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An Improved Method for Skin Cancer Prediction Using Machine Learning Techniques

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ABSTRACT- Among skin diseases the type that causes cancer are the fatal ones and pose the biggest issues. These issues arise since cancers are just much larger quantities of the same cells that are present around the body, which makes diagnosis very difficult until later stages. Now the onset of artificial intelligence and machine learning techniques, in the field of images, has allowed computers to identify sequences and patterns in images that can never be observed by the naked eye. Hence in order to battle skin cancer in its early stages a system has been proposed to identify and predict skin cancer in its earlier stages. A skin cancer prediction system has hence been created and implemented to predict three major types of skin cancer that affect humans. A dataset of the said skin cancer types and other types of skin diseases have been taken and analyzed. Apart from the model, a web application has been constructed for deployment on the web to enable the access of this model to the general masses. The current work is limited to selective dataset and model, which can be further extended.

Keywords: CNN, Skin Cancer, Cost-efficient, Machine Learning

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1. INTRODUCTION

Skin problems are a typical occurrence in the daily lives of humans, which can appear in any part of the body and come in a variety of shapes and sizes. Most of the time, one dismisses them as a common occurrence, unconcerned about the severity of the problem, and in some cases, one is unable to recognize them as a disease [1]. They have a wide range of appearances that even when identified, even trained professionals (doctors or skin specialists) are unsure of the exact disease which has been acquired by the patient at times and thus how to treat them [1]. Hence, treatment of such diseases is very difficult and intensive. Among the myriad of skin diseases, skin cancer is the most fatal of them all. If cancers aren't detected in the early stages, they are effectively incurable and result in deaths [2].

Cancers are a category of disease, which are caused due to abnormal growth in cells, wherein they do not stop multiplying [2]. The constant growth and appearance of new cells leads to congestions and complications from within [2]. Hence cancers in general can be categorized as some of the most fatal diseases, and if not detected in earlier stages almost certainly leads to death [3]. Detection of cancers is an arduous task even for trained medical professionals, as they are simply the extra addition of the same cells and generally cannot be distinguished from one another unless some new characteristics arise [4].

Although skin diseases can be difficult to detect in general by the naked eye of trained professionals, machine learning is a powerful tool that has come to existence. It has proven to be a very powerful tool in image processing and segmentations considering as multiclass problem for human skin disease detection [5]. Image segmentation allows the model to identify new characteristics of the images that were previously unknown and helps identify new traits about an image. Recently it has become a very powerful way of detecting and predicting diseases through images (X Rays, MRI scans etc.) [6][7]. Even among all ML techniques, CNN has proven to be the one of the best and most popular ways to perform image segmentation and analysis [6, 8]. List of models such as ANNs, KNNs, RBFNs, CNNs have been used for classification on lesion images for skin cancer detection still CNNs (deep learning-based model) have been reported to be better comparatively [9][11][13] [22]. The challenge of effective, faster, and remotely accessible machine learning model based on CNN neural analysis to address the problem of skin cancer detection is yet to be addressed.

In this paper a CNNs based model with modified preprocessing steps has been proposed for early detection of skin cancer faster and better results. Apart from that model has been developed with fully automation, web enable and easy accessibility from remote areas for wider use. So, it could be used by people in every area. This will aid in the saving of many lives from fatal diseases as well as faster and more accurate treatment of diseases without spending time on diagnosis.

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2. MATERIALS AND METHODS

2.1 Proposed Solution

To address the research gap in early detection of skin cancer the current work aims to build a model which is used for the prevention and early detection of skin diseases in a fast and cost-efficient way. An application is built where a person can upload an image from the UI, then the image will be sent to the trained model. The model analyses the image and detects the skin disease that person had. A CNN model will be used to analyze the images for the segments and to classify the images into their said categories.

This system will allow any users with internet access to upload an image into the database and get results, identifying the disease for them. This result can then be used by the user to take the necessary precautions needed to cure the acquired disease. This system could also be used by doctors to identify a disease correctly and then verify their diagnosis. New doctors can also learn from this as it'd be more accurate in general and would be a very helpful tool in assisting doctors of the current age, reducing their stress, and allowing them to work more efficiently.

