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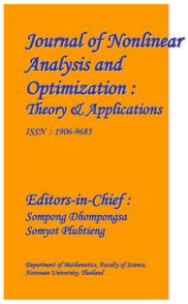

PREDICTION OF SKIN CANCER UTILISING DEEP LEARNING TECHNIQUES

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ABSTRACT
Cancer is a fatal illness caused by uncontrolled cell growth, yet modern science has come a long way in healing it. Thus, cancer's rapid proliferation may invade and demolish adjacent buildings and even travel to distant locations, causing death to those residing there. Furthermore, cancer does not care about a person's gender; it has the potential to affect every single cell in the body at any point in time. One of the many ways in which skin cancer has recently emerged is via the uncontrolled damage to DNA caused by mutations in skin cells. Melanoma, basal cell, and squamous cell skin cancers are the three most common forms of this disease. Also proposed here are innovative segmentation and feature extraction methods for effective pre-processing. Modern technology has also been instrumental in the effective implementation of image conversion, contour detection, and wavelet transform. When processing images utilising data gathered from sensors aboard satellites, it is typical for pre-processing errors to originate in pure mathematics or overestimated pixel sizes.
Key words: Skin cancer, basal cell, DNA.

1. INTRODUCTION
Cancer has lately become a fatal illness in India due to the rapid growth in the number of people afflicted, which is over 2.5 million. One estimate puts the number of new cancer cases diagnosed in India each year at around 0.7 million. On the other side, about 0.3 million Indians lose their lives to cancer every year. The most popular cancer websites, based to data collected by the National Cancer Registry Programme (NCRP), are those for males pertaining to the mouth, lungs, oesophagus, and stomach, and for females pertaining to the cervical, breast, and oral cancers. Among Indian cancer patients, over 50% die from oral and pulmonary cancers, whereas over 50% of female cancer patients die from cervical and breast malignancies.

1.1 SKIN CANCER
Uncontrolled proliferation of aberrant skin cells is the hallmark of skin cancer. Cancerous tumours form when DNA damage to skin cells is not repaired, leading to mutations that trigger mistakes in genes that slow down the growth of the skin cells. In addition, basal cell, squamous cell, and melanomas are the three main subtypes of skin cancer. The two most common types of skin cancer are melanoma and non-melanoma. In this case, melanoma, a cancerous tumour that may metastasise to other organs, produces melanocytes, the cells responsible for skin pigment. It may also spread to other organs and kill the host when given enough time. The opposite is true for non-melanoma tumours, which do not metastasise.
The most deadly form of skin cancer in humans, malignant melanoma, was the culprit in the increased mortality rate. Melanoma rates have been reasonably rising lately, particularly among Caucasian people. According to recent studies, melanoma is now the sixth most important disease for women in Australia and the fifth most important cancer for men in North America [1,2]. The nation with the most people also has an impact via its reports. Melanoma also ranks seventh among female cancers and sixth among male cancers overall [3,4]. However, this kind of skin cancer is curable if detected in its

early stages [5,6]. By taking this course of action, early detection of melanoma skin cancer allows for a straightforward excision, reducing mortality.

2. LITERATURE REVIEW

Because dermoscopy may identify melanoma at an early stage, dermatologists employ it as a diagnostic tool. Furthermore, it is able to depict a plethora of pigmented structures that the human eye is unable to see, including dots, pigment networks, streaks, and blue with white patches [7,8]. Thus, based on those two characteristics alone, the lesion picture you gave cannot be a melanoma. Consequently, dermoscopy pictures are used to categorise lesions with more certainty.

In order to diagnose melanoma in its early stages, dermatologists employ the ABCD rule, which involves assessing four standard parameters: diameter, asymmetry, colours, and border [7]. This method is used in cancer diagnostic systems for melanoma identification.

Also, in order to examine the parameters, [8] employs a novel 7-point checklist approach. Melanoma pictures with reflections and hair make visual identification a challenging job for specialists involved in skin cancer detection; moreover, melanoma boundaries are undetectable. Melanoma image interpretation is both subjective and efficient, even for seasoned physicians [9].

