PROJECT REPORT

1.INTRODUCTION:

1.1.PROJECT OVERVIEW:

This study shows that CAD may also be a viable option in dermatology by presenting a novel method to sequentially combine accurate segmentation and classification models. Given an image of the skin, we decompose the image to normalize and extract high-level features. Using a neural network-based segmentation model to create a segmented map of the image, we then cluster sections of abnormal skin and pass this information to a classification model. We classify each cluster into different common skin diseases using another neural network model. Our segmentation model achieves better performance compared to previous studies, and also achieves a near-perfect sensitivity score in unfavorable conditions.

1.2:PURPOSE:

Although computer-aided diagnosis (CAD) is used to improve the quality of diagnosis in various medical fields such as mammography and colonography, it is not used in dermatology, where noninvasive screening tests are performed only with the naked eye, and avoidable inaccuracies may exist. Our classification model is more accurate than a baseline model trained without segmentation, while also being able to classify multiple diseases within a single image. This improved performance may be sufficient to use CAD in the field of dermatology.

2.LITERATURE SURVEY:

2.1:EXISTING PROBLEM:

Skin diseases are the 4th common cause of skin burden worldwide. Robust and Automated system have been developed to lessen this burden and to help the patients to conduct the early assessment of the skin lesion. Mostly this system available in the literature only provide skin cancer classification. Treatments for skin are more effective and less disfiguring when found early and it is a challenging research due to similar characteristics of skin diseases. In this project we attempt to detect skin diseases .A novel system is presented in this research work for the diagnosis of the most common skin lesions (Melanocytic nevi, Melanoma, Benign keratosis-like lesions, Basal cell carcinoma, Actinic keratoses, Vascular lesion, Dermatofibroma). The proposed approach is based on the pre-processing, Deep learning algorithm, training the model , validation and classification phase. Experiments were performed on 10010 images and 93% accuracy is achieved for seven-class classification using Convolution Neural Networks (CNN) with the Keras Application API.

2.2:REFERENCES:

1. Doi, K. Computer-aided diagnosis in medical imaging: Historical review, current status and future potential. *Comput. Med. Imaging Graph.* **31**, 198–211.

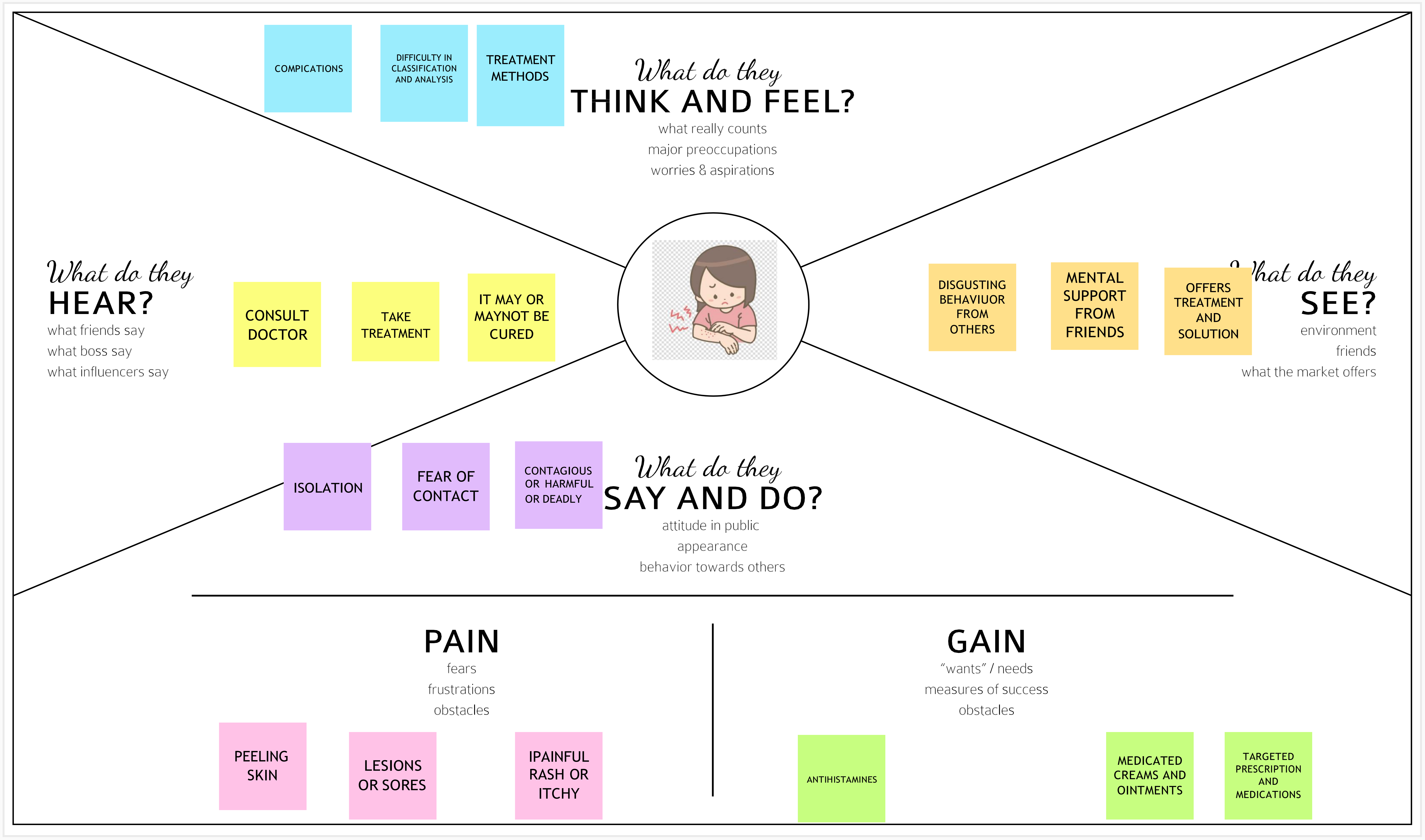
2. Yoshida, H. & Dachman, A. H. Computer-aided diagnosis for CT colonography. *Semin. Ultrasound CT MRI* **25**, 419–431

3. Trabelsi, O., Tlig, L., Sayadi, M. & Fnaiech, F., Skin disease analysis and tracking based on image segmentation. *2013 International Conference on Electrical Engineering and Software Applications*, Hammamet, 1–7.

