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DEEP LEARNING ALGORITHMS IN DERMATOLOGY:EVALUATING THE ACCURACY AND RELIABILITY FOR SKIN CANCER DETECTION

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ABSTRACT
High Incidence of Dermatological Diseases for humans. In the medical industry detecting skin disease and recognizing its type is a very challenging task. Due to the complexity of human skin texture and the visual closeness effect of the diseases, sometimes it is really difficult to detect the exact type. Therefore, it is necessary to detect and recognize the skin disease at its very first observation. In today's era, artificial intelligence (AI) is rapidly growing in medical fields. The CNN model was used by applying transfer learning on the 7 skin diseases to create a skin disease classification system on DL system. The proponents gathered a total of 3,406 images and it is considered as imbalanced dataset because of the unequal number of images on its classes. Furthermore, a web application is designed for instant and proper action. It helps the patient and dermatologists identify the type of disease from the affected region's image at the initial stage of the skin disease. These findings suggest that the proposed system can help general practitioners efficiently and effectively diagnose skin conditions, thereby reducing further complications and morbidity.
Keywords— *Artificial Intelligence, Skin Cancer, Web application, Image processing.*

Introduction
JUPYTER, previously known as Python Notebook, is a web-based, interactive development environment. Originally developed for Python, it has since expanded to support over 40 other programming languages including Julia and R. JUPYTER allows for notebooks to be written that contain text, live code, images, and equations. These notebooks can be shared, and can even be hosted on GitHubfor free. Download a JUPYTER notebook that allows you to edit and experiment with the code. JUPYTER is part of the Anaconda distribution. Machine learning to perform regression, classification, and clustering on some freely available medical datasets concerning breast cancer and diabetes, and we will also take a look at a DNA microarray dataset. The scope of this Project, In KERAS, to build a simple neural network to classify the Wisconsin Skin cancer dataset that was described earlier. Often, deep learning algorithms and neural networks are used to classify images—convolutional neural networks are especially used for image related classification. However, they can of course be used for text or tabular-based data as well. In this we will build a standard feed-forward, densely connected neural network and classify a text-based cancer dataset in order to demonstrate the framework's usage. The only shortcoming faced during the implementation of the algorithm to predict the skin disease the unavailability of the larger dataset than used. If a larger dataset was available then the neural network would have been trained more accurately and the results would have been more precise than they presently are. When a much larger dataset is available then CNN could be applied and the epochs and hidden layers could be increased which would increase the accuracy and precision of the outcome provided by the neural network. Skin Disease a life-threatening cessation of activity in the skin. Early prediction of Skins Disease important, as it allows for the necessary measures to be taken to prevent or intervene during the onset. Artificial intelligence (AI) technologies and big data have been increasingly used to enhance the ability to predict and prepare for the patients at risk. This study aims to explore the use of AI technology in predicting skin disease as reported in the literature.

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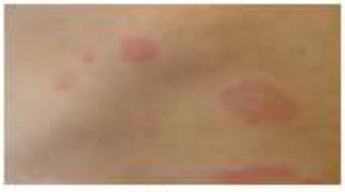
LITERATURE

