PROJECT REPORT

1. Introduction

1.1 Project Overview

Now a day's people are suffering from skin diseases, more than 125 million people suffering from Psoriasis also skin cancer rate is rapidly increasing over the last few decades especially Melanoma is most diversifying skin cancer. If skin diseases are not treated at an earlier stage, then it may lead to complications in the body including spreading of the infection from one individual to the other.
To overcome the above problem, we are building a model which is used for the prevention and early detection of skin cancer, psoriasis. Basically, skin disease diagnosis depends on the different characteristics like colour, shape, texture etc. Here the person can capture the images of skin and then the image will be sent the trained model. The model analyses the image and detect whether the person is having skin disease or not.

1.2 Purpose

The diseases are not considered skin diseases, and skin tone is majorly suffered from the ultraviolet rays from the sun. However, dermatologists perform the majority of non-invasive screening tests simply with the naked eye, even though skin illness is a frequent disease for which early detection and classification are essential for patient success and recovery. The characteristic of the skin images is diversified so that it is a challenging job to devise an efficient and robust algorithm for automatic detection of skin disease and its severity. Automatic processing of such images for skin analysis requires quantitative discriminator to differentiate the diseases.

2. Literature Survey

2.1 Existing problem

A neglected public health problem Skin diseases are among the most common health problems in humans. Considering their significant impact on the individual, the family, the social life of patients, and their heavy economic burden, the public health importance of these diseases is underappreciated.

2.2 References

[1] J. Kawahara and G. Hamarneh, "Multi-resolution-tract CNN with hybrid pretrained and skin-lesion trained layers," in International Workshop on Machine Learning in Medical Imaging, pp. 164–171, Springer, New York, NY, USA, 2016.

[2] S. Verma, M. A. Razzaque, U. Sangtongdee, C. Arpnikanondt, B. Tassaneetrithep, and A. Hossain, "Digital diagnosis of Hand, Foot, and mouth disease using hybrid deep neural networks," IEEE Access, vol. 9, pp. 143481–143494, 2021.

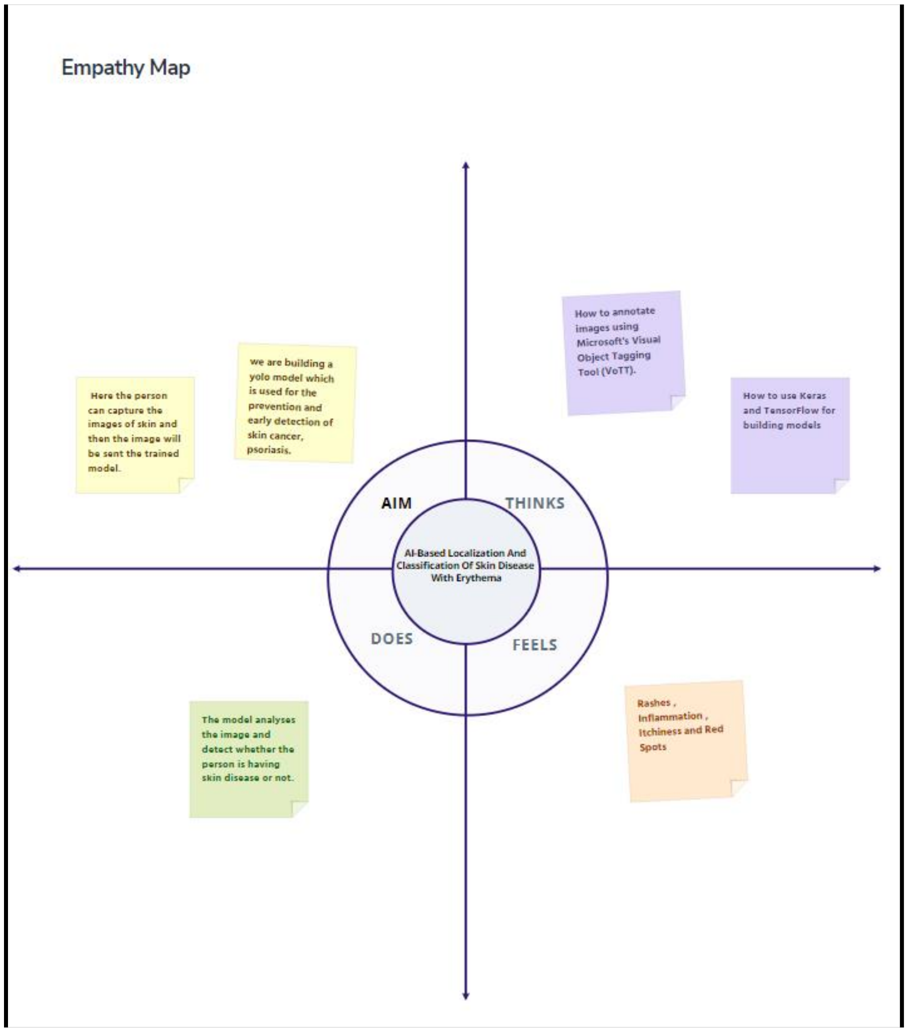
[3] P. P. Rebouças Filho, S. A. Peixoto, R. V. Medeiros da Nobrega´ et al., "Automatic histologically-closer classification of skin lesions," Computerized Medical Imaging and Graphics, vol. 68, pp. 40–54, 2018.