3. Ideation and Proposed Solution 2

3.1 Empathy Map Canvas

1



3.3 Proposed Solution

CAD (Computer Aided Diagnosis)has been a viable option in dermatology by presenting a novel method to sequentially combine accurate segmentation and classification models.

3.4 Problem Solution fit

Skin disease can appear in virtually any part of body and there is a lack of data required to form an association between the probability of a skin disease based on the body part.It is shown that current state-of-the-art CNN models can outperform models created by previous research, through proper data preprocessing, self-supervised learning, transfer learning, and special CNN architecture techniques. Furthermore, with accurate segmentation, we gain knowledge of the location of the disease, which is useful in the preprocessing of data used in classification, as it allows the CNN model to focus on the area of interest. Lastly, unlike previous studies, our method provides a solution to classify multiple diseases within a single image. With higher quality and a larger quantity of data, it will be viable to use state-of-the-art models to enable the use of CAD in the field of dermatology.

4. Requirement Analysis

4.1 Functional requirements:

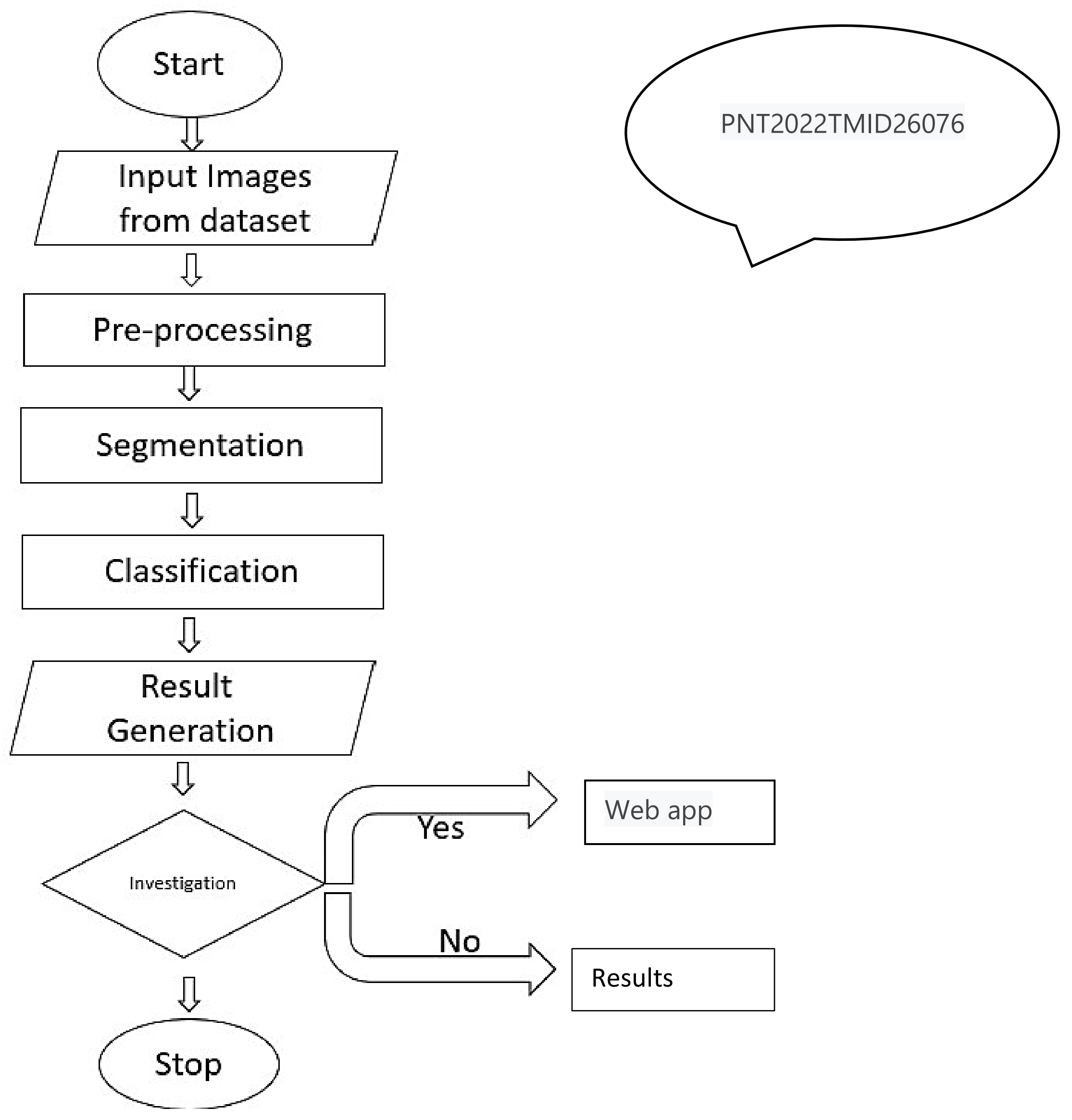
Temperature:If the temperature level exceeds the room temperature then the alert message will be sent using GSM, **Pulse sensor** to measure the pulse amplitude and width signals,**GPS** which is used to used to track the livelocation of the skin disease.**GSM** results in partial or whole-body exposures to electromagneticfield(EMF)communications, **Web camera** collects medical images or images from WebCam are feed into the system**,,Raspberry pi microprocessor** in which all other sensors, GPS and GSM are integrated.

