



Melanoma Detection Using a Deep Learning Approach

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Citation | Manzoor. S, Qayyum. H, Hassan. F, Ullah. A, Nawaz. A, Rahman. A, “Melanoma Detection Using a Deep Learning Approach”, International Journal of Innovations in Science and Technology. Vol 4, Issue 1, pp: 222-232, 2022.

Received | Feb 18, 2022; Revised | Feb 26, 2022 Accepted | Feb 28, 2022; Published | March 01, 2022.

Melanoma is a skin lesion disease; it is a skin cancer that is caused by uncontrolled growth in melanocytic tissues. Damaged cells can cause damage to nearby cells and consequently spreads cancer in other parts of the body. The aim of this research is the early detection of Melanoma disease, many researchers have already struggled and achieved success in detecting melanoma with different values for their evaluation parameters, they used different machine learning as well as deep learning approaches, and we applied deep learning approach for Melanoma detection, we used publicly available dataset for experimentation purpose. We applied deep learning algorithms ResNet50 and VGG16 for Melanoma detection; the accuracy, precision, recall, Jaccard index, and dice co-efficient of our proposed model are 92.3%, 93.3%, 90%, 9.98%, and 97.7%, respectively. Our proposed algorithm can be used to increase chances of survival for patients and can save the money which is used for diagnosis and treatment of Melanoma every year.

Keywords: Melanoma Identification, Melanoma detection, Deep Learning, VGG16, ResNet50, Data Augmentation.

INTRODUCTION

Melanoma is a skin lesion that results in cancer, it starts because of uncontrolled growth of melanocytes cells, the damaged cells cause nearby other cells to be damaged and they result in skin cancer, and this is a most dangerous type of skin cancer which resulted in 75% deaths due to skin cancer [1]. Disease diagnosis and treatment consumes a lot of budget and other resources including time, and human resources, to resolve these issues there is a need to have an automated Melanoma detection system that would assist the patients and the doctors in the terms of Melanoma presence or absence on the skin of the patient [1].

Detection of Melanoma would be a relief to the patients who are geographically far from diagnosis center(s), as they would be able to detect the initiation of Melanoma disease by capturing the picture of the damaged skin to check whether it is Melanoma disease or not, and if the disease is absent then their time and money for reaching diagnosis center would be

saved, and if the disease is detected then the patient would be able to initiate the treatment as soon as possible which would increase the chances of his/her survival [2].

Melanoma classification is a trending topic among medical researchers, various types of algorithms have been applied for detection, they used different types of datasets with different orientations and the researchers have evaluated their algorithms based on different parameters including accuracy, specificity, sensitivity, dice co-efficient, precision, recall, and dice index. Most of the researchers used the dataset of ISBI 2016 which is available at [2], the publicly available dataset is open-source which helps many researchers to proceed in the previous works that result in improved models for disease detection and treatment [3].

Melanoma is an aggressive skin cancer that reduces the expectancy of human life, the disease can be reduced by early detection causing downfall of mortality due to skin cancer [6]. Sara et al., [6] compared different states of art CNN (convolutional neural networks) for dermoscopic images, they utilized GPU to speed up the process of training and testing, they claimed that pre-processing of data and data augmentation results in improved accuracy. Sara et al. [6] focused on data-preprocessing, they applied hair removal and ruler's removal for improving the dataset to achieve better results against their proposed model. To differentiate between melanoma and non-melanoma skin diseases is a big challenge for researchers, but using dermoscopic images this issue can be resolved easily [7], Savy et al., [7] used the dataset of dermoscopic images, the dataset is available at [8], they applied two deep neural networks VGG16 and AlexNet in two different ways of procession i.e., transfer learning and usage of the model as feature extractor, for melanoma detection, they claimed that the transfer learning gives better results for both models, the feature extraction gives 95 % accuracy for AlexNet while using VGG16 the accuracy was 97.5%.

