Identify Melanoma Using CNN

Shashidhara G M [1[0000-0003-1812-1540]], Rashmi Agarwal [2[0000-0003-1778-7519]] and Jitendra Suryavamshi[3[]]

REVA Academy for Corporate Excellence
REVA University, Bangalore, India
[2]rashmi.agarwal@reva.edu.in

Abstract. Skin cancer is a common disease that affects mankind significantly every year there are more new cases of skin cancer than the combined incidence of cancers of the breast, prostate, lung, and colon. With over 5,000,000 new cases every year skin cancer is a concerning public health predicament. Melanoma and non-melanoma are the two main kinds of skin cancer, respectively. Melanoma is a malignant tumor. The 19th most common malignancy in both men and women is melanoma. The deadliest types of skin cancer are melanoma, which can spread quickly. The crucial factor in Melanoma cancer treatment is early diagnosis. Doctors usually prefer the biopsy method for skin cancer detection. During a biopsy, a sample from a suspected skin lesion is removed for medical examination to determine if it is cancerous or not a biopsy is a painful, slow, and time-consuming method. This study proposes an end-to-end decision-based system classifiers for example like neural networks. Convolutional Neural Networks (CNN) will be used to classify melanoma or benign. CNN architectures are appropriate classifiers to distinguish between the images of moles on the skin. This study has used images from both clinical and dermoscopic images Med-node and ISIC. The procedure advised in Melanoma detection shall capture images and preprocess. Segment the acquired preprocessed image and extract the desired feature and classify them as Melanoma or benign. The model has given an accuracy of 94 %, and Sensitivity and Specificity are at 0.87 and 0.89 respectively.

Keywords: Image processing, Deep learning, Convolutional Neural Network, Skin lesion detection, Neural network.

1 Introduction

Melanoma is one among the many deadly category of the skin related cancer, occurs when melanocytes (the cells that provides the skin its brown or tan colour) may start growing out of control. Malignant melanoma is also one of the fastest growing cancers [1]. Melanomas may develop on the skin and the other commonly known places are the neck and face. Chances of getting melanoma on the feet soles, on palms, or under nails are very high. Melanomas are also seen in other parts of the body for example mouth, eyes, anal and genitals. A mole (nevus) is a benign tumor on the skin developed from melanocytes. Every human being may have some moles. Many of the moles (nevi) could be harmless but few of them can turn into melanoma. Normal moles are a typical mole on the skin is often brown, tan, or black in colour. A mole can have a circular or oval shape and can be elevated or flat. Moles often measure less than 6 millimetres (1/4 inch) in diameter. While many moles first occur during childhood or as an adult, other moles are present from birth. The mole will typically remain the same size, colour, and shape for many years after it has developed. Some moles might disappear in the future. The

majority of people have a mole, and many are benign. However, it's crucial to keep an eye out for and be aware of changes in mole's size, colour, form, and texture as shown in Fig. 1.

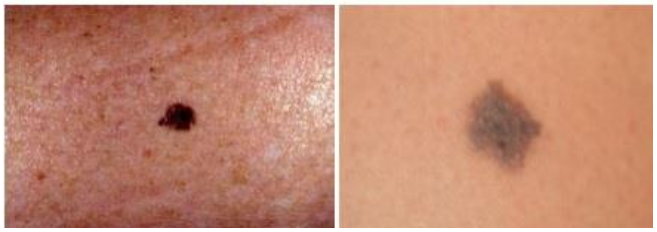

Fig. 1. Benign Mole and Malignant [2][3]

Across the globe, dermatologist advises conducting biopsy and the issue is that the biopsy extraction of the affected skin lesion is an old invasive method that is very painful for the patients. However, if a dermatologist is able to detect and remove the mole early on time more than 90% of malignant melanoma cases can be easily cured. If in case the melanoma skin disease is identified and not treated immediately there would be chances of spreading to the other organs such as liver or lung tumor the existence rate of the patients after surgical operation drops below 20%. With all these challenges on hand, a non-invasive computer-enabled decision system that will help patients in detecting melanoma is the need of the hour.

2 Literature Review

Over time different researchers have worked on skin lesion detection systems using machine learning and deep learning techniques. Melanoma skin cancer if detected early the disease can be cured. In this study, a solution for detecting early-stage melanoma skin cancer using CNN is worked. Image processing is done on 514 raw images from ISIC archive for training and validating our model. The experimental results achieved 74.76% accuracy and 57.56% validation loss [4].

This study is having dataset of 2,056 patients (20.8% with a minimum of one melanoma, 79.2% with zero melanomas) across three continents averaging 16 lesions per patient, consisting of 33,126 dermoscopic images and 584 (1.8%) histopathological confirmed melanomas compared with benign melanoma mimicking data [5].