4.2 Non-Functional requirements:

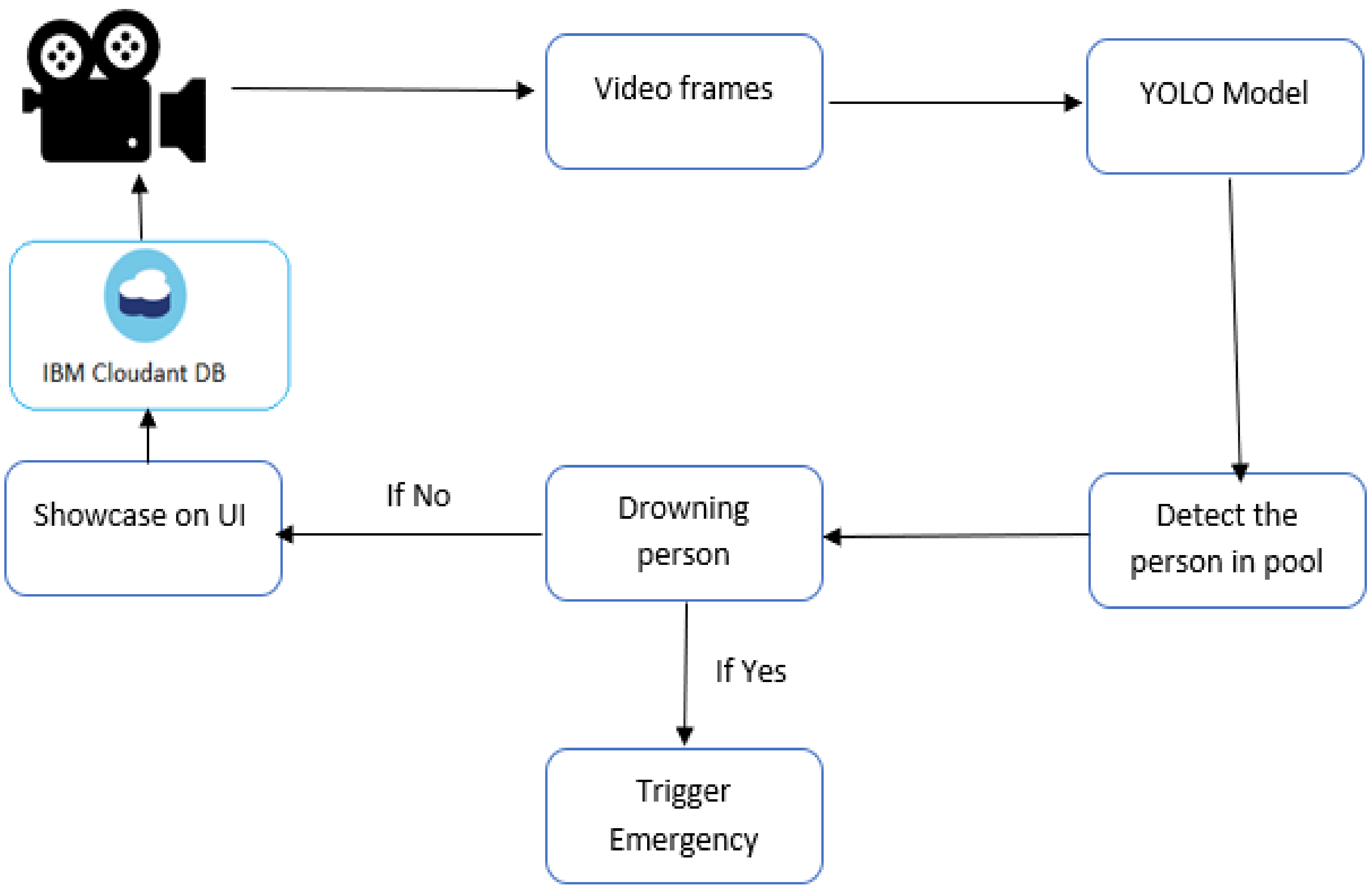
Usability, Security, Reliability, Performance,Availability, Scalability.

5. Project Design

5.1 Data Flow Diagram:



5.2 Solution and Technical Architecture



5.3 User Stories:

User Type	Functional Requirement(Epic)	User Story Number	User Story / Task	Acceptance criteria	Priority	Release
Customer (Mobile user)	Registration	USN-1	As a user, I can register for the application by entering my email, password, and confirming my password.	I can access my account /dashboard	High	Sprint-1
		USN-2	As a user, I will receive confirmation email once I have registered for the application	I can receive confirmation email & click confirm	High	Sprint-1
		USN-3	As a user, I can register for the applicationthrough facebook.	I can register and accessthe dashboard with facebook login.	High	Sprint-2
	Login	USN-4	As a user, I can register for the application through gmail.	I can receive an email confirmation.	High	Sprint-1
Customer Care Executive	Login		As I enter I can view the working of the application and scan for any glitches and monitor the operation and check if all the users are authorised.	I can login only with myprovided credentials.	Medium	Sprint-3
Administrator	Login		Maintaining and making sure the databasecontaining the locations are secure and accurate and updated constantly.	I can login only with myprovided credentials.	High	Sprint-3