2.2 Algorithms and Techniques Used

The algorithms and techniques used for the comparisons are:
CNN (Convolutional Neural Networks): A CNN is a Deep Learning algorithm that can take in an input image, assign importance (learnable weights and biases) to various aspects/objects in the image, and be able to differentiate one from the other [10]. The above algorithms would be used for analyzing and predicting the disease acquired by the user. For the sake of a higher prediction rate and more accurate analysis, more algorithms are being used to identify one disease. Then after comparing the accuracy rates of all the algorithms, the most accurate result will be displayed to the user along with accuracy percentages. The CNN architecture is mentioned in *figure 1*.

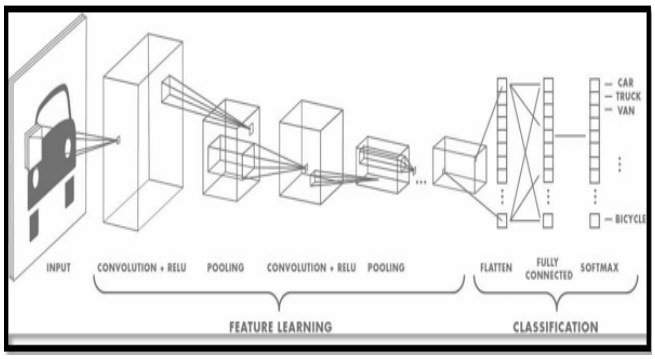

Figure 1: CNN Architecture [10]

2.3 Proposed Architecture

An architecture has been proposed which addresses the gaps identified in the background study. The first step to rectifying the solution is importing the dataset, this dataset contains the images for analysis and their metadata in CSV format. The details of the dataset have been given below in the dataset section and the analysis has been done after.

The next step is preprocessing the data then exploratory data analysis (EDA) which has been obtained. Data preprocessing is wherein we make the raw data into a bit more useful information by setting new variables, cleaning the errors, and filling blank places which can cause errors. EDA is done so that any useful information on the data can be obtained and used for building the CNN model. We have also identified the duplicates in the images from this dataset and actively worked to reduce the effects of this duplication through oversampling of images. The segmented images and their pixel RGB values are then used for the training of the model. To obtain the segmented RGB values of the images we have sorted the pixel RGB values into an array and then appended them in the dataset for evaluation. Oversampling was then done to overcome the class imbalance of the data and the data was reset accordingly to obtain a fully balanced dataset. This new dataset had a total of 46935 images to train with. The new balanced dataset would hence give us better prediction results when compared to the original dataset. The CNN model is made soon after which contains the processes for the classification system and how the image classification will happen in the randomized training set. The data is then augmented and fitted into the model for the classification which basically classifies the randomized data by analyzing the images and processing them through the model. It is trained in several steps in epochs and the data is slowly and accurately classified.

After this step we analyze the correctness of our model by comparing it to the test set and validate it. This step gives us the accuracy of the training model and lets us analyze it for further improvements which can be made to the model. After this we have used this saved model to put it in a system where we can analyze new images by using it. Here we have saved the model and imported it to a different Collaboratory and inserted new images in it for proper analysis of the disease. A proper GUI will be created afterward to streamline this process and enable it for all users across the internet. The flow chart of this basic architecture is given below with detailed steps. [*Figure (2.2)*] The proposed architecture for the model is mentioned in *figure 2*.

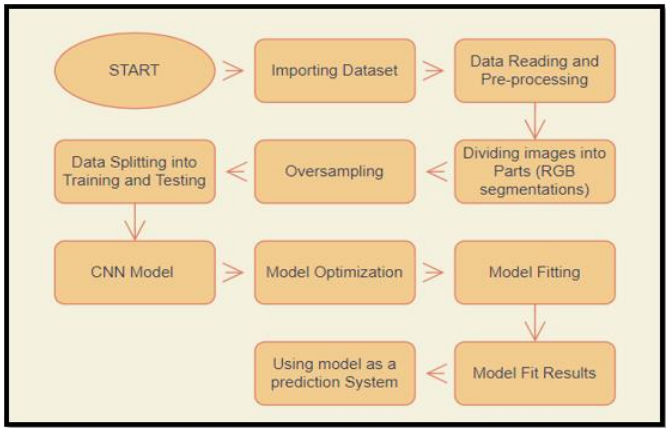

Figure 2: Proposed Architecture

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2.4 Data Preprocessing and Architecture

After getting clear criteria and a set architecture for the model to be made, one can now devise a plan for the implementation of the model and start developing it.