In this study, an ensemble learning approach combines three DCNNs architectures such as Inception V3, Inception ResNet V2, and DenseNet. This model produces good classification performance with 97.23% accuracy, 90.12% sensitivity, 97.73% specificity, 82.01% precision, and 85.01% F1-Score. This method gives encouraging results in classifying skin lesions for cancer diagnosis [6].

A Real-time image augmentation with the algorithm-level method of designing a new loss function. The training dataset has 24,530 dermoscopic images. The proposed EfficientNetB4-CLF model gives the highest accuracy of 89.97% and also the highest mean recall of 86.13% [7].

Generic algorithms can be used to successfully identify appropriate architectures for the diagnosis of melanoma, resulting in an overall prediction performance improvement of 11% and 13%. To help dermatologists, the suggestion was turned into an online application [8].

In this paper, two techniques are used to categorize the stages of melanoma cancer. Stage 1 and stage 2 melanoma are categorized using the first technique. The second technique divides melanoma into three stages: stage 1, stage 2, and stage 3. The suggested system employs the Similarity Measure for Text Processing (SMTP) loss function and a CNN algorithm. The exhibited and compared experimental findings with various loss functions include the proposed SMTP loss function [9].

Images of the dermoscopic kind, containing various cancer samples, are gathered for this investigation from the databanks (ISIC 2016, ISIC2017, and ISIC 2020). Model has been assessed using F1 score, recall, specificity, recall, precision, and accuracy. Accuracy rates for the proposed DCNN classifier were 81.41%, 88.23%, and 90.42% [10].

To analyze the performance of the Deep Generative Adversarial Network developed two CNN models to function simultaneously based on the architecture of ResNet50 and VGG16. DGAN performed very good on the conventional data augmentation by having a performance of 91.1% for the unlabeled dataset and 92.3% for the labeled dataset. On the other side, CNN models with data augmentation performance were at 70.8% for the unlabeled dataset [11].

This research paper limits review to skin cancer classifiers. In particular, CNN for segmentation or for the classification of dermoscopic patterns is not considered here. Further this study dwells upon why the comparability of the presented procedures is very difficult and what type of challenges has to be addressed in the future [12].

This paper has reviewed studies on (AI/ML) algorithms aiming to facilitate the early diagnosis of skin cancers. Researchers evaluated MEDLINE, Embase, Scopus, and Web of Science (from Jan 1, 2000, to Aug 9, 2021) further and have published the summary.

	Sensitivity	Specificity	Positive predictive value	Negative predictive value	Area under the receiver operating characteristic curve	Accuracy*	F1-score†
Melanoma (197 studies provided outcome measures for melanoma alone, 2000–21)							
Mean (95% CI)	0·842 (0·816–0·868)	0·891 (0·871–0·910)	0·814 (0·769–0·859)	0·929 (0·909–0·949)	0·898 (0·882–0·915)	89·5% (88·2–90·8%)	0·807 (0·732–0·882)
Median (IQR)	0·894 (0·792–0·950)	0·920 (0·850–0·965)	0·846 (0·720–0·955)	0·930 (0·900–0·960)	0·910 (0·849–0·950)	91·3% (86·0–95·0%)	0·850 (0·748–0·960)
Range	0·13–1·00	0·36–1·00	0·280–1·000	0·86–1·00	0·71–1·00	59·7–100%	0·280–0·975
Number of studies	146	127	49	17	64	141	24
Squamous cell carcinoma (ten studies provided outcome measures for squamous cell carcinoma alone, 2015–20)							
Mean (95% CI)	0·603 (0·396–0·810)	0·933 (0·865–1·000)	0·415 (0·247–0·582)	0·951 (0·875–1·000)	0·875 (0·777–0·973)	85·3% (77·3–93·3%)	...
Median (IQR)	0·58 (0·394–0·799)	0·965 (0·928–0·979)	0·415 (0·372–0·457)	0·951 (0·931–0·970)	0·906 (0·859–0·922)	86·0% (77·5–93·8%)	...
Range	0·256–1·000	0·800–0·995	0·329–0·500	0·912–0·989	0·730–0·958	71·0–97·8%	...
Number of studies	7	5	2	2	4	4	0
Basal cell carcinoma (29 studies provided outcome measures for basal cell carcinoma alone, 2012–20)							
Mean (95% CI)	0·837 (0·792–0·883)	0·887 (0·783–0·990)	0·834 (0·767–0·902)	0·896 (0·743–1·000)	0·923 (0·879–0·967)	87·6% (80·7–94·6%)	0·846 (0·783–0·909)
Median (IQR)	0·880 (0·766–0·914)	0·938 (0·893–0·988)	0·877 (0·785–0·930)	0·978 (0·939–0·988)	0·946 (0·912–0·970)	91·1% (77·5–97·5%)	0·875 (0·845–0·913)
Range	0·580–0·996	0·342–1·000	0·541–0·986	0·510–0·992	0·76–0·99	70·0–99·7%	0·61–0·93
Number of studies	26	12	17	6	10	11	10
Benign versus malignant (33 studies involved more than two lesion types and provided outcome measures for benign vs malignant, 2018–20)							
Mean (95% CI)	0·870 (0·843–0·897)	0·864 (0·820–0·908)	0·859 (0·804–0·914)	0·892 (0·832–0·951)	0·883 (0·840–0·926)	88·8% (86·3–91·3%)	0·888 (0·817–0·959)
Median (IQR)	0·851 (0·828–0·928)	0·892 (0·842–0·923)	0·871 (0·834–0·906)	0·902 (0·874–0·939)	0·895 (0·855–0·934)	89·5% (83·8–93·1%)	0·833 (0·830–0·957)
Range	0·720–0·995	0·535–0·981	0·582–0·994	0·761–0·970	0·742–0·975	75·9–99·5%	0·826–0·994
Number of studies	28	23	14	6	12	24	5