6.Project Planning and Scheduling

6.1 Sprint Planning and Estimation

Sprint	Functional Requirement (Epic)	User Story Number	User Story / Task	Story Points	Priority	Team Members
Sprint1	Login	USN-1	As a user, I can login to the dashboard by entering my email, password, and confirming my password.	7	High	Samyugtha velu S Nandhini S Nandhini B Sindhuja M Sowndarya P
Sprint1		USN-2	As a user, I will give the correct details about my medical report.	3	High	Samyugtha Velu S Nandhini B Nandhini S Sindhuja M Sowndarya P
Sprint2	Screening	USN-3	As a user, I can find the method more efficient and accurate.	5	Medium	Samyugtha Velu S Nandhini B Nandhini S Sindhuja M Sowndarya P
Sprint1		USN-4	As a user, I can use it with minimal physical interaction with the device.	3	Medium	Samyugtha Velu S Nandhini B Nandhini S Sindhuja M Sowndarya P
Sprint4	Physical Features	USN-5	As a user, I can use the database and software installed in a particular system	5	High	Samyugtha Velu S Nandhini B Nandhini S Sindhuja M Sowndarya P
Sprint2		USN-6	As a user, I can find it portable and light weight	10	Low	Samyugtha Velu S Nandhini B Nandhini S Sindhuja M Sowndarya P
Sprint3	Safety	USN-7	As a user, I can be safe as the detection method is free from radiations	5	Medium	Samyugtha Velu S Nandhini B Nandhini S Sindhuja M Sowndarya P

Sprint3	Testing	USN-8	As a user, I can undergo testing without any fear of pain as this method is pain free.	5	High	Samyugtha Velu S Nandhini B Nandhini S Sindhuja M Sowndarya P

Sprint	Functional Requirement (Epic)	User Story Number	User Story / Task	Story Points	Priority	Team Members
Sprint-3		USN-9	As a user, I also suggest others to use this software.	5	High	Samyugtha Velu S Nandhini B Nandhini S Sindhuja M Sowndarya P
Sprint-2	Cost Effectiveness	USN-10	As a user, I can reach many people affected from skin disease	5	Low	Samyugtha Velu S Nandhini B Nandhini S Sindhuja M Sowndarya P
Sprint-3		USN-11	As a user, I can create awareness among people to undergo frequent medical check up.	5	Medium	Samyugtha Velu S Nandhini B Nandhini S Sindhuja M Sowndarya P
Sprint-4	Results	USN-12	As a user I can rely on the results without any suspicion	5	Medium	Samyugtha Velu S Nandhini B Nandhini S Sindhuja M Sowndarya P
Sprint-4		USN-13	As a user, I can benefit from the result as it will help me know whether treatment is necessary or not.	3	High	Samyugtha Velu S Nandhini B Nandhini S Sindhuja M Sowndarya P
Sprint-1			As a user I can complete the screening process within minutes for a single patient.	7	Medium	Samyugtha Velu S Nandhini B Nandhini S Sindhuja M Sowndarya P
Sprint-4			As a user I can get the results immediately after screening process.	7	Medium	Samyugtha Velu S Nandhini B Nandhini S Sindhuja M Sowndarya P

6.2 sprint delivery schedule

Sprint	Total Story Points	Duration	Sprint Start Date	Sprint End Date (Planned)	Story Points Completed (as on Planned End Date)	Sprint Release Date (Actual)
Sprint-1	20	6 Days	24 Oct 2022	29 Oct 2022	20	29 Oct 2022
Sprint-2	20	6 Days	31 Oct 2022	05 Nov 2022	20	05 Nov 2022
Sprint-3	20	6 Days	07 Nov 2022	12 Nov 2022	20	12 Nov 2022
Sprint-4	20	6 Days	14 Nov 2022	19 Nov 2022	20	19 Nov 2022