2.3 Problem Statement Definition

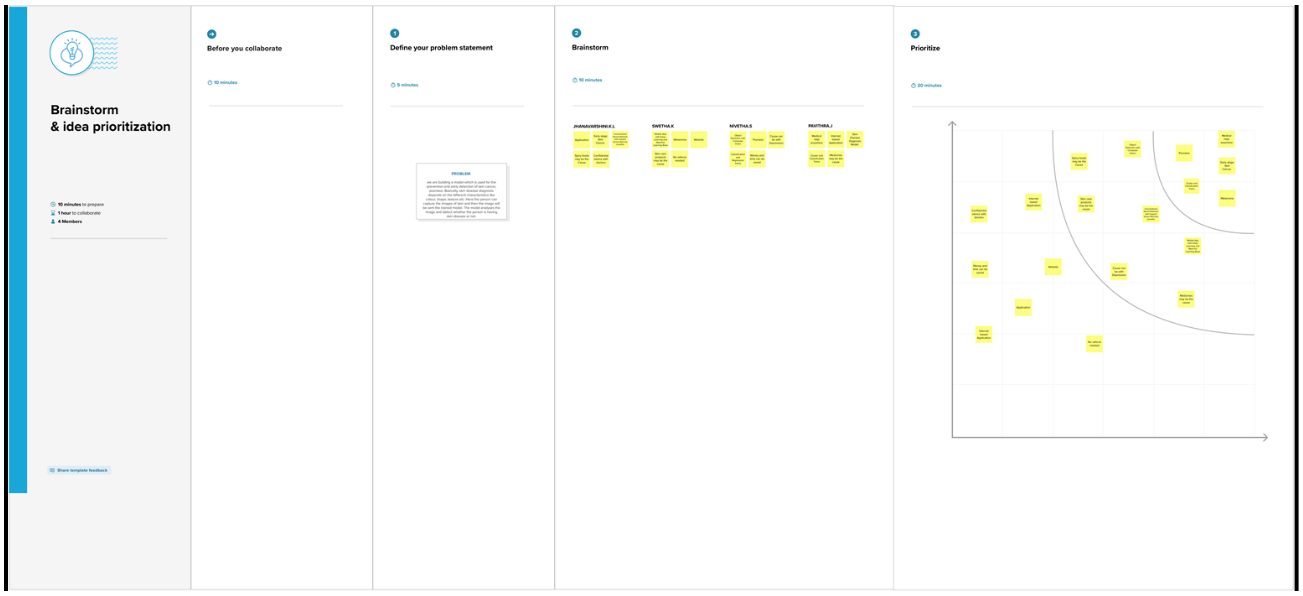
We're trying to find a solution to identify Skin Disease but Developed model is under training because given an image of skin, we can decompose, segment, and classify in a sequential manner which takes to Early detection of skin cancer, psoriasis.

3. Ideation and Proposed Solution

3.1 Empathy Map Canvas


Empathy Map
Here the person can capture the images of skin and then the image will be sent the trained model.
we are building a yolo model which is used for the prevention and early detection of skin cancer, psoriasis.
How to annotate images using Microsoft's Visual Object Tagging Tool (VoTT).
How to use Keras and TensorFlow for building models
AIM
THINKS
AI-Based Localization And Classification Of Skin Disease With Erythema
DOES
FEELS
The model analyses the image and detect whether the person is having skin disease or not.
Rashes , Inflammation , Itchiness and Red Spots