*Accuracy index=(true positives + true negatives)/(true positives + true negatives + false positives + false negatives). †F1 score=2 × (positive predictive value × sensitivity)/(positive predictive value + sensitivity).

Table 2: Outcome measures reported in the included studies for melanoma, squamous cell carcinoma, basal cell carcinoma, and for studies that assessed the classification of benign versus malignant categories (in studies that included more than two lesion types; n=272)

Fig. 2. Summary of Melanoma Studies [13]

CNN in order to process two-dimensional input, CNN is a Multilayer Perceptron (MLP). Because it contains a deep network and is frequently used for processing and interpreting picture, CNN is one of the types of neural networks. CNN architecture is comparable to that of neural networks in that each CNN neuron has a function for bias, weight, and activation. In the CNN architecture the convolution layer with ReLU activation is initiated, Pooling layer is employed for extracting feature, and the fully connected layer with SoftMax activation as the classification layer. Below, the paper will briefly go over each of the CNN layers. The first layer to process the image as an input system model is the convolution layer. The feature map is an image that has been processed using a filter to extract features from the input.

ReLU (Rectified Linear Unit) is a CNN activation layer used to enhance neural network training, which has the advantage of reducing errors. Rel-U sets all of the pixels' values to zero when a pixel picture contains a value other than zero [14] .

The pooling layer has various advantages, including the ability to gradually reduces volume of the output on the feature map and the ability to control over-fitting. It is typically introduced after several convolution layers in the CNN method [15].

The pooling layer also reduces the amount of computation only needed to run in the network and the number of parameters to make learners use.

A convolution layer's features map summarizes the features that are present in a particular region. The ensuing operations are performed on summarized features rather than the precisely positioned features that are created by the convolution layer. This advantage makes the model more resilient to alterations in the arrangement of the features in the input image.

Utilizing maximum or mean pooling, data is reduced utilizing the pooling layer. In contrast to mean pooling, which chooses the average value, max-pooling will choose the maximum value.

Hyperparameter:

The performance of the model can be impacted by the hyperparameter, which has changing values that persist during the training of model. Adaptive Moment Estimation and Nesterov-accelerated Adaptive Moment Estimation, Stochastic Gradient Descent (SGD), Root Mean Square Propagation (RMSprop), are examples of hyperparameters that are frequently employed as optimizers (Nadam).

A recurrent optimization technique called stochastic gradient descent (SGD) aims to improve the model by applying superior functions like differential or subdifferential. Each training sample is treated as a new parameter by SGD. A common technique for creating deep learning models is called Root Mean Square Propagation (RMSprop) [16].

This optimizer is a variation on the Root Propagation algorithm (Rprop). Rprop cannot initially be applied to files containing a lot of data. Moving the gradient average at the model's time is the core of RMSprop. RMSprop and momentum are combined to create the Adam optimizer. Additionally, this optimizer employs an average weight gradient [17].

Adam will be used in this research, compared to other optimizers, Adam is fast and utilizes less memory, and also can handle noisy issues with sparse gradients. Thus, Adam and NAG are combined to create Nadam (Nesterov-accelerated Adaptive Moment Estimation) (Nesterov accelerated gradient).