7. Coding and Solutioning

```
import tensorflow as tf
import tensorflow_hub as hub
import matplotlib.pyplot as plt
import numpy as np
import pandas as pd
import seaborn as sns
from tensorflow.keras.utils import get_file
from sklearn.metrics import roc_curve, auc, confusion_matrix
from imblearn.metrics import sensitivity_score, specificity_score

import os
import glob
import zipfile
import random

# to get consistent results after multiple runs
tf.random.set_seed(7)
np.random.seed(7)
random.seed(7)

# 0 for benign, 1 for malignant
class_names = ["benign", "malignant"]
```

```
def download_and_extract_dataset():
 # dataset from https://github.com/udacity/dermatologist-ai
 # 5.3GB
 train_url = "https://s3-us-west-1.amazonaws.com/udacitydlnfd/datasets/skin-cancer/train.zip"
 # 824.5MB   valid_url = "https://s3-us-west-
1.amazonaws.com/udacitydlnfd/datasets/skin-cancer/valid.zip"

  # 5.1GB
  test_url  = "https://s3-us-west-1.amazonaws.com/udacity-
dlnfd/datasets/skin-cancer/test.zip"
  for i, download_link in enumerate([valid_url, train_url, test_url]):
    temp_file = f"temp{i}.zip"
    data_dir = get_file(origin=download_link,
fname=os.path.join(os.getcwd(), temp_file))
    print("Extracting", download_link)
    with zipfile.ZipFile(data_dir, "r") as z:
      z.extractall("data")
    # remove the temp file
    os.remove(temp_file)

# comment the below line if you already downloaded the dataset
download_and_extract_dataset()
```

```
# preparing data
# generate CSV metadata file to read img paths and labels from it
def generate_csv(folder, label2int):
    folder_name = os.path.basename(folder)
    labels = list(label2int)
    # generate CSV file
    df = pd.DataFrame(columns=["filepath", "label"])
    i = 0
    for label in labels:
        print("Reading", os.path.join(folder, label, "*"))
        for filepath in glob.glob(os.path.join(folder, label, "*")):
            df.loc[i] = [filepath, label2int[label]]
            i += 1
    output_file = f"{folder_name}.csv"
    print("Saving", output_file)
    df.to_csv(output_file)

# generate CSV files for all data portions, labeling nevus and
seborrheic keratosis
```

```
0# as 0 (benign), and melanoma as 1 (malignant)
# you should replace "data" path to your extracted dataset path # don't replace if you used
download_and_extract_dataset() function generate_csv("data/train", {"nevus": 0, "seborrheic_keratosis": 0,
"melanoma": 1}) generate_csv("data/valid", {"nevus": 0, "seborrheic_keratosis": 0,
"melanoma": 1}) generate_csv("data/test", {"nevus": 0, "seborrheic_keratosis": 0, "melanoma": 1})
```

```
.0# loading data train_metadata_filename = "train.csv" valid_metadata_filename = "valid.csv" # load CSV files as
DataFrames df_train = pd.read_csv(train_metadata_filename) df_valid = pd.read_csv(valid_metadata_filename)
n_training_samples = len(df_train) n_validation_samples = len(df_valid) print("Number of training samples:",
n_training_samples) print("Number of validation samples:", n_validation_samples) train_ds =
tf.data.Dataset.from_tensor_slices((df_train["filepath"], df_train["label"])) valid_ds =
tf.data.Dataset.from_tensor_slices((df_valid["filepath"], df_valid["label"]))
```

```
Number of training samples: 2000
Number of validation samples: 150
```

Let's load the images:

```
# preprocess data def
decode_img(img):
  # convert the compressed string to a 3D uint8 tensor   img =
tf.image.decode_jpeg(img, channels=3)
  # Use `convert_image_dtype` to convert to floats in the [0,1] range.   img =
tf.image.convert_image_dtype(img, tf.float32)   # resize the image to the desired size.   return
tf.image.resize(img, [299, 299])
```

```
    ds = ds.batch(batch_size)
    # `prefetch` lets the dataset fetch batches in the background while
the model
    # is training.
    ds = ds.prefetch(buffer_size=tf.data.experimental.AUTOTUNE)
    return ds


valid_ds = prepare_for_training(valid_ds, batch_size=batch_size,
cache="valid-cached-data")
train_ds = prepare_for_training(train_ds, batch_size=batch_size,
cache="train-cached-data")
batch = next(iter(valid_ds))


def show_batch(batch):
    plt.figure(figsize=(12, 12))
    for n in range(25):
        ax = plt.subplot(5, 5, n+1)
        plt.imshow(batch[0][n])
        plt.title(class_names[batch[1][n].numpy()].title())
        plt.axis('off')


show_batch(batch)
```

```
def   process  path     ( filepath      ,    label    ):
    # load the raw data from the file as a string
    img   =  tf  . io  . read  file      ( filepath      )
    img   =  decode  img   ( img )
    return     img ,   label


valid  ds      =  valid  ds     . map( process  path      )
train  ds      =  train  ds     . map( process  path      )
# test  ds = test  ds
for    image ,    label      in    train  ds      . take  ( 1):
        print    ( "Image shape:"       ,    image  . shape  )
        print    ( "Label:"      ,    label    . numpy())
Image shape    :   ( 299 ,    299 ,    3 )
Label   :    0
```