For these reasons, as well as to aid clinicians in establishing the correct diagnosis from the images, computer-aided diagnosis (CAD) has become an essential tool in the identification of melanoma. In addition to enhancing detection accuracy, these sorts of diagnostic tools also help to decrease the time it takes to diagnose the condition [10].

3. METHODOLOGY

3.1 Image database

The selected melanoma skin lesion images that are available in the skin cancer image database.

3.2 User interface module

The different kinds of skin cancer images such as melanoma skin lesion and other type of skin cancer images have been collected by this module from the skin cancer image database that has the reasonable volume of pixels in the input melanoma skin cancer images. Moreover, all these skin cancer images have been forwarded into the next component called image data pre-processor that is used to pre-process the input skin melanoma images for performing the classification.

3.3 Data pre-processor

Image conversion, contour detection, wavelet transform, ABCD parameters, segmentation, and feature extraction are the six subcomponents used in this data pre-process.

Here, the proposed model uses separate new and existing methods for performing image conversion, contour detection, wavelet transformation, for framing ABCD rules, segmenting the input melanoma images and extract the necessary features from input image. This data pre-processor is sent to the next module called classification module to perform image classification process.

Image Conversion: Many file formats are used to store the medical images along with various conversion problems due to the presence of different image formats. The Image conversion techniques are necessary to perform for fast image conversion. Here, the input images can be converted from any format to the standard formats such as JPG, PNG and BMP formats. It can be rotated the input images in 90 degree increments and also rotates automatically for compensating with the orientation of EXIF. Moreover, it also can be resized or enlarged the input medical images by a number of images or to a fixed size which is retaining the original ratio optionally. The file type of input skin images are also added as a command in the context menu which is available in the menu bar.

Contour Detection: Contour detection is playing major role in image processing. In this scenario, split the input images by using classification and the segmentation techniques into many parts which is related to the detection of the connected contours that are also separating these various parts. Here, image input detection is an easy when detects the local image edges by using the various image analysis techniques. On the other hand, the image edge detection of continuous contours that is very difficult task and also need in detailed analysis about the input images.

Wavelet Transform: This sub component is responsible for performing wavelet transform by applying the standard techniques that are available in the literature. Generally, it is an important task in image compression application. It is more suitable method when it is compared to the Fourier

transform. Moreover, the Fourier transform is not to calculate the spectral data value practically. Because of, it needs the necessary information about the previous and future of the signal over the entire time. In addition, it is not able to observe the frequency values which are dynamic with time because the resulting function after performing the Fourier transform in different independent time. Moreover, the wavelet transforms are working based on the wavelets with different frequency in certain time duration.

Image Segmentation: The suggested prediction model's data pre-processor uses this sub-component to carry out the picture segmentation task. Partitioning an original skin image into several segments, such as sets of pixels and as super-pixels, is achieved through the image segmentation method. A less complicated and more easily analysed representation of an input skin image is the primary goal of this segmentation procedure. Additionally, it is utilised to insert the numerous picture objects and their respective borders (e.g., lines, curves, etc.) into the input photos. Lastly, it covers the whole input skin image and assigns new labels to every pixel.

Feature Extraction: This sub component is responsible to extract the necessary features which can contribute more in the image classification process in terms of decision making in the proposed prediction model. Here, it starts with a set of measured data and also built the derived features that must be useful, informative and non-redundant. Generally, it performs a dimensionality reduction in this data pre-processor.

3.4 Clustering module

This module is responsible for grouping the segmented images which are having more relevant pixels and super pixels. The clustering module is applied an existing fuzzy c-means clustering method that is used to group the pre-processed skin melanoma images effectively.

3.5 Classification module

The classification module is consists of four additional components namely SVM Classifier, EMSVM Classifier, ANN-BPN Classifier and FTCM Classifier. These four sub components are also used different classification algorithms such as SVM Classification algorithm, Enhanced Multiclass SVM classification algorithm.

Artificial Neural Network based Back Propagation Network and Fuzzy Temporal Cognitive Map classification algorithms for classifying the melanoma images.