In Connection of automated skin disease classification, ANNs to extract features and trained a linear classifier on them using 1300 images of Dermo fit Image Library to perform 10-ary classification. Similar approach was used by Ge et al. on Mole Map dataset to do 15-ary classification.[1] Esteva used a pre-trained Inception v3 on around 130,000 images. Although their results for two binary-classification tasks are merely "on par with all tested experts", yet this work was the first credible proof-of-concept based on a large dataset that DL can make a practical contribution in real-world diagnosis. Zilong et al. review the few techniques for skin cancer detection using images.[2] This study was not limited to melanoma detection, it provides an over about different types of cancers that use images for their diagnosis. Few studies for melanoma diagnosis were included in this paper.[3] In addition to this, a review presented by Sultana et a provides an overview of a few deep learning methods and discusses some benchmark datasets.[4] However, it did not give information about non published, internet collected and combine datasets. Another systematic literature on classifying a skin lesion using CNNs by Brinker. has been done, it provides a brief overview of the different methods of deep learning.[5] Sudden cardiac arrest can leave serious brain damage or lead to death, so it is very important to predict before a cardiac arrest occurs.[6] However, early warning score systems including the National Early Warning Score, are associated with low sensitivity and false positives.(FT) We applied shallow and deep learning to predict cardiac arrest to overcome these limitations.[7] We evaluated the performance of the Synthetic Minority Oversampling Technique Ratio. We evaluated the performance using a Decision Tree, a Random Forest, Logistic Regression, Long Short-Term Memory model, Gated Recurrent Unit model, and LSTM–GRU hybrid models.[8] Our proposed Logistic Regression demonstrated a higher positive predictive value and sensitivity than traditional early warning systems.[9]. Despite advances in healthcare, the incidence of in-hospital cardiac arrest (IHCA) has continued to rise for the past decade. Identifying those patients at risk has proven challenging. Our objective was to conduct a systematic review of the literature to compare the IHCA predictive performance of machine learning (ML) models with the Modified Early Warning Score (MEWS).[10] Design: The systematic review was conducted following the Preferred Reporting Items of Systematic Review and Meta-Analysis guidelines and registered on Method: Data extraction was completed using the Critical Appraisal and Data Extraction for Systematic Reviews of Prediction Modelling Studies checklist.

2.1 Skin Dermatological Disease

Skin lesions are abnormalities in the surface of the skin. They are good markers of life quality and even are symptoms of deadly diseases. Since professional medical help can be inaccessible for some people due to shortage of professional dermatologists or high cost of professional help, development of tools for automated diagnostics of dermatological diseases could be beneficial for the humanity and could provide low-cost medical help around the world. Visual information is the primary source for dermatological disease- diagnostics, therefore it is possible to create automated dermatological disease diagnostics tools by analyzing skin images using methods of computer vision and machine learning.



[a] .

[b]

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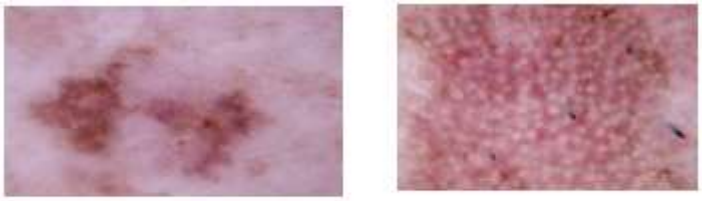
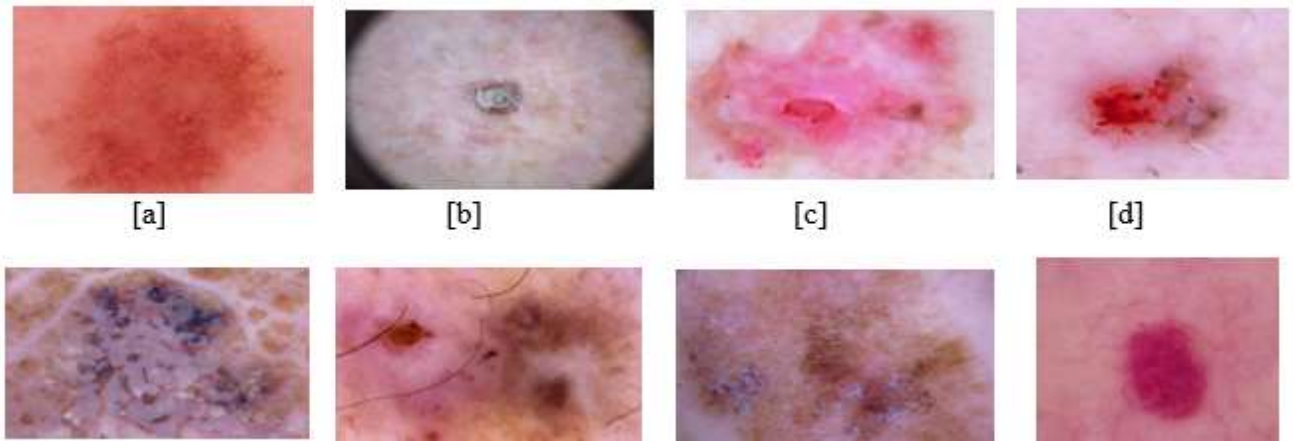


[c] [d]

Fig.1 Stages of Skin Transformation from Non-Skin Disease to Skin Cancer Symptoms.