3. Objective and Methodology

The objective of this study is to analyze and classify the mole images sourced either photographed using a smartphone or a dermoscopic device. Provide access to a computer-enabled automated, reliable system that can detect melanoma via digital images. The Model using CNN shall be able to process and classify both clinical and dermoscopic images. Analyze images of lesions in a very short time can be a very useful tool in the area of medical diagnosis. The model with end-to-end decision system can detect melanoma patients' lives can be saved at very low cost.

The paper follows CRISP-DM framework. It is a process model which explains approaches in data mining. It is the most widely used model in analytics. It was conceived in 1996 IBM Corporation released a new methodology called Analytics Solutions Unified Method for Data Mining/Predictive Analytics (ASUM-DM). It refines and extends CRISP-DM and has six steps [18] . Further each of the process steps is being discussed in detail from business understanding to data understanding, data preparation, modeling, model evaluation, and deployment feasibility.

4. Business Understanding

Melanoma is a an skin growth or tumor produced due to melanocytes transformation into malignant. Melanomas usually occur on the skin. The number of cases of melanoma skin cancer diagnosed worldwide is expected to rise by 18% to 340,271 with the number of deaths increasing 20% to 72,886 by 2040 [19]

Malignant melanoma is the deadliest and speedily increasing skin cancers across the globe. The easy solution would be to get diagnosed early is very much significant to get cured with a simple excision if detected early. The paper objective is to determine that any image source be it clinical or dermoscopic are used to determine benign or malignant. Melanoma cases diagnosed worldwide is expected to rise by 18% to 340,271, the number of deaths increasing 20% to 72,886 by 2040. Close to half a million (466,914) people are expected to be diagnosed with melanoma skin cancer an increase of 62% against 2018 data while 105,904 are expected to die from this deadly skin cancer disease which will be an increase of 74%.

Many studies conducted have used either dermoscopic or clinical images, very minimal studies have been done using both the images together. An inclusive model that can process any mole image and classify as melanoma or benign. Medical practitioners and patients need an easy method at a faster rate in identifying the melanoma and stop the disease spreading further. Need to detect early and classify a normal mole to evolving Melanoma. Highly-trained specialists are required to accurately diagnose Melanoma early which is a very big challenge due to the shortage of experts. Melanoma is more dangerous and has increased over the last decade and early detection of a mole becoming cutaneous melanoma will help reduce mortality rates. The prevalence rate is

the proportion of people in the population who have a specific disease or attribute at a specific time or within a specific period (CDC Centers for Disease Control and Prevention 2019). In the United States fifth, most common cancer among men and women is melanoma. White people are more impacted with melanoma than black people which is 20 times more than later. Most women are diagnosed with melanoma much before the age of 50 however the average age of diagnosis is 65. The development of melanoma occurs when people grow older which is a very common phenomenon. This is also seen younger population who are 30 plus age. Melanoma is the common cancer diagnosed among young adults and older people, mainly in women. Around 2400 cases estimated in 2020 are projected to be diagnosed in the age group of 15 to 29. Skin cancer cases including melanoma have been progressively increasing for several decades. The number of melanoma diagnoses among persons in their 30s decreased somewhat for males and stayed stable for women. Increased sun protection practices and a decline in indoor tanning are probably contributing factors to the decline of melanoma among younger people. Melanoma makes for about 1% of all skin cancer diagnoses in the US. But out of all skin cancer disorders, melanoma is the one that claims the most lives. In the United States, it is anticipated that 7,650 deaths from melanoma (5,080 males and 2,570 women) will take place. But thanks to early detection and treatment, the number of melanoma deaths fell by about 4% annually from 2015 to 2019.

5 Data Understanding and Data Preparation

The datasets are digital photos taken in 2018 and 2019 from a pool of consecutive lesions samples taken from the ISIC. These photographs were captured using digital cameras in a variety of resolutions while operating in nonpolarizing or polarizing modes. Images with poor image quality, ambiguity, or clarity were not included in the dataset. Figure No.3 shows various examples of melanoma photos for classification. The images are manually evaluated and classified as either benign skin lesions or melanoma.

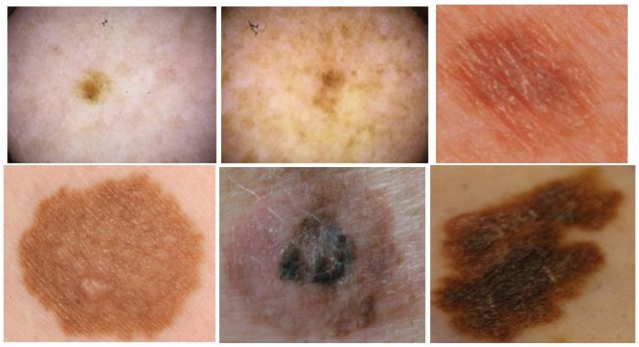

Fig. 3. sample Melanoma and Nevus/ Benign Images (ISIC Archive, 2019) [2]

Images were labelled as benign, naevus, and Melanoma from below sites were used from [3], [2]. 170 images were put into the dataset relying upon their analysis label which has been extracted from the metadata of the pictures. 70 images of melanoma and 100 images labeled as nevus and benign are used in this study. 170 images are non-dermoscopic melanoma and out of that100 are nevi. The image dimensions range from 201 x 257 to 3177 x 1333 pixels. The dataset has been prearranged into 2 classes containing malignant melanoma Images and the other nevus images. The images from ISIC and from the Med-node archive have been chosen randomly and clubbed for the training, test, and validation.