ANN-BPN Classifier: This sub component is used to classify the skin melanoma images effectively by using the existing neural network classifier called ANN-BPN classification algorithm. The three layers of the neural network here are the input, output, and hidden layers. A single process layer, the hidden layer, connects the input and output layers. This hidden layer compresses data by making use of a smaller number of neurons than are present in the input and output layers combined. In addition, the training activities over the neural network are used to accomplish the image compression operation. To build a hierarchical neural network with two additional process layers, the back-propagation neural network is further extended.

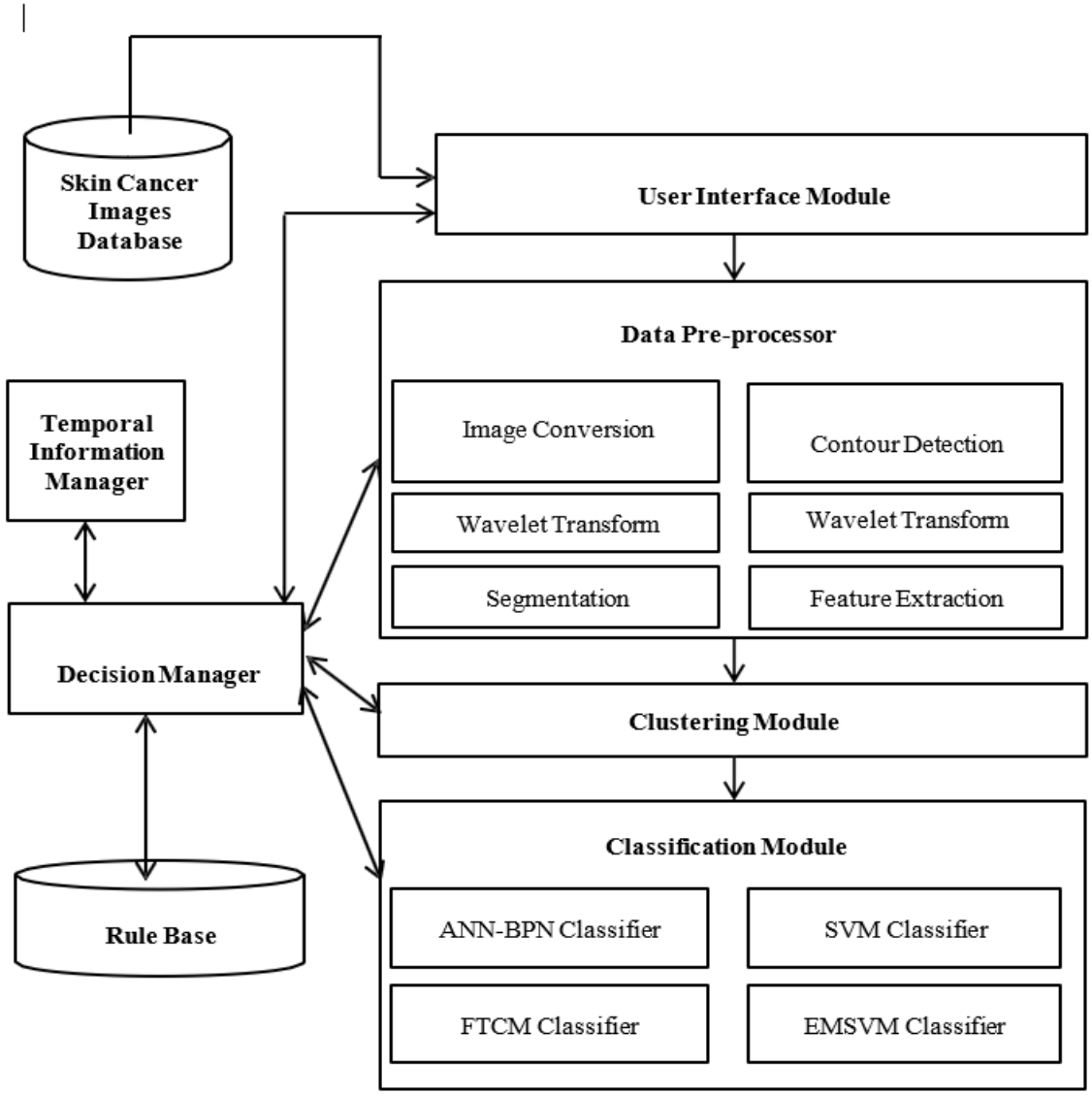

Figure 3.1 System Architecture

4. RESULTS AND ANALYSIS:

In the performance analysis, skin cancer datasets is consider as it predicts the malignant and benign cancer.

```
Downloading skin-cancer-malignant-vs-benign, 340467838 bytes compressed
[==================================================] 340467838 bytes downloaded
Downloaded and uncompressed: skin-cancer-malignant-vs-benign
Data source import complete.
```

Figure.