2.2 Skin and Describing Lesions

A promising approach to skin disease diagnosis is through identification of morphological elements in the affected skin which later are used in diagnostics. The crucial advantage of using morphological elements is their number, because there are only some of them in comparison with the number of diseases causing them. The more classes should be distinguished, the more labeled data is required to apply modern machine learning methods. However, availability of labeled medical data is widely acknowledged bottleneck. Morphological elements are divided into primary and secondary ones. Primary morphology refers to the appearance characteristics of a skin lesion while secondary morphology refers to the temporal changes in the skin lesion. Therefore, primary morphology is more indicative of a skin lesion structure and appearance and identifying primary morphological elements is a priority. Skin cancer is the most common form of cancer in the United States. In fact, In Fig 2 it is estimated by the American Cancer Society in Nevada more than 200,000 cases of skin cancer will be diagnosed this year.



[a] [b] [c] [d]

[e] [f] [g] [h]

Fig 2. Skin Cancer Disease Datasets [a] Actinic-keratosis [b] Basal Cell Carcinoma, [c], [d] benign Keratosis [e] Dermatofibrosarcoma [f] Melanoma [g] Melanocytic-nevi [h] Vascular Lesions

2.3 Skin Morphology Classification

Although skin morphology is widely discussed in dermatology studies, different specialists tend to choose slightly different classification for their research. Most of existing classifications include following types with consistent definitions: macule, patch, papule, nodule, plaque, wheal, vesicle, bulla, and pustule.

1.Bulla is a fluid-filled circumscribed elevation of skin that is over 0.5 cm in diameter;
2.Macule is a small flat area with colour or texture differing from surrounding skin;
3.Nodule is a solid mass in the skin that is palpated or elevated and is, in diameter of both width and depth, greater than 0.5 cm;
4.Papule is a solid elevation of skin that is less than 0.5 cm in diameter;
5.Patch is a large flat area with colour or texture differing from surrounding skin;
6.Plaque is an elevated area of skin without substantial depth but is greater than 2 cm in diameter;
7.Pustule is an evident accumulation of pus in skin;

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8.Vesicle is a fluid-filled circumscribed elevation of skin that is less than 0.5 cm in diameter;
9.Wheal is a white elevated compressible and faded area often surrounded by a red flare.

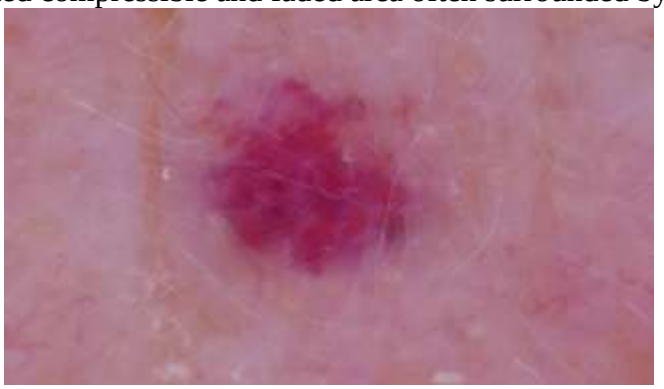

Fig.3 Basal Ceil Carcinoma Disease

III . PROPOSED WORKFLOW

The proposed convolutional architecture contains the input layer followed by a convolutional layer with 16 kernels along with activation function as RELU, in the subsequent layer 25% of the nodes is dropped by dropout layer. Again, the convolutional layer was performed with eight kernels with previous parameters, also applied the dropout layer with 25%. For prediction probability calculations, added an output layer. The cleaned data is split into 80% training and 20% testing for training and testing purposes. The same dataset is tested with different deep learning classifiers such as VGG16 & CNN

Image Acquisition:

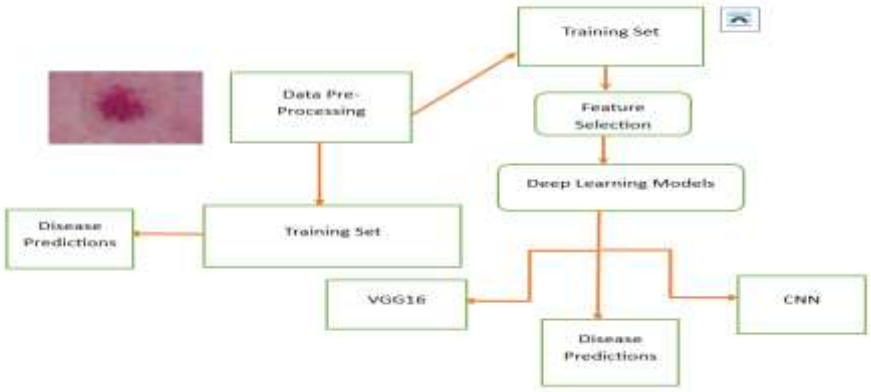

Fig.5 Proposed Methodology

Skin lesions are abnormalities in the surface of the skin. They are good markers of life quality and even are symptoms of deadly diseases. Since professional medical help can be inaccessible for some people due to shortage of professional dermatologists or high cost of professional help, development of tools for automated diagnostics of dermatological diseases could be beneficial for the humanity and could provide low-cost medical help around the world. Visual information is the primary source for dermatological disease diagnostics, therefore it is possible to create automated dermatological disease diagnostics tools by analyzing skin images using methods of computer vision and machine learning.

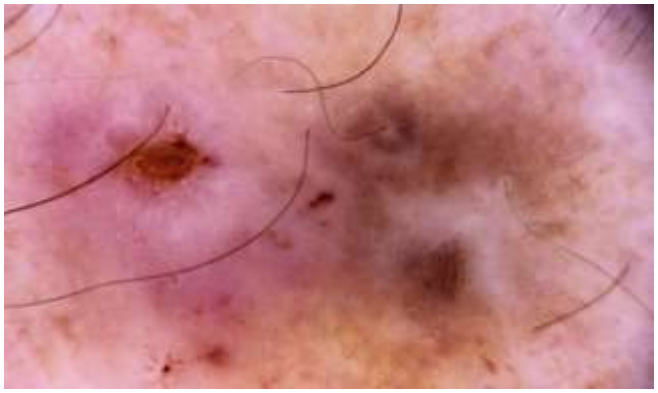

Fig.4 Image Aspect

3.1 Image Aspect

Morphological elements are divided into primary and secondary ones. Primary morphology refers to the appearance characteristics of a skin lesion while secondary morphology refers to the temporal changes in the skin lesion. Therefore, primary morphology is more indicative of a skin lesion structure and appearance and identifying primary morphological elements is a priority Dataset Resizing.

3.2 Data Collection

This dataset consists of 10015 Dermatoscope images categorized into 7 different classes. A complete dataset is employed to train the system model. A dataset is split into training set and validating/testing set. Validation/testing set will tune the parameters and is used only to assess the effectiveness and efficiency of the system.

3.3 Labels

Labels are the last yield. The yield classes is likely to be the 1names. When information researchers discuss marked information, they mean the gatherings of tests that have been labelled to at least one name.

3.4 Over-fitting

A significant thought in Deep Learning is that the estimation of the objective capacity that has been prepared utilizing preparing information, sums up to new information. Speculation works best if the sign or the example that is utilized as the preparation information has a high sign to commotion proportion.

3.4 Data Preprocessing

The methodology proposed in this research paper starts with data preprocessing. Data preprocessing step includes (i) a data driven method to select patient records and selecting important variables for analysis and (ii) The collected data from patient records are not clean and may include noise, incorrect, missing values, or inconsistent data. So, we have to apply different method of data cleaning to clean such anomalies. (iii) The data are not ready for mining even after cleaning, because they are in different formats, which directly can't be used, so data must be transform into formats suitable for mining. The transformation applied to achieve this is normalization; smoothing, aggregation, etc. are used.