3.2 Ideation and Brainstorming


Brainstorm
& idea prioritization
10 minutes to prepare
1 hour to collaborate
4 Members
Share template feedback
Before you collaborate
10 minutes
Define your problem statement
5 minutes
Brainstorm
10 minutes
JHANAVARSHINI.K.L
Application
Early stage Skin Cancer
Spicy foods may be the Cause
Confidential advice with doctors
SWETHA.K
Melanoma
Website
Skin care products may be the cause
No referral needed
NIVETHA.S
Object Detection with Computer Vision
Psoriasis
Cause can be with Depression
Classification and Regression trees
Money and time can be saved
PAVITHRA.J
Medical help anywhere
Internet based Application
Skin Disease Diagnosis Model
Cluster and Classification Trees
Medicines may be the cause
Prioritize
20 minutes

PROBLEM

we are building a model which is used for the prevention and early detection of skin cancer, psoriasis. Basically, skin disease diagnosis depends on the different characteristics like colour, shape, texture etc. Here the person can capture the images of skin and then the image will be sent the trained model. The model analyses the image and detect whether the person is having skin disease or not.

3.3 Proposed Solution

Two-phase analysis model. The original image primarily enters a pre-processing stage, where normalization and decomposition occur. Afterwards, the first step is segmentation, where cluster of abnormal skin are segmented and cropped. The second step is classification, where each cluster is classified into its corresponding class. Developed Model is Still under training.

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. A Solution model used for the prevention and early detection of skin cancer and psoriasis by image analyses to detect whether the person is having skin disease or not. The location of the disease that is present in an image and improved performance by CNN model to focus on particular subsections of the images.

4. Requirement Analysis

4.1 Functional requirements

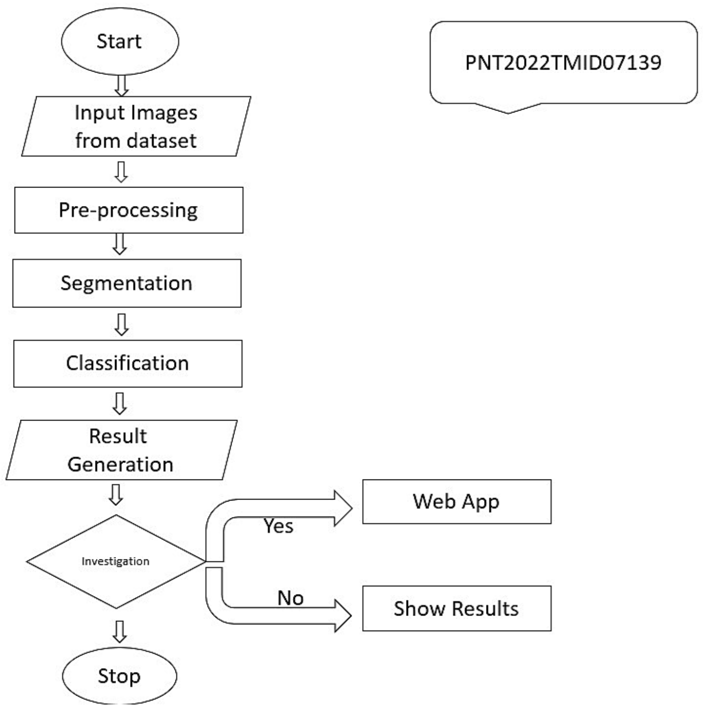
Image Acquisition, Pre-processing Steps such as Colour gradient generator on an image , Cropping and isolating region of interest and Thresholding and Clustering on image, Visual feature extraction, System Training YOLO Model for Skin disease classification with deep learning and CNN, Separate access of application for admin, Diagnosis of Skin disease and Data retrieval and Data manipulation.

4.2 Non-Functional requirements

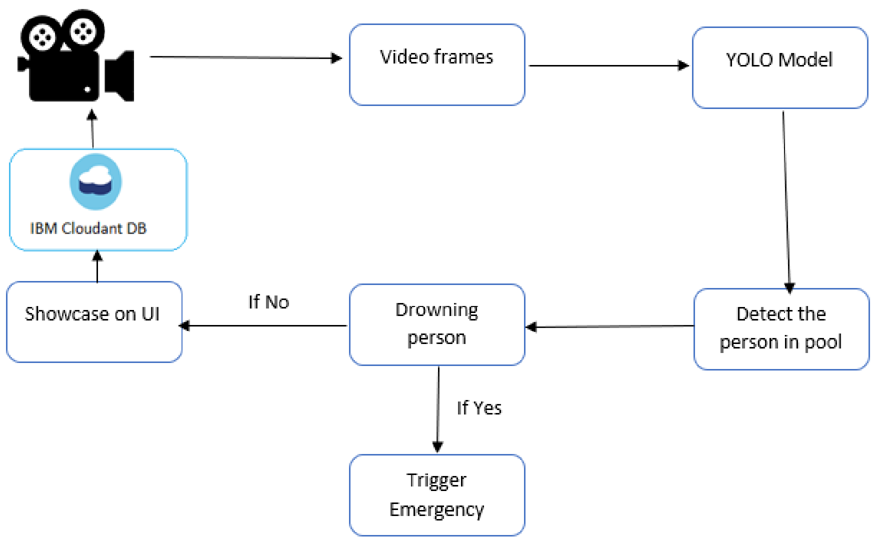
Software Quality Attributes, Prediction, Accuracy.