When transforming images, image augmentation is a crucial technique used that may produce numerous transformed copies of the same old image. Depending on the procedures used for picture augmentation, such as shifting, rotating, flipping, etc., each image copy differs from the other images in some ways. This technique is frequently used for creating deep learning models because applying this image augmentation in small amounts of variations on the original image does not deviate from its target class but only offers another new perspective of capturing the real object practically in day-to-day clinical life.

Images of a nevus with a raised mole with different colors of tan and brown were included. The shapes of the images are oval, round, dome-shaped were part of the data set. The images were largely free from hair. The ISIC data set of benign moles was in a pointed and round shape with bluish color in the background. Malignant melanomas were a combined data set from ISIC and Mednode in equal numbers. The idea was to include the data set variation of two different sources and derive the model.

By ensuring that no identical image is ever used twice during training, the image data generator will go through the image data and randomly change each unique image before it is provided to the model. Rotations, shears, flips, and zooms are just a few of the transformations that can be set when the data generator is instantiated as parameters. This transformation helps to avoid the model from learning noise in the data, such as where features are placed in the image, and makes the model more robust as it trains on slightly distorted images.

One another main obstacles is the big size of the images. The input feature dimension is 1760 * 1470 and the Med-node image dimensions range from 201 * 257 to 3177 * 1333 pixels. This feature size will be very big for computation to process and push to the neural network especially CNN as it also depends on the number of hidden units. The images have three RGB (Red, Green, and Blue) channels, but because of their great computational capacity, they can only be read as a single channel. The data set's image extent is very large in both dimensions of width and height. For instance, a photograph with a width of 1760 and a height of 1470 is highly difficult to process and requires more computing power to register several pictures, which is time-consuming and waste-

ful of resources. The photographs must be scaled as a result of the aforementioned factors so that the machine can process the images using less memory and graphical processing resources. The approach is defined to address these two issues while reading the photos. in such a way that just one-color channel is retained. Grayscale images are generated from original images for easy process.

There are three layers present in the suggested system. The input layer, which is the initial layer, here the data sets for training are placed. Information from the input layer is gathered that provides by adding weight before moving on to hidden levels. While the patterns are identified, the hidden layer's neurons extract the data's features from it. Using the patterns as foundation right classes are chosen by output layers. As last step binary classification is used, to select classes 1 and 0. Class 0 in this study denotes a benign nevus or mole, whereas class 1 denotes a malignant melanoma with cancerous cells.

Each of the preprocessed images is saved along with their classes. From the dataset, benign and malignant images are taken for further processing. Images are discarded if they are not labeled. At last, the images recorded are fed to CNN. The CNN feature that allows you to reduce the size of the image is important and practical. By choosing a stride of 2, for example, you can confuse the image by taking into account both the horizontal and vertical orientations separately.

Image size is reduced to speed up computation, pooling layers are frequently utilized. Convolutions and pulls are then applied to extract more complicated features. After features flattened to single layer images are fed to fully connected neural network of the model, The intended outcome, which is either benign or cancerous, is then discovered after using the SoftMax**.**

6 Modeling

The pre-processing model in this study involves merely normalizing the photos, which is benign. The photos are scaled here in this step. Before processing the photos, the data must be multiplied by the rescale factor. The proposed model would struggle to process the original images' RGB coefficients, which range from 0 to 255, at a standard learning rate, thus the values are scaled to be between 0 and 1, or 1/255, instead. In this study, the proposed CNN model has the first layer the convolutional (Conv2D) layer which is like a set of learnable filters opted for 32, 6x6 filters for the two first conv2D layers. Each filter transforms a part of the image (defined by the kernel size) using the kernel filter. The kernel filter matrix is applied to the whole image. Filters can be seen as a transformation of the image. From these altered images, CNN can pick out elements that are valuable everywhere (feature maps).

The pooling (MaxPool2D) layer of CNN is the second crucial layer. This layer merely serves as a down sampling filter, selecting the maximal value after examining

the two nearby pixels. These are employed to lower computational expenses and, to a lesser extent, to lower overfitting. After the first two layers followed with Max pool size 2x2 combining convolutional and pooling layers, CNN is able to combine local features and learn more global features of the image.