3.5 Data Splitting

For each experiment, we split the entire dataset into 70% training set and 30% test set. We used the training set for resampling, hyper parameter tuning, and training the model and we used test set to test the performance of the trained model. While splitting the data, we specified a random seed (any random number), which ensured the same data split every time the program executed.

3.6 Splitting of Data

After cleaning the data, data is normalized in training and testing the model. When data is spitted then we train algorithm on the training data set and keep test data set aside. This training process will produce the training model based on logic and algorithms and values of the feature in training data. Basically, aim of feature extraction is to bring all the values under same scale.A dataset used for machine learning should be partitioned into three subsets — training, test, and validation sets.

A. Training set:

A data scientist uses a training set to train a model and define its optimal parameters it has to learn from data.

. B. Test set:

A test set is needed for an evaluation of the trained model and its capability for generalization. The latter means a model's ability to identify patterns in new unseen data after having been trained over a training data. It's crucial to use different subsets for training and testing to avoid model over fitting.

3.7 Neural Network

It consists of multiple neuron-like structures. The input image is feed to multiple neurons. The output we get is a single classified one. Various computations are taken place in the intermediate neurons The layers with intermediate neurons are known as Hidden Layers The weights are added for the proper output. In the neural network, the final output is known, so if the calculated output is wrong a back propagation is made and the approximate weights are updated. The activation function is used to speed up the process. In this, we use three convolutional neural network models. Convolutional neural networks are a subclass of neural networks. They, are great at capturing local information and predicting based on trained data. We use three models namely Inceptionv3, Mobile Net, Res net.

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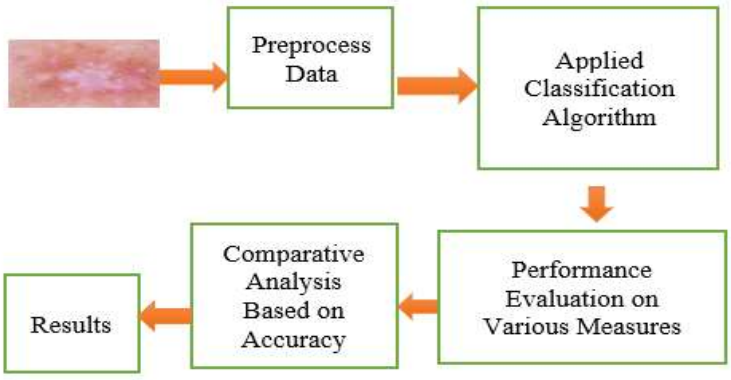

Fig 5. Block Diagram of Data Pre-Processing

VGG16 Model

Transfer learning generally refers to a process where a model trained on one problem is used in some way on a second related problem. In deep learning, transfer learning is a technique whereby a neural network model is first trained on a problem similar to the problem that is being solved. One or more layers from the trained model are then used in a new model trained on the problem of interest. the benefit of decreasing the training time for a neural network model and can result in lower generalization error. The weights in re-used layers may be used as the starting point for the training process and adapted in response to the new problem. This usage treats transfer learning as a type of weight initialization scheme. This may be useful when the first related problem has a lot more labeled

data than the problem of interest and the similarity in the structure of the problem may be useful in both contexts.

4.1 Basic model

The model's architecture features a stack of convolutional layers followed by max-pooling layers, with progressively increasing depth. This design enables the model to learn intricate hierarchical representations of visual features, leading to robust and accurate predictions. Despite its simplicity compared to more recent architectures, VGG-16 remains a popular choice for many deep learning applications due to its versatility and excellent performance.