Codella et al., [9] used the publicly available dataset of dermoscopic images which was challenge of ISBI (International Symposium on Biomedical Imaging) named "Skin lesion towards Melanoma detection" [10], they proposed a combined visual recognition system for disease detection consisting of segmentation and classification, they compared their results with other state-of-art methods of machine learning and deep learning including convolutional neural networks, deep-residual network, and fully connected U-Net architecture, they evaluated their model on the basis of Accuracy and Jaccard index, they experimented and claimed the results of Jaccard index and accuracy for Optimized Single was 0.836 and 94.9% respectively, while for after applying data augmentation the Jaccard index and accuracy reduced to 0.828 and 94.7%, the results of Jaccard index and accuracy further reduced after noise removal and became 0.812 and 94.1% respectively, for ensemble of 10 U-Nets the Jaccard index and accuracy became 0.841 and 95.1 % respectively, and for state-of-art the Jaccard index and accuracy became 0.843 and 95.3% respectively. David et al., [11] used the dataset of dermoscopic images of ISBI (2016) publicly available at ISIC [2], they applied segmentation on the input images with the help of a suitable mask and then classified the images into Melanoma, and Non-Melanoma skin diseases, the segmentation, and classification were applied in five steps a) lesion segmentation, b) dermoscopic feature selection, c) dermoscopic feature segmentation, d) disease classification task, e) disease classification using a mask. After training, the model was evaluated based on sensitivity, accuracy, specificity, dice coefficient, and Jaccard index, the value of sensitivity, specificity, accuracy, dice coefficient,

and Jaccard index for feature segmentation was 0.396, 0.968, 0.962, 0.128, and 0.070 respectively, while the values of sensitivity, specificity, accuracy, dice coefficient, and Jaccard index for disease classification with the mask were 0.547, 0.937, 0.855, 0.624, and 0.783, respectively. However, there are numerous limitations of the systems that are discussed above such as Codela et al., applied SVM for classification, and it used 50% threshold for binary dataset. They applied late fusion with unweighted SVM score, in this way its accuracy could not boost up and resulted 72.3% accuracy. Neol et al., shown poor performance in the lesion attribute detection step, the poor results were shown due to poor correlation of clinicians who were responsible for the experimentation. Here Jaccard value for some instances was divided by zero which is not useful. David et al., applied skin lesion mask but did not apply suitable data preprocessing techniques to remove noise, hair, and bubbles; due to this reason, its sensitivity and average precision was very low. Sara et al., applied a few data pre-processing techniques, the pre-processing techniques consist of illumination and contrast, but hair removal technique was not applied which resulted in lower performance regarding the accuracy, and other parameters. Resnet50 shows better results but it has some consequences like it has 23 million layers and it takes weeks for training purpose. Vgg16 is a deeper network, and it consists of 16 deep layers of network and it can classify the input image into 1000 different classes, so it takes weeks for training purposes.

Parkash et al.,[17] deployed CNN for detection of Melanoma disease, CNN used in this research consist of multi-layer perceptron. CNN is capable of handling two-dimensional data. CNN is also considered in deep learning techniques as its network is much deep containing multiple layers. Initially after applying pre-processing technique of removing hair, and noise the disease distribution was considered to check the attributes of the input dataset, the dataset contained 7 skin disease including melanoma, nevi, and other skin disease. They applied the results with the graph which shows the effects of skin disease, it analyzes that the skin disease is a cancer or not? When it is known that the input image is a skin cancer then it is compared with the input dataset to check the skin cancer is Melanoma or non-Melanoma [18].

Jwan et al.,[18] worked on classification of skin lesion using deep convolutional neural network, their methodology comprises of four steps including image pre-processing, image segmentation, feature extraction, and last one classification stage with labels Melanoma and Non-Melanoma. The Melanoma skin cancer consists of Melanoma, Melanocytic Nevus, Benign, and Vascular Lesion. While Non-Melanoma skin cancer comprises of Dermatofibroma, Actinic Keratosis, Basal Cell Carcinoma, and Squamous Cell. ABCDE rule was deployed for Melanoma detection, during first step two sides of input image, if both sides of an image are same then it is first clue that the input image belongs to Non-Melanoma skin cancer, if both sides of the input image are not same then it belongs to the Melanoma skin cancer. At second stage the input image is checked for its edges and visibility, if the edges of image are sharp then it belongs to Non-Melanoma Skin Cancer and if the edges are not same then it belongs to Melanoma Skin Cancer. At third stage the shades of input image are analyzed if the shades of image are consistent then it belongs to Non-Melanoma Skin Cancer and if its shades are not consistent throughout the image then it belongs to Melanoma Skin Cancer. At fourth and last stage of the process diameter of the object within the input image is analyzed

if its size is smaller than 6mm then it belongs to Melanoma Skin Cancer, and if its size is greater than 6mm then it belongs to Melanoma Skin Cancer [18].