Dropout is a regularization technique in which, for each training sample, a portion of the layer's nodes are randomly disregarded (their weights are assigned to zero). As a result, a piece of the network is dropped at random, forcing the network to acquire features in a distributed manner. Additionally, this method enhances generalization and lessens overfitting. Dropout in the suggested model is set to 0.3.

'relu' is the rectifier (activation function max (2,2). The activation of rectifier function will add non-linearity in the network. Final feature maps are converged into single ID vector by using the Flatten layer. In order to employ fully connected layers after several convolutional/maxpool layers, this flattening step is required. It incorporates every local feature discovered in the earlier convolutional layers. Ultimately fully-connected (Dense) layer is used as an ANN classifier. Adam optimizer provides better results. This algorithm is an extension of stochastic gradient descent adopted for deep learning applications.

7 Model Evaluation

The images labeled as "Naevus " and "malignant" were used. The sourced dataset has been organized into 2 classes one with Malignant Melanoma Images and the other Naevus Images with 70/30 for train and validation.

According to the model summary in this paper, the first layer has 3488 parameters. From the above model, the summary understands that the output of each layer of Conv2D and MaxPooling2D layer is a 3D tensor of shape (height, width, channels). The dimension's width and height would shrink as learning goes deeper in the network. The first argument 32 controls the number of output channels for each Conv2D layer. The conv layers are employed to reduce the number of parameters and find local patterns.

Flatten has been employed to connect conv to dense. Dropout 0.3 has been used to avoid overfitting. A dense layer has been employed after conv layers; dense layer helps in classifying the extracted features provided by conv layers. The proposed CNN model has the first layer the convolutional (Conv2D) layer which is like a set of learnable filters, the first two conv2d layers has 32, 6 * 6 filters. Using the kernel filter, each filter alters a specific area of the image. The entire image is subjected to the kernel filter matrix.

Filters can be thought of as a picture alteration. From these transformed photographs, CNN can pick out elements that are valuable everywhere (feature maps). The pooling

(MaxPool2D) layer of CNN is the second crucial layer and serves as down sampling filter, choosing the maximum value from the two nearby pixels. These are employed to lower computing costs and may, to a certain extent, lower overfitting.

The Model has run for 60 epochs with training loss at 0.177 and accuracy at 0.94. The model is able to learn until the 60th epoch with validation loss reducing from 0.45 to0.38 and Validation accuracy at 0.88. This proposed CNN model has better performance even after combined two data sets from ISIC and Med-node. From the literature review, it is learned that many studies have either used one of the datasets while training the model. This model can perform better even with the images having a small mole, large moles, and raised moles with different colors of tan and brown moles.

9.1 Model Performance

The model performance in Fig. 4. has achieved an accuracy of 94 % with training loss at 17.6%, The Validation loss is at 38% for the 60th Epoch and has been decreasing meanwhile the Validation accuracy is increasing which is a good indication that the model is still learning.

Since the validation loss is at 38% the confusion matrix as depicted in Fig. 5. has very less false positives which are labeled as melanoma instead of nevus. However, the model is able to detect the true positive better. The model also is a better type II error the false negative rate is also low.

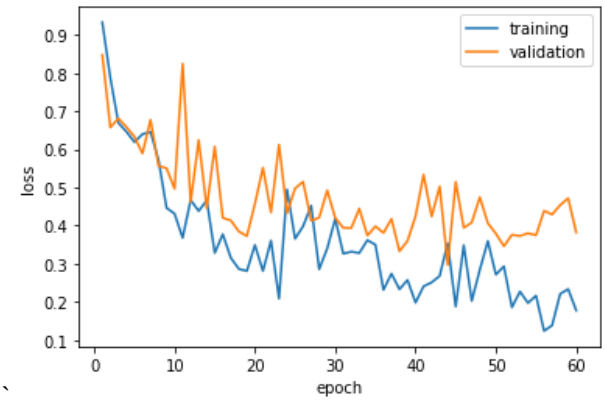

Fig. 4. Training _Validation Plot

Other Metrics Equations and Results

Sensitivity = TP/(TP+FN) 14/ (14+2) = 0.87

Specificity = TN/(TN+FP) 17/ (17+2) = 0.89
Precision = TP/(TP+FP) 14 / (14+2) = 0.87
Negative Predictive Value = TN/(TN+FN) 17/ (17+2) = 0.89
Accuracy = TP+TN/(TP+TN+FP+FN) 14+17/ (14+17+2+2) = 0.88

