*), specificity (*SPE*), accuracy (*ACC*), precision (*PRE*), and *F – score*.

$$\text{Accuracy} = \text{ACC} = \frac{\text{TP} + \text{TN}}{\text{TP} + \text{TN} + \text{FN} + \text{FP}} \times 100 \quad (8)$$

$$\text{Sensitivity} = \text{SEN} = \frac{\text{TP}}{\text{TP} + \text{FN}} \times 100 \quad (9)$$

$$\text{Specificity} = \text{SPE} = \frac{\text{TN}}{\text{TN} + \text{FP}} \times 100 \quad (10)$$

$$\text{Precision} = \text{PRE} = \frac{\text{TP}}{\text{TP} + \text{FP}} \times 100 \quad (11)$$

$$\text{F – score} = \frac{2\text{TP}}{2\text{TP} + \text{FP} + \text{FN}} \times 100 \quad (12)$$

Where:

True Positive=TP: Correctly classified as having skin cancer.

True Negative=TN: Correctly classified as not having skin cancer.

False positive =FP: classified as having skin cancer but not cancer.

False negative =FN: classified as not having skin cancer but having cancer.

Based on Table1 with 50 images being tested from the training dataset, there were 50 correct images and 0 incorrect images in the classification as in TABLE I.

TABLE I. TRAINING DATA

No	Input	Category	Output	Result
1	0.jpg	benign	benign	TRUE
2	1.jpg	benign	benign	TRUE
3	10.jpg	benign	benign	TRUE
4	100.jpg	benign	benign	TRUE
5	1000.jpg	benign	benign	TRUE
6	1001.jpg	benign	benign	TRUE
7	1002.jpg	benign	benign	TRUE
8	1004.jpg	benign	benign	TRUE
9	1005.jpg	benign	benign	TRUE
10	1006.jpg	benign	benign	TRUE
11	1007.jpg	benign	benign	TRUE

12	1008.jpg	benign	benign	TRUE
13	1009.jpg	benign	benign	TRUE
14	101.jpg	benign	benign	TRUE
15	1010.jpg	benign	benign	TRUE
16	1011.jpg	benign	benign	TRUE
17	1012.jpg	benign	benign	TRUE
18	1013.jpg	benign	benign	TRUE
19	1014.jpg	benign	benign	TRUE
20	1015.jpg	benign	benign	TRUE
21	1016.jpg	benign	benign	TRUE
22	1017.jpg	benign	benign	TRUE
23	1018.jpg	benign	benign	TRUE
24	1019.jpg	benign	benign	TRUE
25	102.jpg	benign	benign	TRUE
26	1247.jpg	malignant	malignant	TRUE
27	1248.jpg	malignant	malignant	TRUE
28	1249.jpg	malignant	malignant	TRUE
29	125.jpg	malignant	malignant	TRUE
30	1250.jpg	malignant	malignant	TRUE
31	1252.jpg	malignant	malignant	TRUE
32	1053.jpg	malignant	malignant	TRUE
33	1054.jpg	malignant	malignant	TRUE
34	1055.jpg	malignant	malignant	TRUE
35	1057.jpg	malignant	malignant	TRUE
36	1158.jpg	malignant	malignant	TRUE
37	1159.jpg	malignant	malignant	TRUE
38	116.jpg	malignant	malignant	TRUE
39	1161.jpg	malignant	malignant	TRUE
40	1162.jpg	malignant	malignant	TRUE
41	1163.jpg	malignant	malignant	TRUE
42	1165.jpg	malignant	malignant	TRUE
43	1167.jpg	malignant	malignant	TRUE
44	1168.jpg	malignant	malignant	TRUE
45	1169.jpg	malignant	malignant	TRUE
46	117.jpg	malignant	malignant	TRUE
47	1171.jpg	malignant	malignant	TRUE
48	1172.jpg	Malignant	malignant	TRUE
49	1174.jpg	Malignant	malignant	TRUE
50	1175.jpg	Malignant	malignant	TRUE

Based on TABLE II with 50 images being tested from the testing dataset, there were 50 correct images and 0 incorrect images in the classification.

TABLE II. TESTING DATA

No	Input	Category	Output	Result
1	1.jpg	benign	benign	TRUE

2	10.jpg	benign	benign	TRUE
3	1003.jpg	benign	benign	TRUE
4	1006.jpg	benign	benign	TRUE
5	1013.jpg	benign	benign	TRUE
6	1018.jpg	benign	benign	TRUE
7	1019.jpg	benign	benign	TRUE
8	1023.jpg	benign	benign	TRUE
9	1025.jpg	benign	benign	TRUE
10	1029.jpg	benign	benign	TRUE
11	1033.jpg	benign	benign	TRUE
12	1034.jpg	benign	benign	TRUE
13	1042.jpg	benign	benign	TRUE
14	1044.jpg	benign	benign	TRUE
15	105.jpg	benign	benign	TRUE
16	1055.jpg	benign	benign	TRUE
17	1061.jpg	benign	benign	TRUE
18	1070.jpg	benign	benign	TRUE
19	1074.jpg	benign	benign	TRUE
20	1077.jpg	benign	benign	TRUE
21	1080.jpg	benign	benign	TRUE
22	1087.jpg	benign	benign	TRUE
23	1088.jpg	benign	benign	TRUE
24	1092.jpg	benign	benign	TRUE
25	11.jpg	benign	benign	TRUE
26	1227.jpg	malignant	malignant	TRUE
27	1228.jpg	malignant	malignant	TRUE
28	1229.jpg	malignant	malignant	TRUE
29	1234.jpg	malignant	malignant	TRUE
30	1238.jpg	malignant	malignant	TRUE
31	1242.jpg	malignant	malignant	TRUE
32	1251.jpg	malignant	malignant	TRUE
33	1254.jpg	malignant	malignant	TRUE
34	1256.jpg	malignant	malignant	TRUE
35	1262.jpg	malignant	malignant	TRUE
36	1266.jpg	malignant	malignant	TRUE
37	1267.jpg	malignant	malignant	TRUE
38	1268.jpg	malignant	malignant	TRUE
39	1280.jpg	malignant	malignant	TRUE
40	1286.jpg	malignant	malignant	TRUE
41	1289.jpg	malignant	malignant	TRUE
42	129.jpg	malignant	malignant	TRUE
43	1292.jpg	malignant	malignant	TRUE
44	1295.jpg	malignant	malignant	TRUE
45	1297.jpg	malignant	malignant	TRUE
46	13.jpg	malignant	malignant	TRUE

47	1300.jpg	malignant	malignant	TRUE
48	1310.jpg	malignant	benign	FALSE
49	1320.jpg	malignant	malignant	TRUE
50	1320.jpg	malignant	malignant	TRUE

V. CONCLUSION

Classification of melanoma cancer images is carried out in two stages. The first stage is training the dataset to produce a model [15]. The second stage is the process of classification in which the system takes the image data, then initializes the model from the results of the training and makes predictions using our model. The system then takes the prediction results along with their probabilities and displays the prediction results along with the image. The experiment was conducted on 660 images of 360 benign and 300 malignant test datasets using a different model [16]. The experiment obtained the highest accuracy of 100% in the training results using the proposed model. Meanwhile, the testing results obtained 98% accuracy when using 50 images. This model can be applied to binary classification of any colored image. We will use different models with changes in the number of epochs and show good accuracy, and we will use GAN to increase the dataset and obtain good results. These results will be helpful for radiologists in making more accurate skin cancer diagnoses.

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