2.4.1 The Dataset

The HAM10000 dataset [13] consists of 10015 dermatoscopic images of a size of 450 × 600. Cases include a representative collection of all important diagnostic categories in the realm of pigmented lesions. It consists of seven diagnostic classes as follows:

1. **Melanoma (MEL):** Melanoma is a disorder in which melanocytes develop malignant (cancer) cells (cells that color the skin). There are a variety of cancers that begin in the skin. Melanoma can develop anywhere on the body's surface. Melanoma risk is influenced by unusual moles, sun exposure, and medical history [14].
2. **Melanocytic Nevi (NV)**: This mole is usually big and is caused by a disease involving melanocytes, or pigment-producing cells (melanin). Melanocytic nevi may be rough, flat, or elevated in appearance. They can be present at birth or develop later in life. Most cases do not necessitate treatment; however, some do necessitate mole removal [15].
3. **Basal Cell Carcinoma (BCC):** Basal cell carcinoma is a kind of skin cancer. Basal cell carcinoma starts in the basal cells, which are a type of skin cell that creates new skin cells when the old ones die. Basal cell carcinoma usually shows as a small, translucent lump on the skin, but it can also occur in different ways [16].
4. **Actinic Keratosis, and Intra-Epithelial Carcinoma (AKIEC):** A rough, scaly area on the skin is called Actinic Keratosis develops after years of sun exposure. It commonly appears on the cheeks, lips, ears, scalp, neck, and backs of hands. An actinic keratosis, also known as a sun keratosis, develops slowly and commonly appears in adults over the age of 40 [17].
5. **Benign Keratosis like Lesions (BKL):** A seborrheic keratosis is a benign (noncancerous) skin development. It might be white, tan, brown, or black in hue. Most of them are elevated and appear to be adhered to the skin. They may resemble warts. Seborrheic keratoses can occur on the chest, arms, back, or other parts of the body.
6. **Dermatofibroma (DF):** Dermatofibroma (superficial benign fibrous histiocytoma) is a common cutaneous lesion with an unknown cause that affects women more frequently. Dermatofibroma mainly affects the extremities (particularly the lower legs) and is asymptomatic, though it can cause itching and pain [18].
7. **Vascular lesions (VASC).:** Birthmarks are vascular lesions, which are very common anomalies of the skin and underlying tissues. Hemangiomas, Vascular Malformations, and Pyogenic Granulomas are the three main types of vascular lesions [19].

Other than the type of cancers presents in the dataset, the information on the age of the people, their gender, the location of the affected disease, the method of diagnosis of the disease and the images of the disease are given to us. These form the details of the entire dataset.

2.4.2 Dataset Operations

A set of operations were performed for better visibility of the dataset which are fully labelling all the diseases as numbers according to the type of disease, from numbers 0 to 6. The NULL values were found in the dataset and replaced with the mean of the data, hence a total of 57, NULL values were normalized. The rest of the information of the dataset was also obtained and analyzed accordingly for any useful information. Another process was done in order to obtain the information on duplicate data. For this comparison between image IDs was done and similar IDs were found within the dataset. This gave us the information that around 4501 images were duplicates, these were then normalized during the process of oversampling. The data was then grouped according to the disease type for further use.

The original images were converted to a Red-Blue-Green (RGB) format after segmentation and this flattened dataset of segmented 28 x 28 images was then used to train the model. The data was readily available for our system however for any further predictions one would have to segment the image and then use them for classification. Hence this new dataset was appended to our original dataset for association and model training along with properly labelled data.

The work is focused to discriminate three skin cancer variants from these lesions which are Basal Cell Carcinoma, Melanoma and Actinic Keratosis. These three are the more common types of skin cancer that are known with melanoma being the most fatal type among them [12]. A small data analysis of the dataset was conducted and it was observed that the data was quite unbalanced with some lesion types having vastly more data compared to the other ones.

2.5 Exploratory Data Analysis

In this paper we have used 11 main libraries for the entire work i.e., NumPy, pandas, os, seaborn, matplotlib, keras, sklearn, TensorFlow, glob, Image, and the drive library. The NumPy and pandas libraries have been used to import, extract, read and refine the data available in the datasets. The seaborn and matplotlib libraries are used for EDA and to show meaningful analysis of the used dataset. Keras, sklearn and TensorFlow are the most important libraries used which are needed for the machine learning model building, testing, and training for final use. The drive and os libraries are simply for connections and data transfer [20].