In this research paper we proposed a hybrid model consisting of two classifiers ResNet50 and VGG16, after applying necessary data pre-processing techniques, we applied the down sampling technique to get a balanced dataset, we used the balanced dataset for training and testing purposes to classify the input images into Melanoma and Non-Melanoma skin diseases, this process yielded the accuracy, precision, and recall for evaluating the model. The remaining paper is organized as, in section 2, we discuss the proposed methodology followed by the data pre-processing, filling in missing values, feature extraction and classification. Section 3 presents the detail of experimental results and discussion. Finally, we conclude our work in section 4.

Materials and Method

This section presents a detailed description of the proposed sepsis detection system. The main objective of the proposed framework is to differentiate between Melanoma and non-Melanoma cases of input data. We proposed the methodology by using the dataset of dermoscopic images provided ISIC 2018 (International Skin Imaging Collaboration) which is publicly available at [2], the dataset contained the record of 7 skin diseases including Melanoma, Basal Cell Carcinoma, Benin, Actinic Keratosis, Dermatofibroma, Melanocytic Nevus, and Vascular Lesion. The dataset contained about 10015 images of 600 X 450 resolution, with the disease range between Benin and Malignant. Firstly, we applied data pre-processing techniques including filling in the empty values by calculating the mean of related values of the column. Then we checked the distribution of all the seven diseases throughout the mentioned dataset, we found that the dataset was unbalanced with majority values of Melanocytic nevi, so we applied down sampling technique, in down-sampling technique the selection ratio of 4000:1000 samples was applied, means we selected just 1000 samples of each 4000 samples for Melanocytic nevi to reduce its majority entries in the dataset, in this way the dataset became regularized and balanced enough to apply the algorithm for skin lesion classification. Normalization technique was applied to the dataset to get a suitable dataset. Label encoding for 7 classes of skin diseases to differentiate between Melanoma and Non-Melanoma skin diseases, the data augmentation technique helped to overcome the negative effects of down sampling technique, the dataset was divided into the proportion of 70% training dataset and 30% testing dataset, then we applied the mask on images to select the region of interest (i.e., affected skin part) then two classifiers VGG16 and ResNet50 were applied for classification of Melanoma disease, Figure 1 shows the methodology.