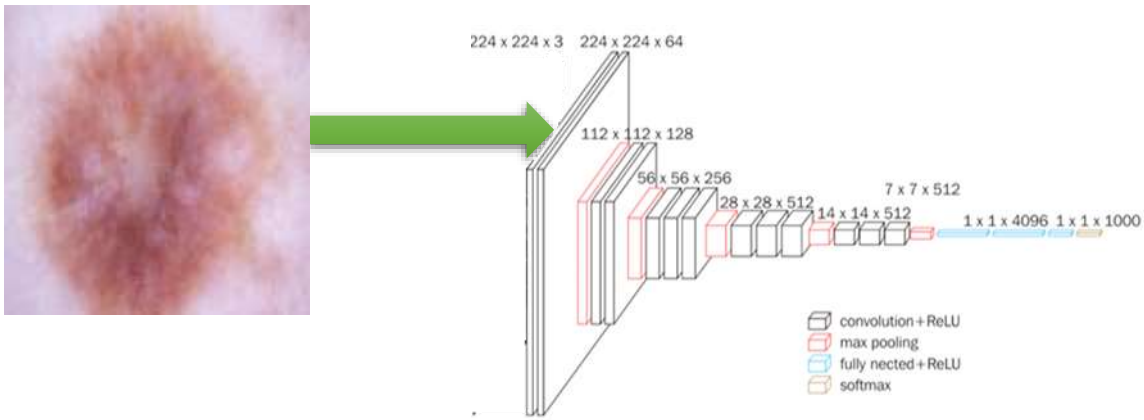

Fig 6. VGG16 Model

4.2 VGG16 EXPRESSION

VGG16 consists of 16 layers with a very deep convolutional network architecture:

Accuracy = (TP+TN) + (P+N)

where * represents convolution, $TP\ and\ TN$ are the True Positive and True Negative biases.

All predicted true positive and true negative divided by all positive and negative. True Positive (TP), True Negative (TN), False Negative (FN) and False Positive (FP) predicted by all algorithms are presented in table.

True positive (TP) indicates that the positive class is predicted as a positive class, and the number of sample positive classes was actually predicted by the model.

False negative indicates (FN) that the positive class is predicted as a negative class, and the number of negative classes in the sample was actually predicted by the model.

False positive (FP) indicates that the negative class is predicted as a positive class, and the number of positive classes of samples was actually predicted by the model.

True negative (TN) indicates that the negative class is predicted as a negative class, and the number of sample negative classes was actually predicted by the model layers.

Table 1 Melanoma Skin Cancer Detection

	Feature Type	Classification Accuracy %	
Melanoma Skin Cancer (Benign & Malignant)	Colour Features	100	50
	Shape Features	100	48
	Texture Features	100	46

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Table 2 Proposed modified VGG-19 model hyperparameters

Hyper Parameters	**Value**	
	VGG16	**Res-Net 50**
Learning Rate	le-3	le-3
Number of Epoch	25	180
Batch Size	8	8
Image Size	224*224*3	224*224*64
Weight	Image Net	Image Net
Metrics	Accuracy	Accuracy
Loss	Categorical Cross	Categorical Cross

The implementation of the algorithm to predict the skin disease the unavailability of the larger dataset than used. If a larger dataset was available then. The neural network would have been trained more accurately and the results would have been more precise than they presently are. When a much larger dataset is available then CNN could be applied and the epochs and hidden layers could be increased which would increase the accuracy and precision of the outcome provided by the neural network.
The equation for this model is:
$Y=\beta0+\beta1X1+\beta2X2+\cdots+\beta n\ X\ n$
where Y is the dependent variable, X1, X2⋯,Xn are the independent variables, and β0,β1,⋯,βn are the coefficients.

IMAGE USING DERMOSCOPY	**SVM Linear Kernel Classifier**	**Bayes Net Classifier**
Sensitivity (%)	90.33	80
Specificity (%)	90.9	84
Accuracy (%)	86.83	80

Table 3 Proposed modified VGG-19 model

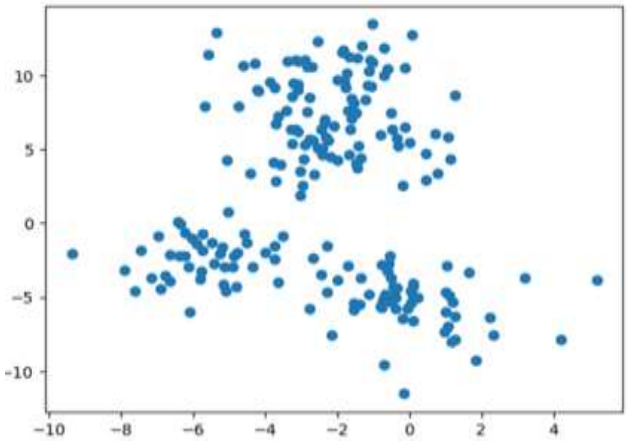

Fig.7 Datasets – Performance metrics

V. Software WEB Application Development

The Anaconda website provides the necessary links to download the software for free in either Windows, Mac, or Linux. It also has starter videos, documentation, training, and support. To download