Upon analysis of the dataset, we obtained the first graph (fig 2.3) that gives us the count of the cell types that we have classified. Here we have 7 types of lesions that we are going to classify for the work namely: Melanocytic Nevi, Melanoma, Benign Keratosis-like lesions, Basal cell carcinoma, Actinic Keratosis, Vascular lesions, and Dermatofibroma.

The *figure 3* shows us that Melanocytic nevi has the highest amount of cell count and hence the greatest number of images consist of it. This is hence also the most acquired lesion by inferring this data and from a general study. The next is melanoma which is the most serious condition of skin cancer that exists and is far less common. The rest of the diseases,

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although common, are not very serious conditions and hence have fewer samples in the dataset. Except for melanoma and basal cell carcinoma, the rest are non-cancerous types of lesions and aren't serious conditions.

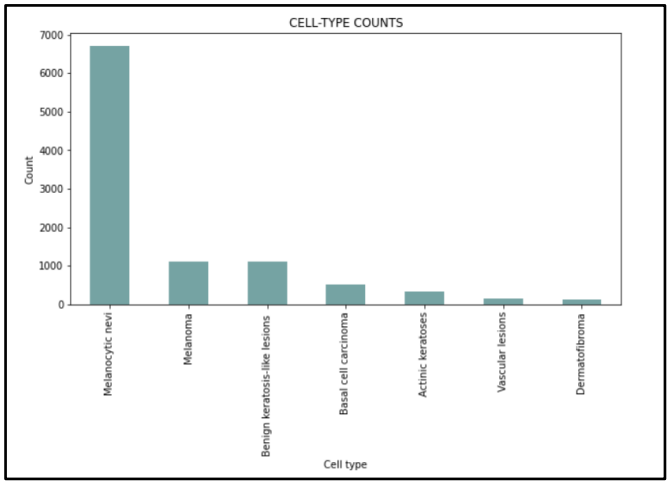

Figure 3: Cell/Image count of the different cell types

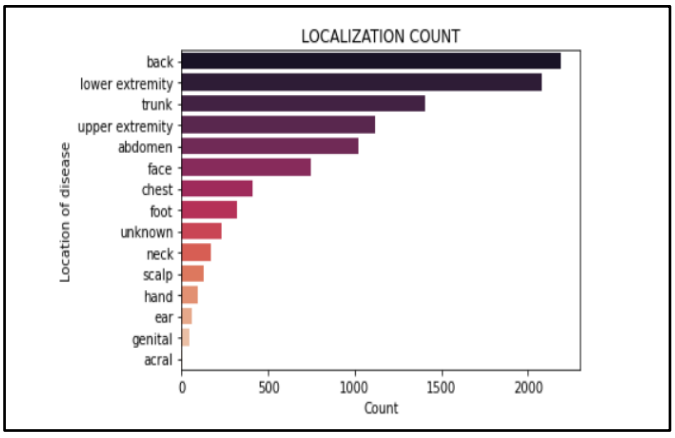

Figure 4: Localization of the cells in different parts of the body

The above *figure 4* shows us the areas that were affected the most by these diseases. Here we observe that the images taken originate mostly from the back, the lower extremity, and the trunk areas, indicating that the disease may have started there due to the areas not receiving much care from being less visible. The other common areas like the face, the foot and the chest are less affected than these due to them being visible locations and receiving more care. Now we come to the distribution of the images of disease among the various age groups. The following two *figures 5 and 6* show us the age of the people who have acquired the diseases and their distribution.

The scatterplot below shows us which disease is acquired among the various age groups from the list. Here each dot corresponds to a certain age and a cell type as mentioned in *figure 6*.