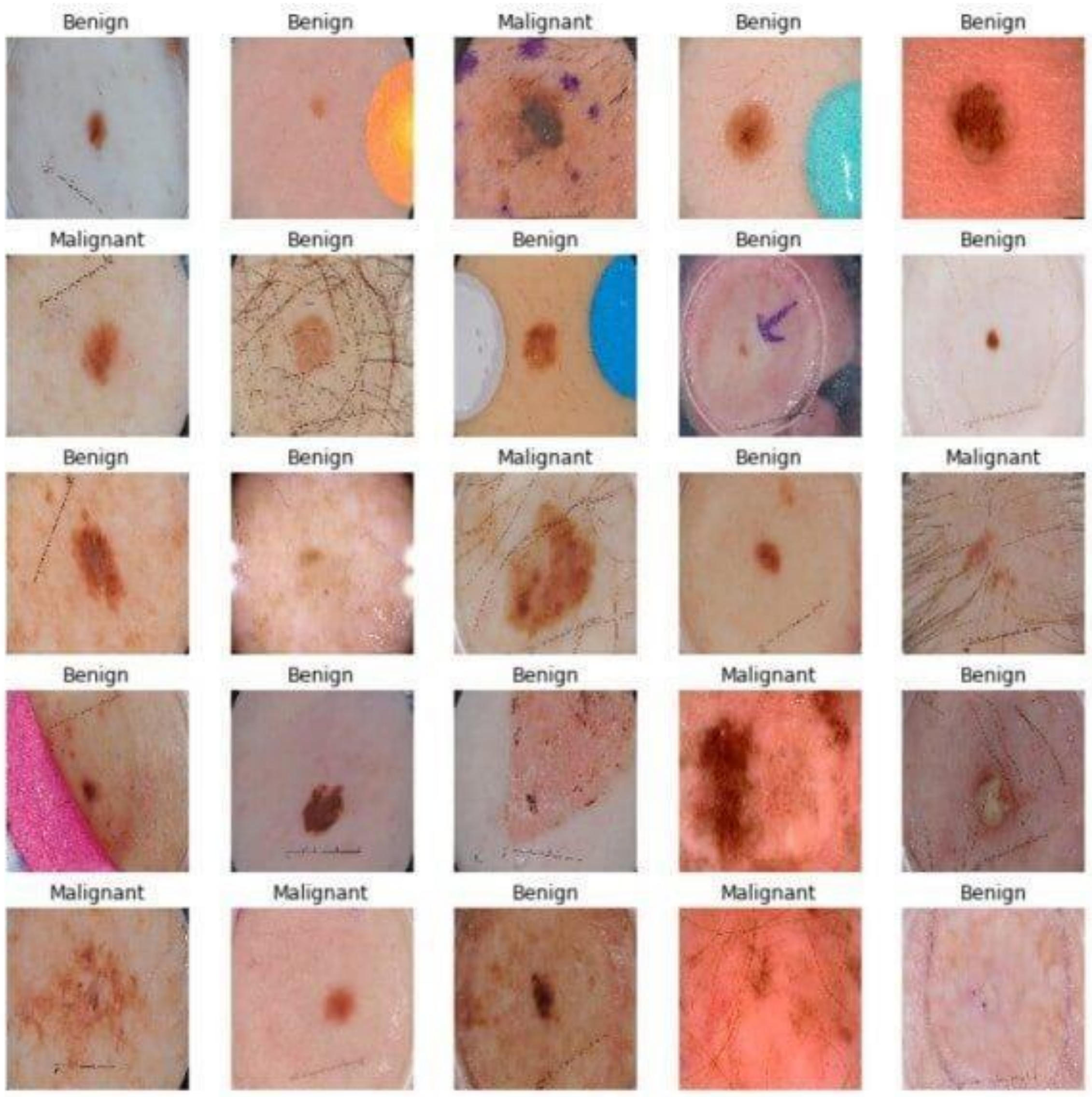
```
# building the model
# InceptionV3 model & pre-trained weights module_url =
"https://tfhub.dev/google/tf2preview/inception_v3/feature_vector/4" m = tf.keras.Sequential([
hub.KerasLayer(module_url, output_shape=[2048], trainable=False),    tf.keras.layers.Dense(1, activation="sigmoid")
])

m.build([None, 299, 299, 3])
  m.compile(loss="binary_crossentropy", optimizer=optimizer, metrics=["accuracy"]) m.summary()
Model: "sequential"
```

```
Layer (type)             Output Shape          Param #
================================================================= keras_layer (KerasLayer)    multiple
21802784  _________________________________________________________________ dense (Dense)
multiple              2049     =================================================================
Total params: 21,804,833

Trainable params: 2,049

Non-trainable params: 21,802,784
```



7.Training the Model

We now have our dataset and the model, let's get them together:

```
model_name = f"benign-vs-malignant_{batch_size}_{optimizer}" tensorboard =
tf.keras.callbacks.TensorBoard(log_dir=os.path.join("logs", model_name))

# saves model checkpoint whenever we reach better weights modelcheckpoint =
tf.keras.callbacks.ModelCheckpoint(model_name + "_{val_loss:.3f}.h5", save_best_only=True, verbose=1)


history = m.fit(train_ds, validation_data=valid_ds,            steps_per_epoch=n_training_samples // batch_size,
validation_steps=n_validation_samples // batch_size, verbose=1, epochs=100,

        callbacks=[tensorboard, modelcheckpoint])
```

Here is a part of the output during training:

```
Train for 31 steps, validate for 2 steps

Epoch 1/100

30/31 [============================>.] - ETA: 9s - loss: 0.4609 - accuracy: 0.7760

Epoch 00001: val_loss improved from inf to 0.49703, saving model to benign-vs-malignant_64_rmsprop_0.497.h5

31/31 [==============================] - 282s 9s/step - loss: 0.4646 - accuracy: 0.7722 - val_loss: 0.4970 -
val_accuracy: 0.8125

<..SNIPED..>

Epoch 27/100

30/31 [============================>.] - ETA: 0s - loss: 0.2982 - accuracy: 0.8708

Epoch 00027: val_loss improved from 0.40253 to 0.38991, saving model to benign-vs-malignant_64_rmsprop_0.390.h5

31/31 [==============================] - 21s 691ms/step - loss: 0.3025
-  accuracy: 0.8684 - val_loss: 0.3899 - val_accuracy: 0.8359

<..SNIPED..>

Epoch 41/100

30/31 [============================>.] - ETA: 0s - loss: 0.2800 - accuracy: 0.8802

Epoch 00041: val_loss did not improve from 0.38991

31/31 [==============================] - 21s 690ms/step - loss: 0.2829
-  accuracy: 0.8790 - val_loss: 0.3948 - val_accuracy: 0.8281

Epoch 42/100

30/31 [============================>.] - ETA: 0s - loss: 0.2680 - accuracy: 0.8859

Epoch 00042: val_loss did not improve from 0.38991

31/31 [==============================] - 21s 693ms/step - loss: 0.2722 - accuracy: 0.8831 - val_loss: 0.4572 -
val_accuracy: 0.8047
```