To perform the prediction and classification of skin cancer, the following packages are imported as mentioned as urlopen, unquote, urlparse, HTTPError, etc.

```
import os
import sys
from tempfile import NamedTemporaryFile
from urllib.request import urlopen
from urllib.parse import unquote, urlparse
from urllib.error import HTTPError
from zipfile import ZipFile
import tarfile
import shutil

CHUNK_SIZE = 40960
```

The basic library files of pandas and numpy are imported and it uses matplotlib to visualize the images and graphs. Seaborn of SNS and gloab are used to retrieve the images of skin cancer along with random function of seed library.

```
# importing basic libraries

import pandas as pd
import numpy as np
import os

import matplotlib.pyplot as plt
import seaborn as sns

from glob import glob ## glob is used to retrieve files

# set seed
np.random.seed(21)
```

```
# Loading train images
img_benign_train = [read(os.path.join(directory_benign_train, filename)) for filename in os.listdir(directory_benign_train)]
img_malignant_train = [read(os.path.join(directory_malignant_train, filename)) for filename in os.listdir(directory_malignant_train)]

# Loading test images
img_benign_test = [read(os.path.join(directory_benign_test, filename)) for filename in os.listdir(directory_benign_test)]
img_malignant_test = [read(os.path.join(directory_malignant_test, filename)) for filename in os.listdir(directory_malignant_test)]

#img_benign_train
type(img_benign_train)
```

- A numpy array uses considerably less memory than a list.
- A variety of mathematical procedures that this list cannot handle are supported by Numpy arrays. While element-wise operations are feasible in np arrays, they are not feasible in lists. (Np arrays contain only homogeneous elements, whereas lists can contain heterogeneous elements). Because of their homogeneity, calculations are substantially more convenient.
- They are capable of executing operations considerably quicker than lists.

Then data labels classify the skin cancer as benign ‘0’ and malignant ‘1’.

```
y_benign_train = np.zeros(X_benign_train.shape[0])
y_malignant_train = np.ones(X_malignant_train.shape[0])

y_benign_test = np.zeros(X_benign_test.shape[0])
y_malignant_test = np.ones(X_malignant_test.shape[0])

y_malignant_train
```

array([1., 1., 1., ..., 1., 1., 1.])

```
Shape of X_train:  (2637, 224, 224, 3)
Shape of y_train:  (2637,)
Shape of X_test:  (660, 224, 224, 3)
Shape of y_test:  (660,)
array([0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0.,
       0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0.,
       0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0.,
       0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0.,
       0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0.,
       0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0.,
       0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0.,
       0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0.,
       0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0.,
       0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0.,
       0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0.,
       0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0.,
       0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0.,
       0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0.,
       0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0.,
       0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0.,
       0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0.,
       0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0.,
       0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0.,
       0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0.,
       0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0.,
       0., 0., 0., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1.,
       1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1.,
       1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1.,
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       1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1.,
       1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1.,
       1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1.])
```

Data shuffles are crucial because we want our samples to be independent of one another and not to be impacted by samples that came before or after. Since the dataset's creator and sorting order are unresolved it's best to shift the training and test sets to get biased-free independent points. Shuffling while producing epochs also ensures that the risk of creating batches that are not representative of the whole dataset is reduced.

Based on the training datasets, the following images are displayed in figure 4.1.