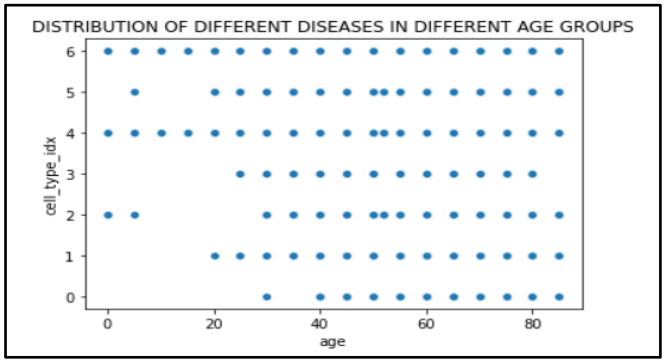

Figure 5: Overall Disease Distribution

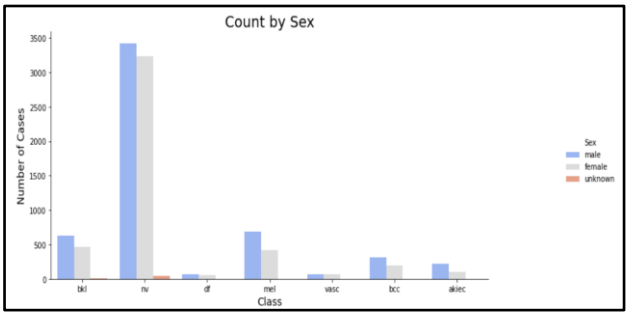

Figure 6: Individual Diseases among Gender

Now about the gender statistics for the dataset, we first see that the number of males in the images taken is slightly higher than that of females, with some data being unknown. The following graphs show us the distribution of the diseases acquired by males and females *(Figure 5 and 6)*. Here we see no major difference in the graphs and both genders are equally susceptible to all the diseases.

This analysis has helped identify the imbalance in the data and hence balance the data using oversampling with the help of the analysis done. After this an oversampling of the data was done which would help in obtaining a balanced dataset for better classification. The random oversampling produced the final dataset of 46934 images from the original dataset of 10015 images.

2.6 Data Preprocessing

The first thing we do before starting our main machine learning model is pre-processing the data. Here we make it so that the data becomes much simpler for the main model to read and use. This makes the learning process faster and produces desirable results for us.

The first step in the process of pre-processing is to make the data balanced. This is necessary so that the model can train equally for all types of classes. Hence to ensure that, oversampling is done which randomly selects data and duplicates them and adds them to the dataset. This new training set has a much larger number of images and becomes a dataset of 46937 images.

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2.9 Train-Test Data Splitting

```
X_train, X_test, Y_train, Y_test = train_test_split(X, y, test_size=0.20,random_state=100)
```

We then split the entire dataset into a train and a test dataset. We have split the one here into an 80:20 ratio of train: test. This allows us to check the data from the 20% left and the rest is randomized to train the classifier model so that it becomes capable of analyzing individual images on its own. We have then normalized the dataset accordingly and performed one-hot encoding to reshape and label the data accordingly which makes this dataset finally ready to be analyzed.

2.9.1 The Training Model

The model has a total of 9 layers which are a combination of 2D convolutional layers, MaxPooling and Dense. The CNN architecture used for the model is mentioned in *figure 7*.

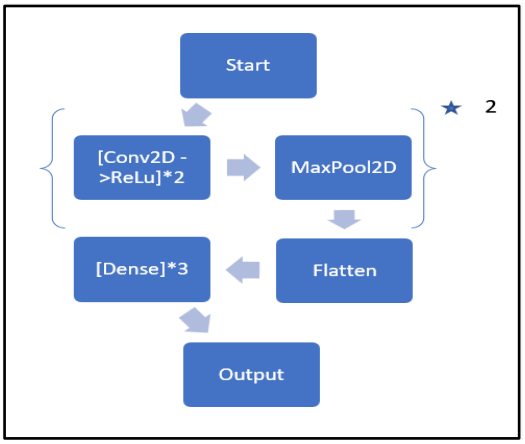

Figure 7: CNN Model Architecture

We utilized the Keras Sequential API, which allows you to start from the input and add one layer at a time. The convolutional (Conv2D) layer is the first. It's like a series of programmable filters. For the first two conv2D layers, we chose 32 filters, and for the latter two, 64 filters. Using the kernel filter, each filter transforms a portion of the image (specified by the kernel size). On the entire image, the kernel filter matrix is applied. Filters can be thought of as image transformations. From these modified images, the CNN can extract features that are useful elsewhere (feature maps) [20, 21].