5. Project Design

5.1 Data Flow Diagram



5.2 Solution and Technical Architecture



5.3 User Stories

Functional Requirement (Epic)	**User Story Number**	**User Story / Task**	**Story Points**	**Priority**
Prerequisites	USN-1	Install Python IDE, Python packages, Microsoft Visual Object Tagging Tool, Yolo Structure	3	High
Data Collection	USN-2	Dataset should be collected from google or using a Chrome extension such as Fatkun Batch Downloader	3	High
Annotate Images	USN-3	Create A Project in VOTT (Microsoft's Visual Object Tagging Tool)	2	Medium
Training YOLO	USN-4	train our model using YOLO weights	2	Medium
	USN-5	To Download and Convert Pre-Trained Weights	3	High
	USN-6	To Train YOLOv3 Detector	3	High
Cloudant DB	USN-7	Register & Login to IBM Cloud	3	High
	USN-8	Create Service Instant and Credentials	2	Medium
	USN-9	Launch DB and Create database	3	High
Development Phase	USN-10	To build a web application	3	High
	USN-11	Building HTML pages with python code	2	Medium
	USN-12	To run the application	3	High
Testing Phase	USN-13	As a user login to dashboard	2	Medium
	USN-14	As a user import the images with skin diseases to the software application	2	Medium
	USN-15	YOLO processes the image and give the necessary details	3	High

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
Sprint-1	Prerequisites	USN-1	Install Python IDE, Python packages, Microsoft Visual Object Tagging Tool, Yolo Structure	3	High	Jhanavarshini.K.L Swetha.K Pavithra.J Nivetha.S
Sprint-1	Data Collection	USN-2	Dataset should be collected from google or using a Chrome extension such as Fatkun Batch Downloader	3	High	Jhanavarshini.K.L Swetha.K Pavithra.J Nivetha.S
Sprint-1	Annotate Images	USN-3	Create A Project in VOTT (Microsoft's Visual Object Tagging Tool)	2	Medium	Jhanavarshini.K.L Swetha.K Pavithra.J Nivetha.S
Sprint-2	Training YOLO	USN-4	train our model using YOLO weights	2	Medium	Jhanavarshini.K.L Swetha.K Pavithra.J Nivetha.S
Sprint-2		USN-5	To Download and Convert Pre-Trained Weights	3	High	Jhanavarshini.K.L Swetha.K Pavithra.J Nivetha.S
Sprint-2		USN-6	To Train YOLOv3 Detector	3	High	Jhanavarshini.K.L Swetha.K Pavithra.J Nivetha.S
Sprint-3	Cloudant DB	USN-7	Register & Login to IBM Cloud	3	High	Jhanavarshini.K.L Swetha.K Pavithra.J Nivetha.S
Sprint-3		USN-8	Create Service Instant and Credentials	2	Medium	Jhanavarshini.K.L Swetha.K Pavithra.J Nivetha.S
Sprint-3		USN-9	Launch DB and Create database	3	High	Jhanavarshini.K.L Swetha.K Pavithra.J Nivetha.S

Sprint-3	Development Phase	USN-10	To build a web application	3	High	Jhanavarshini.K.L Swetha.K Pavithra.J Nivetha.S
Sprint-3		USN-11	Building HTML pages with python code	2	Medium	Jhanavarshini.K.L Swetha.K Pavithra.J Nivetha.S
Sprint-3		USN-12	To run the application	3	High	Jhanavarshini.K.L Swetha.K
Sprint-4	Testing Phase	USN-13	As a user login to dashboard	2	Medium	Jhanavarshini.K.L Nivetha.S
Sprint-4		USN-14	As a user import the images with skin diseases to the software application	2	Medium	Jhanavarshini.K.L Pavithra.J
Sprint-4		USN-15	YOLO processes the image and give the necessary details	3	High	Jhanavarshini.K.L