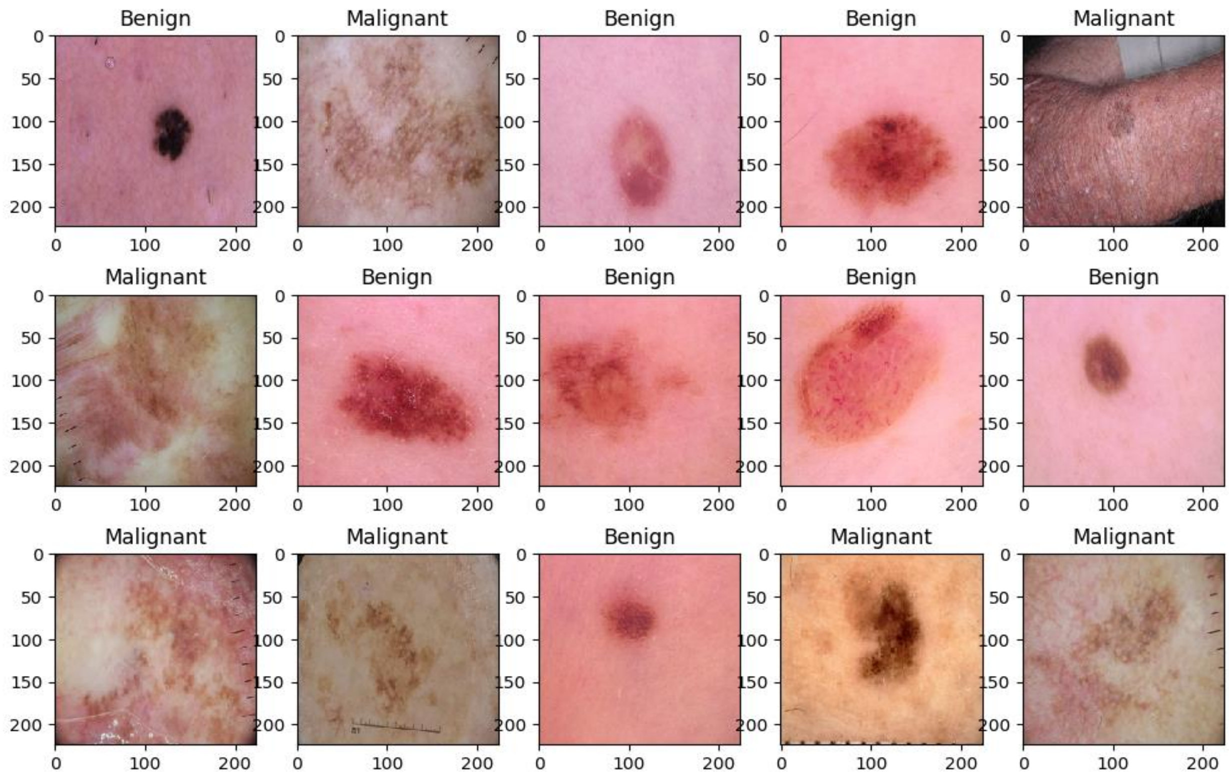

Figure. 4.1 Training datasets.

- Convolutional Layer: Image transformation is achieved through the employment of filters and feature maps. We refer it this as the Convolutional Layer. One application of the Pooling Layer's Max Pooling is down sampling. Both processing expenses and overfitting are somewhat decreased by it.
- Dropout: During training, a regularization technique that sets some nodes' weights to 0 at random drops some nodes. This compels the network to acquire features through dispersed means. Enhances generalization and avoids over fitting.
- The flatten layer is employed to transform feature maps into one-dimensional vectors, enabling their utilisation in prediction tasks. Simple ANNs with non-linear Relu activation functions are referred described as "dense layers with Relu."
- Dense layer with Softmax: An ANN layer with the binary activation function Softmax for final classification.

```
Model: "sequential"
_________________________________________________________________
 Layer (type)                Output Shape              Param #
=================================================================
 conv2d (Conv2D)             (None, 224, 224, 64)      1792

 max_pooling2d (MaxPooling2  (None, 112, 112, 64)      0
 D)

 dropout (Dropout)           (None, 112, 112, 64)      0

 conv2d_1 (Conv2D)           (None, 112, 112, 64)      36928

 max_pooling2d_1 (MaxPoolin  (None, 56, 56, 64)        0
 g2D)

 dropout_1 (Dropout)         (None, 56, 56, 64)        0

 flatten (Flatten)           (None, 200704)            0

 dense (Dense)               (None, 128)               25690240

 dense_1 (Dense)             (None, 128)               16512

 dense_2 (Dense)             (None, 2)                 258

=================================================================
Total params: 25745730 (98.21 MB)
Trainable params: 25745730 (98.21 MB)
Non-trainable params: 0 (0.00 Byte)
_________________________________________________________________
```