Model Evaluation

First, let's load our test set, just like previously:

```
# evaluation # load
testing set
test_metadata_filename = "test.csv" df_test =
pd.read_csv(test_metadata_filename) n_testing_samples =
len(df_test)
print("Number of testing samples:", n_testing_samples)
test_ds = tf.data.Dataset.from_tensor_slices((df_test["filepath"], df_test["label"]))
 def prepare_for_testing(ds, cache=True, shuffle_buffer_size=1000):
```

```
if cache:    if isinstance(cache, str):      ds = ds.cache(cache)
```

```
 isinstance(cache, str):      ds = ds.cache(cache)
        else  :
```

```
          ds   =  ds . cache  ()
   ds   =  ds . shuffle    ( buffer_size      =shuffle_buffer_size          )
   return     ds

test_ds      =  test_ds    . map( process_path      )
test_ds      =  prepare_for_testing          ( test_ds    ,    cache  ="test    - cached   - data"   )
```

8.Results

```
Number of testing samples            :   600
```

`600` images of the shape `(299, 299, 3)` can fit our memory, let's convert our test set from `tf.data` into a NumPy array:

```
# convert testing set to numpy array to fit in memory (don't do that when testing # set is too large)
y_test = np.zeros((n_testing_samples,))
X_test = np.zeros((n_testing_samples, 299, 299, 3)) for i, (img, label) in
enumerate(test_ds.take(n_testing_samples)):
 # print(img.shape, label.shape)   X_test[i] = img   y_test[i] =
label.numpy()
 print("y_test.shape:", y_test.shape) # load the weights with the least
loss
m.load_weights("benign-vs-malignant_64_rmsprop_0.390.h5") print("Evaluating the model...")
loss, accuracy = m.evaluate(X_test, y_test, verbose=0) print("Loss:", loss, "  Accuracy:", accuracy)
```

Output:

```
Evaluating the model...
Loss: 0.4476394319534302   Accuracy: 0.8
```

The below function does that:

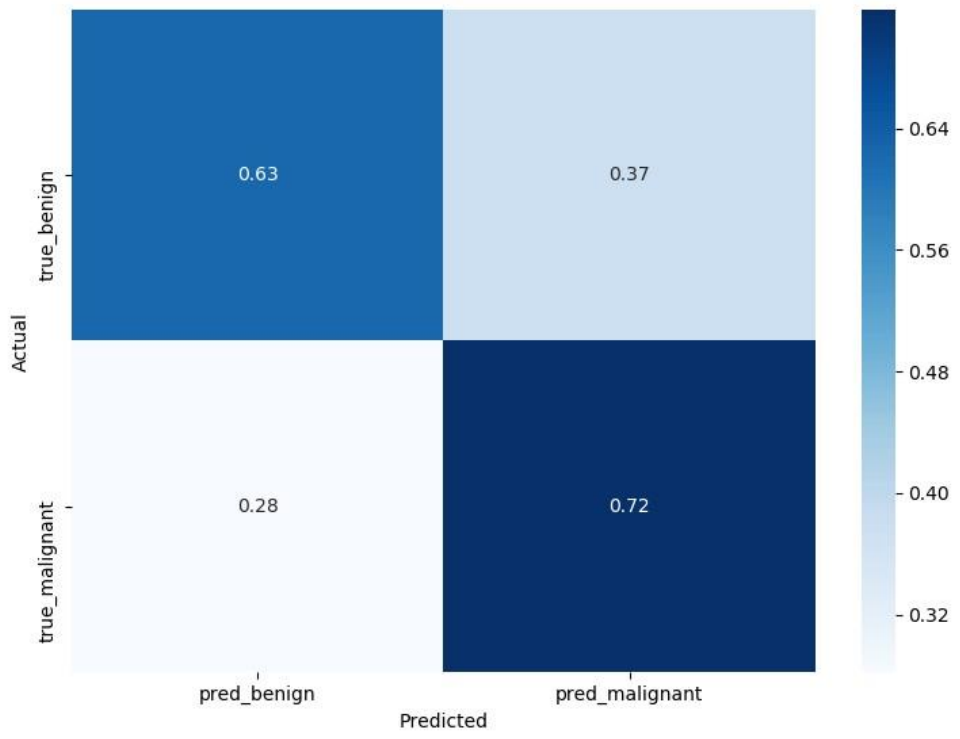
```
def get_predictions(threshold=None):
    """
    Returns predictions for binary classification given `threshold`
    For instance, if threshold is 0.3, then it'll output 1 (malignant)
for that sample if
    the probability of 1 is 30% or more (instead of 50%)
    """
    y_pred = m.predict(X_test)
    if not threshold:
        threshold = 0.5
    result = np.zeros((n_testing_samples,))
    for i in range(n_testing_samples):
        # test melanoma probability
        if y_pred[i][0] >= threshold:
            result[i] = 1
        # else, it's 0 (benign)
    return result

threshold = 0.23
# get predictions with 23% threshold
# which means if the model is 23% sure or more that is malignant,
# it's assigned as malignant, otherwise it's benign
y_pred = get_predictions(threshold)
```

Now let's draw our confusion matrix and interpret it:

```
def plot_confusion_matrix(y_test, y_pred):
    cmn = confusion_matrix(y_test, y_pred)
    # Normalise
    cmn = cmn.astype('float') / cmn.sum(axis=1)[:, np.newaxis]
    print(cmn)
    fig, ax = plt.subplots(figsize=(10, 10))
    sns.heatmap(cmn, annot=True, fmt='.2f',
                xticklabels=[f"pred_{c}" for c in class_names],
                yticklabels=[f"true_{c}" for c in class_names],
                cmap="Blues"
                )
    plt.ylabel('Actual')
    plt.xlabel('Predicted')
    # plot the resulting confusion matrix
    plt.show()

plot_confusion_matrix(y_test, y_pred)
```