and install Anaconda, The 32-Bit or 64-Bit Graphical Installer It is important to notice that Python 3 is the latest version and is being constantly updated and supported. The previous version, Python 2 is still offered, but is no longer being maintained. Once the installation is completed, you can search for the Anaconda Navigator on your device and open it.

5.1 Anaconda Navigator and IDEs

The Anaconda Navigator, is a GUI, like the "menu" page of Anaconda, where you can easily access and launch different
IDEs without needing to type commands in a terminal window. There are many different IDEs specially designed for Python programming and the following ones are automatically installed with Anaconda. To access an IDE, click on its icon in the Navigator Home tab.

5.2 JUPYTER Notebook and JUPYTER LAB

JUPYTER Notebook is a web-based IDE that uses your default web browser. Each block of code can be run separately, making it highly Flexible and easy to experiment with This allows for different types of texts to be used in the same Notebook. Thus, code outputs, visualizations, equations, and normal text can be used all in one place. This makes it effective to create and share documents and to present your code and results in an organised and aesthetically pleasing way. Since it is web-based, it also make sit easy to share Notebooks with others and is optimal for collaborations. JUPYTER-Lab is an extension of the JUPYTER Notebook with many more features. In JUPYTER-Lab, JUPYTER Notebooks are integrated with other applications, like a command-line Terminal, a code **Console** and **Text Editor**.

VI. RESULTS AND DISCUSSION

The cleaned data is split into 80% training and 20% testing for training and testing purposes. The same dataset is tested with different deep learning classifiers such as VGG16 & CNN. In this paper, we proposed a CNN to predict the accuracy of whether a patient had a cardio arrest or not. 89.91 training accuracy and 86.83% testing accuracy

Fig.8 Skin Web-App Home Page

Fig 9 Login Page For Patient's Details

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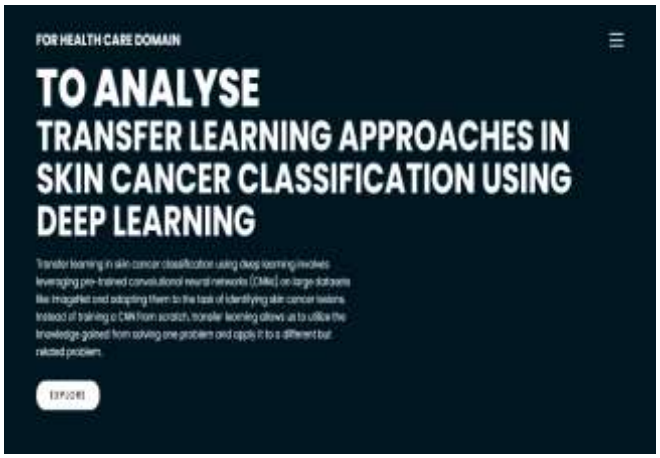

Fig 10 Landing Page of Skin Cancer Classification

Fig 11 Patient Skin Upload and Stored in Database as Label

Fig 12 Patient Information Form with Report Prediction

VII. CONCLUSION AND FUTURE ENHANCEMENTS

In this analysis, the majority of findings focused on deep learning for the binary identification of Skin Disease. The intended framework originally classified the skin lesion as either benign or malignant after performing two operations on it. Skin lesions are abnormalities in the surface of the skin. They are good markers of life quality and even are symptoms of deadly diseases. Since professional medical help can be inaccessible for some people due to shortage of professional dermatologists or high cost of professional help, development of tools for automated diagnostics of dermatological diseases could be beneficial for the humanity and could provide low-cost medical help around the world.

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