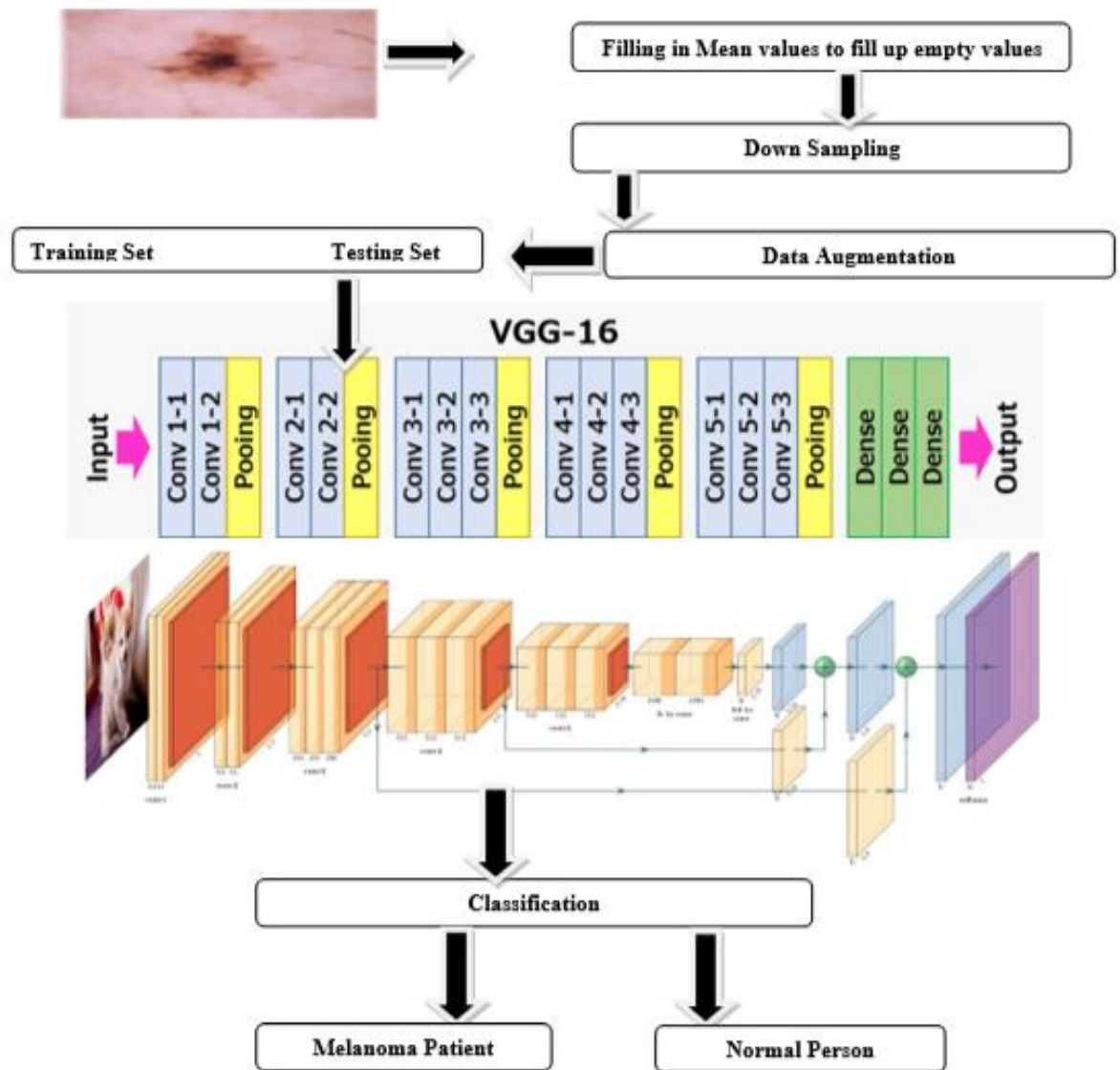


Figure 1. Proposed System.

Down Sampling

Down sampling is the reduction of the sampling rate of a signal, it reduces the majority samples of a specific value by picking up one from N number of entries [12].

Sub Sampling

The subsampling is a method that selects fewer samples of majority valued label, in our case we choose 1 sample from every 4 samples of majority labels, named Melanocytic nevi [12].

Data Augmentation

The data augmentation technique is used to overcome and neglect the negative effects of strong imbalanced classes and results in enhancement of the performance of the proposed model [6].

VGG 16

VGG16 is a convolutional neural network that uses the ImageNet library, it is comprised of a convolution with maximum pool layers that are connected throughout the whole network, and at the end, and it holds 2 fully connected layers that are used for the prediction purpose [13]. During the period of training the input image is fixed to the size of 224x224 RGB, the input image is pre-processed in a single step of reducing the mean RGB from the input image. The input image after pre-processing is passed through the stack of convolutional layers where it is filtered through filter of 3x3 size which rotates all over the image by moving up, down, left, and right, it's as effective as filter of 7x7 size [13]. Max pooling consisting of five max pooling layers is applied on the image to assist the spatial pooling process. Max pooling is applied on the window of 2x2 pixels [13].

RESNET50

ResNet50 is a convolutional neural network (CNN) which consists of 50 layers of the network, it is available in a pre-trained model which is initially trained on more than 1 Million images from the library of ImageNet, the pre-trained model is then fit for testing and classification purpose [13].

RESULTS AND DISCUSSION

Dataset

We used the input dataset downloaded from ISIC 2018 (International Skin Imaging Collaboration) which is publicly available at [2], the dataset contained the record of seven skin diseases including Melanoma, Benin, Actinic Keratosis, Basal Cell Carcinoma, Dermatofibroma, Melanocytic Nevus, and Vascular Lesion.