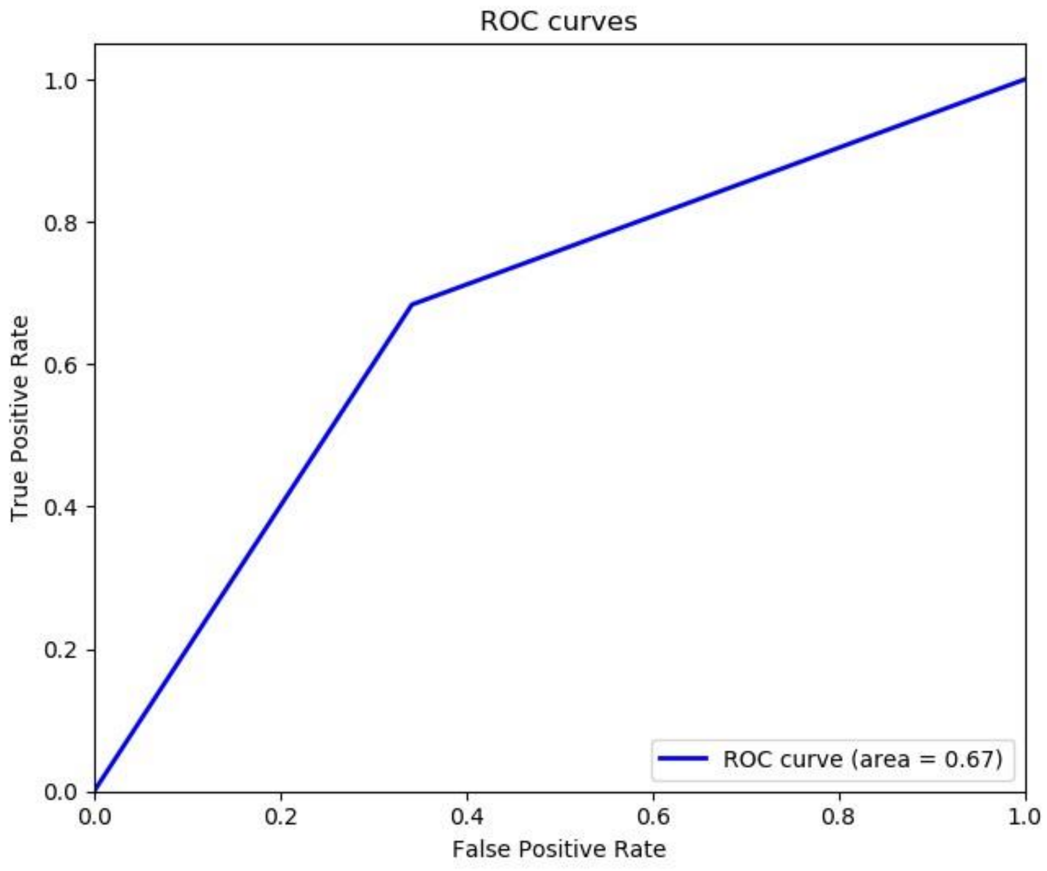


```
def plot_roc_auc(y_true, y_pred):
    """
    This function plots the ROC curves and provides the scores.
    """
    # prepare for figure
    plt.figure()
    fpr, tpr, _ = roc_curve(y_true, y_pred)
    # obtain ROC AUC
    roc_auc = auc(fpr, tpr)
    # print score
    print(f"ROC AUC: {roc_auc:.3f}")
    # plot ROC curve
    plt.plot(fpr, tpr, color="blue", lw=2,
                label='ROC curve (area = {f:.2f})'.format(d=1,
f=roc_auc))
    plt.xlim([0.0, 1.0])
    plt.ylim([0.0, 1.05])
    plt.xlabel('False Positive Rate')
    plt.ylabel('True    Positive Rate')
    plt.title('ROC curves')
    plt.legend(loc="lower right")
    plt.show()

plot_roc_auc(y_test, y_pred)
```

Output:

```
ROC AUC: 0.671
```



ROC AUC: 0.671

9. Advantages and Disadvantages

9.1 Advantages

Instant Response, improves prediction of Skin Disease, no referral needed, Saves Money and Time, and Confidential Advice.

9.2 Disadvantages

Network Connectivity and Accuracy

10. Conclusion

We have shown that even without a large dataset and high-quality images, it is possible to achieve sufficient accuracy rates. In addition, we have shown that current state-of-the-art CNN models can outperform models created by previous research, through proper data pre-processing, self-supervised learning, transfer learning, and special CNN architecture techniques. Furthermore, with accurate segmentation, we gain knowledge of the location of the disease, which is useful in the pre-processing of data used in classification, as it allows the CNN model to focus on the area of interest. Lastly, unlike previous studies, our method provides a solution to classify multiple diseases within a single image. With higher quality and a larger quantity of data, it will be viable to use state-of-the-art models to enable the use of CAD in the field of dermatology.

11. Future Scope

This implementation of the Structural Co-Occurrence matrices for feature extraction in the skin diseases classification and the pre-processing techniques are handled by using the Median filter, this filter helps to remove the salt and pepper noise in the image processing; thus, it enhances the quality of the images, and normally, the skin diseases are considered as the risk factor in all over the world. Our proposed approach provides 97% of the classification of the accuracy results while another existing model such as FFT + SCM gives 80%, SVM + SCM gives 83%, KNN + SCM gives 85%, and SCM + CNN gives 82%. Future work is dependent on the increased support vector machine's accuracy in classifying skin illnesses, and SCM is used to manage the feature extraction technique.

12. Appendix

GitHub Link:

https://github.com/IBM-EPBL/IBM-Project-3710-1658592520