Rate of learning An annealer is used to reduce the learning rate by a specific percentage after a certain number of training iterations/epochs.

```
0.5264                                                                  33/33
[==============================] - ETA: 0s - loss: 1.9614 - accuracy:
0.5270                                                                  33/33
[==============================] - 23s 503ms/step - loss: 1.9372 - accuracy: 0.5276 - val_loss: 0.6671 -
val_accuracy: 0.5455
dict_keys(['loss', 'accuracy', 'val_loss', 'val_accuracy', 'lr'])
0.8136363636363636
```

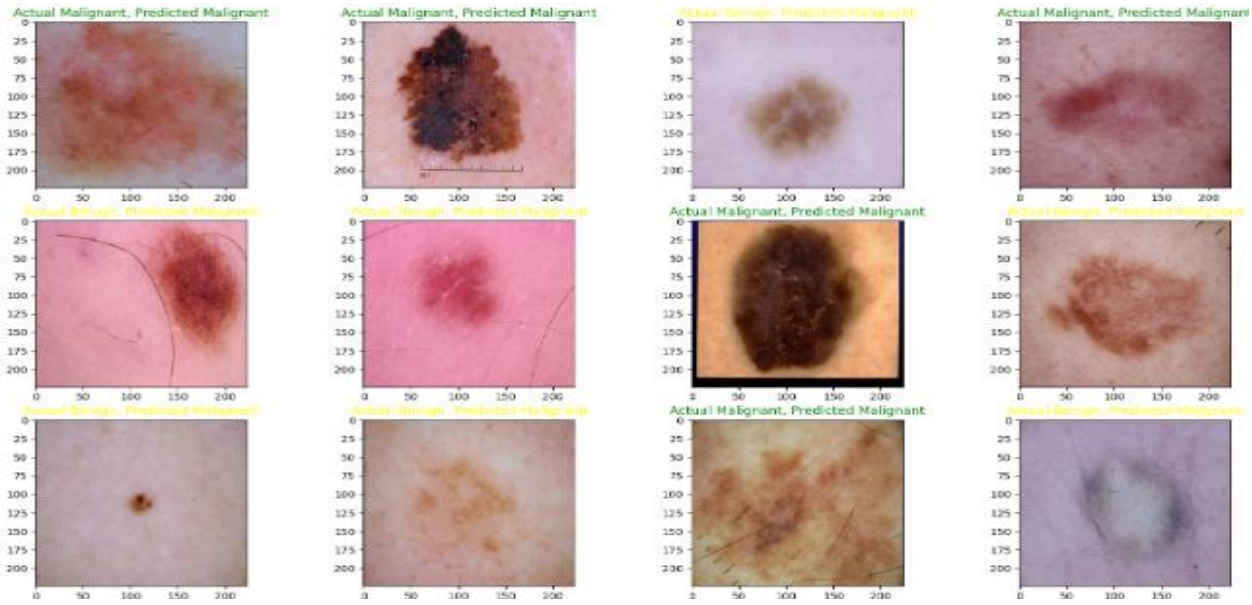

Figure 4.2. Training datasets

A green title indicates an accurate forecast. The yellow title indicates that a benign cancer was mistakenly diagnosed as malignant (but this is still acceptable because medical professionals would still closely monitor it). Red title signifies inaccurate prediction of Malignant Cancer as Benign (This is the most serious circumstance since we do not want a Malignant Cancer to go unreported or receive less care).

5. CONCLUSION

This study explains and designs the overall system architecture for the proposed prediction system. All of the parts and functions of the suggested prediction model are laid out in this system architecture document. The whole system design consists of interconnected modules that work together to provide an optimal setting for cancer illness prediction. When designing this system, the architects took into account a widely used and standardised picture database for the suggested model's pre-processing and classification tasks.

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