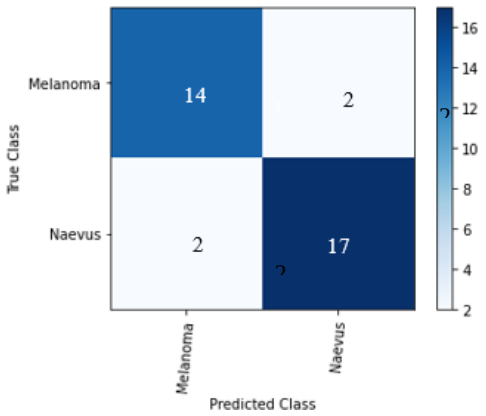

Fig. 5. Confusion Matrix

8 Deployment

The data pipeline appears to arrange the deployment for the future as the business requirement is to create a front-end API as an application. The Complete deployment is not the scope of this project study however have considered the below deployments as a reference for future work. The goal of this stage is to actualize end-to-end applications in which images are taken from smartphones or digital cameras and appropriately classified after the images are run through the preprocessing data generator layer and further fed through the model to detect Melanoma via a Flask API displayed in the UI / dashboard. One of the deployment- Overview of Fully Automated Approach for Early Detection of Pigmented Skin Lesion Diagnosis Using ABCD [20].

Dermatologists all over the world use ABCD as the primary tool for diagnosis while patients use it as a self-examination tool and as a common reference for various skin cancer diagnosis models. This ABCD model is made up of the four main warning signs that can be detected visually and more accurately identified by the computer-embedded deep learning modeled automated system to diagnose melanoma. The features will then be detected using the ABCD rule based on the image area identified during the preprocessing and segmentation.

9 Analysis and Results

The proposed CNN model performance on both Clinical and dermoscopic images has achieved an accuracy of 94 % with training loss at 17.6%, the validation loss is at 38% for the 60th Epoch and has been decreasing meanwhile the validation accuracy is increasing which is a good indication that the model is still learning.

Since the validation loss is at 38% as per the confusion matrix has very less false positives which are labeled as melanoma instead of nevus. However, the model is able to detect the true positive better. The model also is a better type II error the false negative rate is also low.

Overall, the model is able to provide an accuracy of 0.94 which is the best among the studies done on melanoma detection particularly using images from two different data sets from ISIC and Med-node.

Comparing the results from literature review and from the current study are depicted in Table 1. the results from the current study are at par however the improvements have to be made in accuracy and also in classifying right class.

Table 1. Results Summary

Results Tabulation	Specificity	Sensitivity	Precision	Negative Predictive Value	Model Accuracy
Results from this Study	0.89	0.87	0.87	0.89	0.88
Results from Literature Review	0.89	0.894		0.93	0.91

10. Conclusions and Future Scope

Skin cancer is a health problem that has caused concern on a global scale, and early detection of the disease is greatly aided by a reliable automatic melanoma decision system. The deep convolutional neural network that can be utilized for skin cancer classification has inspired the suggested Sequential CNN model. The analysis's findings demonstrate that the new model is more effective than the evaluated studies and pretrained classification models. The overall ACC for Sequential CNN is 94%. This investigation strongly suggests using AI to identify the deadliest type of cancer since the current proposed model is good reliable in predicting the precise classification with a high true positive rate. We can speed up processing by employing images that are 128 by 128 pixels in size, have three channels, and an inference time of about 0.1 seconds per image. As a result, the suggested technique can perform even better on substantial and evenly distributed skin cancer datasets. Currently, in this study we have analyzed

only malignant and benign moles in the next study would like to include all types of melanomas and grade them with severity levels including data from Asian countries. Currently, the data used is from western countries [21]. Further would like to deploy end to end model starting from capturing images in digital cameras and a UI to process and produce the results of detection within minutes with higher accuracy.

References

[1] American Cancer Soceity, "What Is Melanoma Skin Cancer ?," pp. 1–14, 2020.

[2] "ISIC Archive," 2019. https://www.isic-archive.com/#!/topWithHeader/onlyHeaderTop/gallery?filter=%5B%22benign_malignant%7Cbenign%22%2C%22benign_malignant%7Cmalignant%22%5D (accessed Aug. 10, 2022).

[3] "Dermatology database used in MED-NODE," 2015. https://www.cs.rug.nl/~imaging/databases/melanoma_naevi/ (accessed Aug. 10, 2022).

[4] A. Aima and A. K. Sharma, "Predictive Approach for Melanoma Skin Cancer Detection using CNN," *SSRN Electronic Journal*, pp. 546–552, 2019, doi: 10.2139/ssrn.3352407.