The pooling (MaxPool2D) layer is the second most essential layer in CNN. Simply said, this layer is a down sampling filter. It compares the values of two adjacent pixels and chooses the one with the highest value. These are used to cut down on computing costs and, to a degree, overfitting. The pooling size (i.e., the area size pooled each time) must be chosen; the larger the pooling dimension, the more essential down sampling is. CNN can aggregate local features and learn more global properties of an image by combining convolutional and pooling layers. This also helps in reducing the computation complexity of the system by reducing the number of variables.

'Relu' stands for rectifier (maximum activation function) (0, x). The rectifier activation function is utilized to give the network non-linearity. It removes all the negative values from the pattern identification and segmentation phase to reduce unwanted variables and get a clear crisp output. To transform the final feature maps into a single 1D vector, utilize the Flatten layer. This flattening phase is required so that completely linked layers may be used following convolutional/max pool layers. It incorporates all the previously discovered local characteristics from the convolutional layers.

Finally, we used the features in three dense (completely connected) layers to create an artificial neural network (ANN) classifier. The net produces the probability distribution of each class in the last layer (Dense (10, activation = "SoftMax")). This uses the SoftMax activation function which is the best activation function for a CNN model, as it predicts a multinomial probability distribution. It normalizes the data the best for further computation for the ANN classification done by the Dense layer.

2.7 Optimizer

After the model building step, we use an optimizer to iteratively improve the parameters to reduce the loss. The Adam optimizer is used here because it combines the advantages of two other extensions of stochastic gradient descent. Specifically:

1. Adaptive Gradient Algorithm (AdaGrad) increases performance on problems with sparse gradients by maintaining a per-parameter learning rate (e.g., natural language and computer vision problems).
2. Root Mean Square Propagation (RMSProp) also preserves per-parameter learning rates that are adjusted based on the average of recent gradient magnitudes for the weights (e.g., how quickly it is changing). This indicates that the technique is effective for both online and non-stationary issues (e.g., noisy).

Adam understands the value of AdaGrad and RMSProp. Adam is a popular deep learning method since it produces good results quickly. Our model's performance is assessed using the metric function "accuracy." This metric function is like the loss function, with the exception that the metric evaluation results are not used for training the model (only for evaluation).

2.8 Model Training and Testing

In this final step the *x_train* and *y_train* have been fitted into the model. A batch size of 10 and 50 epochs were chosen for this fitting process. This ensures that we have sufficient epochs to train and no overfitting happens. The model is fitted in steps in 20 different epochs and each epoch helps in increasing the accuracy of the model. Here the learning rate changes sequentially after certain conditions have been made and changes are made accordingly.

Increasing the epochs would essentially increase the accuracy up to a certain point after which the accuracy would remain constant for the system and barely increase.

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3. RESULTS

Using HAM10000 dataset [13], exploratory data analysis has been done, then resizing of images has been performed to fit as a column in the data frame. Afterwards the dataset has been split into train and test sets and preprocessing is performed such as normalization and one hot encoding. After the preprocessing and splitting up the data into train and test sets, CNN model is built. The number of convolutional layers used is 2.

The model predicts the entered image to be that of a person suffering from Melanoma, Melanocytic Nevi, Basal Cell Carcinoma, Benign keratosis-like lesions, Actinic keratoses, Vascular lesions and Dermatofibroma. However, due to further classification of the model into cancerous and non-cancerous systems it will give the output among the three cancerous types in the end. The predictions sometimes vary as the initial stages of a few diseases look like others.

3.1 Training Model

Upon training the model we find that the accuracy of the model starts from 64% and rises all the way to 91.9% in just 5 epochs. The learning rate for our model starts at 0.001 and is set to fall to 0.00001 at minimum. This ensures that our model gets the best possible results in the least amount of time.

3.2 Model Evaluation

The model achieved an accuracy score of 97.89% and suffered a net loss of 15.5% during training.