Experimental Environment

For experimentation, all the extra layers of the network were frozen except the fc layer and dense layer, after that the top two layers were tune. The epochs-based training and testing were applied for the classification purpose, each model has a different time for each step of processing, 481 epochs were applied for training purposes while 433 epochs were applied for testing purposes. On each epoch of the network layer, the steps of padding, conv2d, batch normalization, max pooling, and zero padding were applied to get the suitable results of the model. Table 1 depicts the processing time of each model for 100 epochs.

Table 1. Environment for experimentation.

Model Name	Processing time for 100 epochs
VGG16	490 SECONDS
ResNet50	780 SECONDS
ResNet50 +VGG16	1153 SECONDS

Evaluation Metrics

The evaluation parameters for comparison of the proposed hybrid model with other models include accuracy, precision, recall, dice-coefficient, and Jaccard index.

Accuracy

Accuracy is the ability of a model to obtain positive results i.e., Melanoma in our case, it is the ratio of the sum of true positive and true negative values of predictions to the total values of the predictions. Equation 3 shows the formula to calculate the accuracy [4]. In equation (1), "A" means Accuracy, TP. stands for True Positive, TN. stands for True negative, FP. stands for False Positive, and FN. stands for False Negative.

$$A = (TP. + TN.) / (TP. + TN. + FP. + FN.) \quad (1)$$

Precision

Precision is the testing parameter used for the evaluation of a model which tells the model is how much precise in identifying the patients with true negative (TN.) results. This gives negative values when the patient's body have no disease symptoms. The precision is the ratio of all the true negative (TN.) values to the total sum of true positive (TP.), and false positive (FP.) values, equation 2 shows the formula to calculate the value of precision [4].

$$P = TP. / (TP. + FP.) \quad (2)$$

Recall

In medical diagnosis the recall of a model means the capability of a model to correctly identify the true positive values of disease within the body of a patient. This gives positive value for the patient's test. This is a ratio of true positive (TP.) values to the sum of true positive (TP.), and false negative (FN.) values, equation 2 shows the formula to calculate the value of precision [4].

$$R = TP. / (TP. + FN.) \quad (3)$$

Jaccard Index

Jaccard Index is the ratio of the size of the union of sample sets divided by the size of the union of sample sets, it is used for measurement of similarity between the sample sets, and equation (4) shows the formula to calculate the Jaccard index [5].

$$J(A, B) = |A \cap B| / |A \cup B| \quad (4)$$

Dice Coefficient

The Dice coefficient is like the Jaccard index, it shows the similarity measurement within the limit of 1 to 0, this shows how two models are like one another, and equation (5) shows the formula to calculate the dice coefficient [5].

$$D(A, B) = 2 * |A \cap B| / (|A| + |B|) \quad (5)$$

We evaluated our model based on accuracy, precision, recall, Jaccard index, and dice coefficient. First, we calculated the accuracy of our proposed model as well other classifiers and compared the results of our proposed model with other models, the accuracy of VGG16, ResNet50, and ResNet50 + VGG16 was 58%, 70%, and 92.3% respectively, the precision for VGG16, ResNet50, and ResNet50 + VGG16 came out to be 0.77, 0.72, and 0.93 respectively, the recall for VGG16, ResNet50, and ResNet50 + VGG16 resulted in the values of 0.70, 0.74, and 0.90 respectively. The Jaccard index of VGG16, ResNet50, and ResNet50 + VGG16, became 0.77, 0.80, and 0.998 respectively. The Dice coefficient for ResNet50, VGG16, and ResNet50 + VGG16 was 0.83, 0.73, and 0.974 respectively. Table 2 shows the comparison of accuracy, precision, recall, Jaccard score, and F1-Score for VGG16, ResNet50, and ResNet50 + VGG16.

Table 2. Comparison of vgg16, resnet50 and vgg16+resnet50.