[5] V. Rotemberg *et al.*, "A patient-centric dataset of images and metadata for identifying melanomas using clinical context," *Sci Data*, vol. 8, no. 1, pp. 1–8, 2021, doi: 10.1038/s41597-021-00815-z.

[6] R. A. Pratiwi, S. Nurmaini, D. P. Rini, M. N. Rachmatullah, and A. Darmawahyuni, "Deep ensemble learning for skin lesions classification with convolutional neural network," *IAES International Journal of Artificial Intelligence*, vol. 10, no. 3, pp. 563–570, 2021, doi: 10.11591/ijai.v10.i3.pp563-570.

[7] T. C. Pham, A. Doucet, C. M. Luong, C. T. Tran, and V. D. Hoang, "Improving Skin-Disease Classification Based on Customized Loss Function Combined with Balanced Mini-Batch Logic and Real-Time Image Augmentation," *IEEE Access*, vol. 8, pp. 150725–150737, 2020, doi: 10.1109/ACCESS.2020.3016653.

[8] E. Pérez and S. Ventura, "An ensemble-based convolutional neural network model powered by a genetic algorithm for melanoma diagnosis," *Neural Comput Appl*, vol. 7, pp. 10429–10448, 2021, doi: 10.1007/s00521-021-06655-7.

[9] R. Patil and S. Bellary, "Machine learning approach in melanoma cancer stage detection," *Journal of King Saud University - Computer and Information Sciences*, vol. 34, no. 6, pp. 3285–3293, 2022, doi: 10.1016/j.jksuci.2020.09.002.

[10] R. Kaur, H. Gholamhosseini, R. Sinha, and M. Lindén, "Melanoma Classification Using a Novel Deep Convolutional Neural Network with Dermoscopic Images," *Sensors*, vol. 22, no. 3, pp. 1–15, 2022, doi: 10.3390/s22031134.

[11] M. Heenaye-Mamode Khan *et al.*, "Multi-Class Skin Problem Classification Using Deep Generative Adversarial Network (DGAN)," *Comput Intell Neurosci*, vol. 2022, 2022, doi: 10.1155/2022/1797471.

[12] T. J. Brinker *et al.*, “Skin cancer classification using convolutional neural networks: Systematic review,” *J Med Internet Res*, vol. 20, no. 10, pp. 1–8, 2018, doi: 10.2196/11936.

[13] O. T. J. Mphil *et al.*, “Review Artificial intelligence and machine learning algorithms for early detection of skin cancer in community and primary care settings : a systematic review,” *Lancet Digit Health*, vol. 4, no. 6, pp. e466–e476, 2021, doi: 10.1016/S2589-7500(22)00023-1.

[14] A. F. Agarap, “Deep Learning using Rectified Linear Units (ReLU),” no. March 2018, 2018.

[15] Y. N. Fu’adah, N. C. Pratiwi, M. A. Pramudito, and N. Ibrahim, “Convolutional Neural Network (CNN) for Automatic Skin Cancer Classification System,” *IOP Conf Ser Mater Sci Eng*, vol. 982, no. 1, 2020, doi: 10.1088/1757-899X/982/1/012005.

[16] J. C. Duchi, P. L. Bartlett, and M. J. Wainwright, “Randomized smoothing for (parallel) stochastic optimization,” *Proceedings of the IEEE Conference on Decision and Control*, vol. 12, pp. 5442–5444, 2012, doi: 10.1109/CDC.2012.6426698.

[17] Y. Yu and F. Liu, “Effective Neural Network Training with a New Weighting Mechanism-Based Optimization Algorithm,” *IEEE Access*, vol. 7, pp. 72403–72410, 2019, doi: 10.1109/ACCESS.2019.2919987.

[18] “Cross-industry standard process for data mining - Wikipedia,” 2021. https://en.wikipedia.org/wiki/Cross-industry_standard_process_for_data_mining (accessed Aug. 10, 2022).

[19] Global Coalition for Melanoma Patient Advocacy and Euro Melanoma, “2020 Melanoma Skin Cancer Report- Stemming the Global Epidemic,” p. 16, 2020.

[20] M. S. Mabrouk, A. Y. Sayed, H. M. Afifi, M. A. Sheha, and A. Sharwy, “Fully Automated Approach for Early Detection of Pigmented Skin Lesion Diagnosis Using ABCD,” *J Healthc Inform Res*, vol. 4, no. 2, pp. 151–173, 2020, doi: 10.1007/s41666-020-00067-3.

[21] S. Zhang, S. Huang, H. Wu, Z. Yang, and Y. Chen, “Intelligent Data Analytics for Diagnosing Melanoma Skin Lesions via Deep Learning in IoT System,” *Mobile Information Systems*, vol. 2021, 2021, doi: 10.1155/2021/8700506.