3.2 Graphical Analysis and comparison (Model Accuracy and Model Loss)

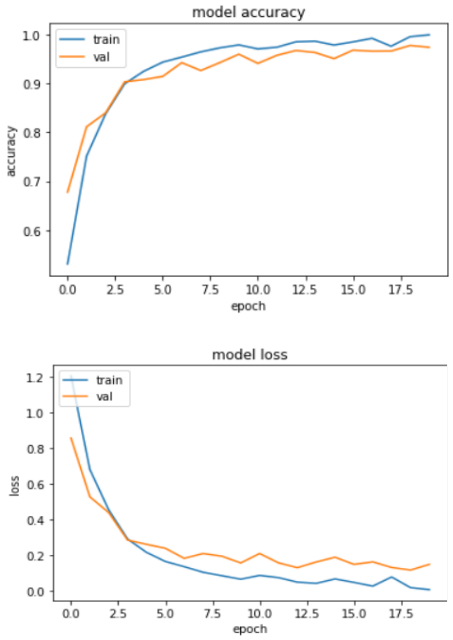

Figure 8: Model Accuracy and Loss Graph

The *Figure 8* shows us the graph of the accuracy rate and the loss rate of the system over time during training, in classifying the images respectively. Our model has hence achieved an accuracy of 97.89%. In the paper by Mohammed et.al, the average accuracy rates of all the given models for the survey amount to 89.17% [7]. Hence the model prepared could be said to be better than the average model for skin disease detection worldwide. For skin cancer related CNN models only is around 95.4% which could be said as the real benchmark to be obtained [7]. This model having 97.89% accuracy could be said as an above average model for skin cancer detection. The best models for skin cancer detection can up to 99% with higher computation models and better algorithms.

3.4 Model Usage

The above model is now loaded onto the streamlit library that is an open-source application framework specialized for machine learning setups and analysis. This forms the frontend of the system which will be deployed and can be accessed on multiple devices.

The interface is simple for the system, it has a total of 5 sections to browse into. The first section is a simple directions section where it is shown how to use the webpage. The second section is a live image capturing section where we can capture the image of the affected body part through an integrated camera to the system. The space bar would click the image for it, and then the diagnosis is listed below the affected image. The third section would be that of an image uploading system wherein an already present image can be uploaded into it and it would give the result of that image. A briefing of how the model has been made and an EDA for it is provided in the fourth section and the final section is just a credits section. The application is very simple to use and with the instructions on how to use it, basically anyone can operate it if they have an internet connection. This image is then analyzed by the model and the following result is obtained as shown in *figure 9*.

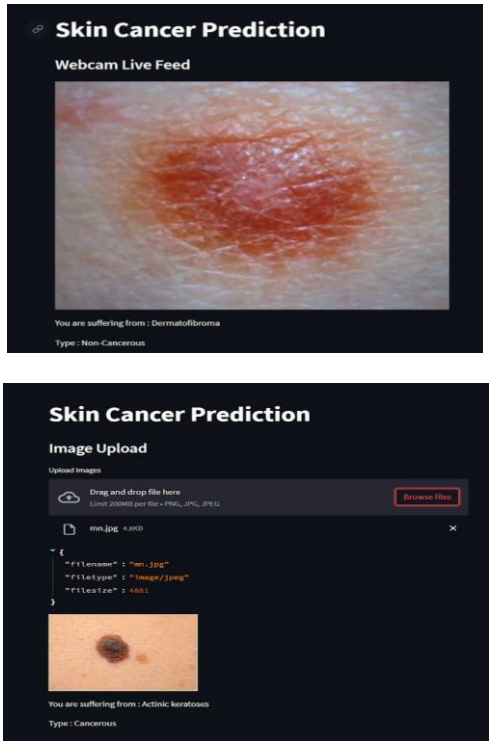

Figure 9: a) Webcam Live Feed b) Image Upload

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4. CONCLUSION

This research work demonstrates a method that uses techniques related to computer vision to distinguish different kinds of skin lesions for now. Deep learning algorithms have been used for learning algorithms for training and testing purposes. The accuracy attained is 97.89%. The feasibility of building a skin disease classification system has been investigated using CNN model. Better accuracy can be obtained by providing a training set with more variance and by increasing its size.

This model has then been used to insert more images and obtain results from its which proves its usability and purposes which have been stated above in the report. We can now use this model to obtain images from other people and use those images to diagnose the people and train the model even more. This will allow us to simulate the model and fulfil the main purpose for which this model was built.

5. FUTURE WORK

This final model can now be deployed on Heroku or Firebase etc. to gain access to the facilities provided by the model to get a proper diagnosis for themselves. The creation of an android application would also greatly benefit the cause and help in spreading awareness and better healthcare of this serious disease.

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CONFLICT OF INTEREST

Authors declare no conflict of interest.

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