Model Name	Accuracy	Precision	Recall	Jaccard Index	Dice coefficient
VGG16	58%	0.77	0.70	0.77	0.73
ResNet50	70%	0.72	0.74	0.80	0.83
ResNet50 GG16	92.3%	0.93	0.90	0.998	0.974

Comparison with other methods

We compared the performance of our method with the results of Adria et al. [14], they calculated accuracy for three methods M1 training from scratch, M2 ConvNet as Feature extractor, and M3 Fine-tuning with ConvNet, the accuracy for M1, M2, and M3 were 66%, 68.67%, and 81.33% respectively, and precision values for M1, M2, and M3 were 0.677, 0.495, and 0.797 respectively. We compared our results with the results of the CNN model of Chanki et al., [15], the accuracy and precision for CNN [15] were 83.51% and 0.922 respectively. We compared our results with the results of Chiem et al., [16], the accuracy of SVM(Quadratic), SVM(Polynomial), and SVM (Gaussian RBF) were 74.36%, 85.3%, and 68% respectively. Table 3 and 4 show the comparison of the proposed model with other methods.

Table 3. Comparison of proposed model with other models

Model Name	Accuracy	Precision
M1 [14]	66 %	0.677
M2 [14]	68.67 %	0.495
M3 [14]	81.33 %	0.797
CNN [15]	83.51 %	0.922
ResNet50 + VGG16	92.3 %	0.93

Table 4. Comparison of accuracy of proposed model with other models

Model Name	Accuracy
SVM (Quadratic) [16]	74.36%
SVM (Polynomial) [16]	85.3%
SVM (Gaussian RBF) [16]	68%
ResNet50 + VGG16	92.3 %

We compared the results of accuracy of our proposed hybrid model with the results of different researchers during the period of 2017-2020. The accuracy of Subha, S., et al. [19], Xiao, F. et al. [20], Harangi, B., et al. [20], Pacheco et al. [20], and Rashid et al. [20], and Li et al. [20] was 80.2%, 84.8%, 90%, 64%, 86%, and 91% respectively. Table 5 shows the comparison of accuracy of our model with other models. The accuracy of our model was 92.3%.

Table 5. Comparison of accuracy of proposed model with other models

Model Name	Accuracy
CNN [19]	80.2%
LBP, ResNet 50, DesNet[20]	84.8%
GoogelNet [20]	64.3%
CNN SENet[20]	91.3%
GANs[20]	86%

ResNet50 [20]	91%
ResNet50 + VGG16	92.3 %

We compared the processing time of our proposed model with other models including ResNet 50, VGG 16, CNN. The processing time of our model, ResNet 50, VGG16, and CNN was 1153 seconds, 780 seconds, 490 seconds, and 1290 seconds respectively. Table 6 shows the comparison of processing time of our model with other models.

Table 6. Environment for experimentation.

Model Name	Processing time for 100 epochs
VGG16	490 SECONDS
CNN [22]	1290 SECONDS
ResNet50	780 SECONDS
ResNet50 +VGG16	1153 SECONDS

CONCLUSION

In the current study we have proposed a hybrid model consisting of two deep learning models ResNet50 and VGG16 for the detection of melanoma using dermoscopic images dataset as input. Additionally, we applied down sampling and sub sampling balancing techniques to get a useful dataset to train and test the proposed model. We compared the results of VGG16, ResNet50, CNN, CNN_SeNet, DesNet, GoogleNet, ResNet, GANs, and ResNet50 + VGG16, the hybrid model gave better results for all the evaluation parameters including accuracy, precision, recall, Jaccard index, and dice coefficient. The accuracy of our proposed model is 92.3% and other models showed less accuracy, CNN showed minimum accuracy with 80.2%, while CNN_SENet showed second most-highest accuracy with value 91.3%. The comparison of proposed model with other models for processing time depicts that the proposed model consumes less resources than other models. In future, we aim to apply customized deep learning models for the other diseases as well. The proposed model can be used for the development of android and iOS application, and it can be extended to web application. The application would be user friendly so that every mobile user can operate it to check for Melanoma or Non-Melanoma skin disease by just capturing the image of infected part of the skin of human body.

Acknowledgment. Acknowledgments are considered necessary.

Author's Contribution.

All the authors of this article have contributed equally.

Conflict of interest. Authors claim that there exists no conflict of interest for publishing this manuscript in IJIST.

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