6.2 Sprint Delivery Schedule

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

7. Coding and Solutioning

```
pip3 install tensorflow tensorflow_hub matplotlib seaborn numpy pandas sklearn imblearn
```

```
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"]
```

Preparing the Dataset

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

Output:

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

```
# 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])


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
# training parameters
batch_size = 64
optimizer = "rmsprop"
```

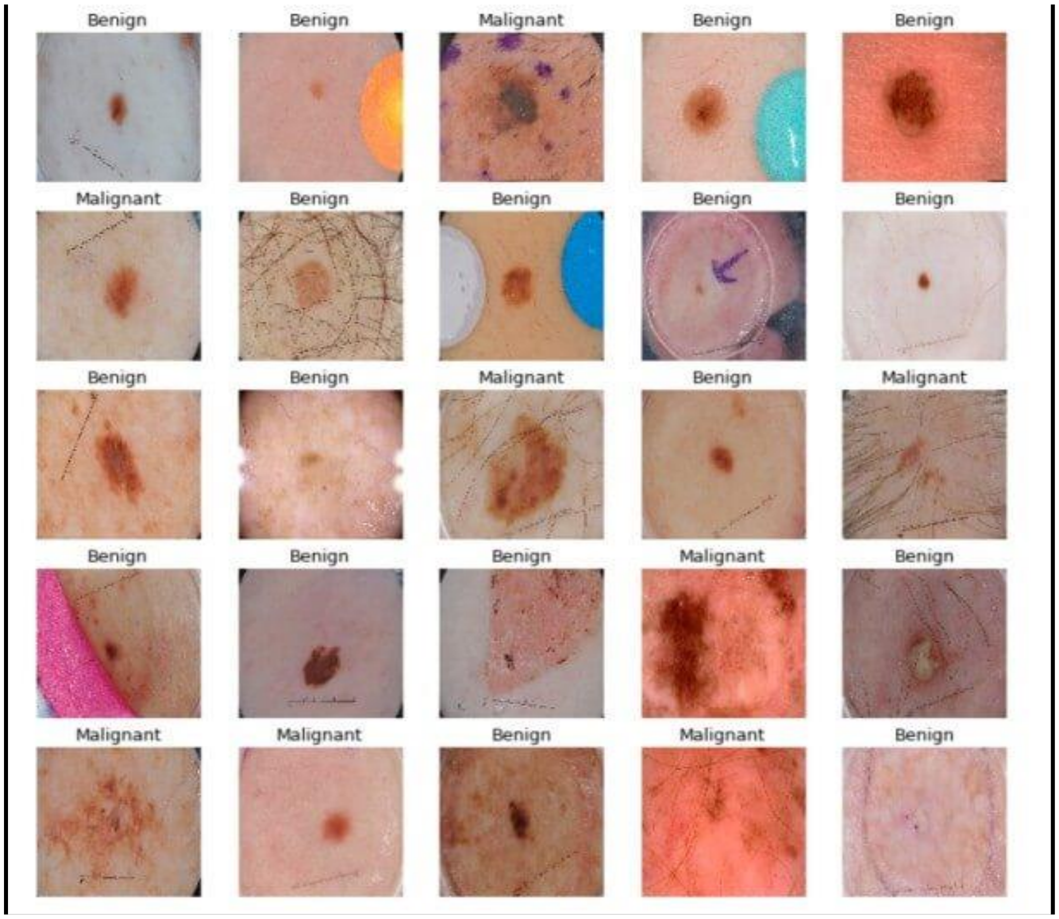
```
def prepare_for_training(ds, cache=True, batch_size=64, shuffle_buffer_size=1000):
  if cache:
    if isinstance(cache, str):
      ds = ds.cache(cache)
    else:
      ds = ds.cache()
  # shuffle the dataset
  ds = ds.shuffle(buffer_size=shuffle_buffer_size)
  # Repeat forever
  ds = ds.repeat()
  # split to batches
  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)
```

Output:



```
# building the model
# InceptionV3 model & pre-trained weights
module_url = "https://tfhub.dev/google/tf2-preview/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()
```

Output:

```
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
_________________________________________________________________
```

Training the Model

```
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])
```

Output:

```
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:

```
# 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)
    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")
```

```
Number of testing samples: 600
# 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)
    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")

# 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:

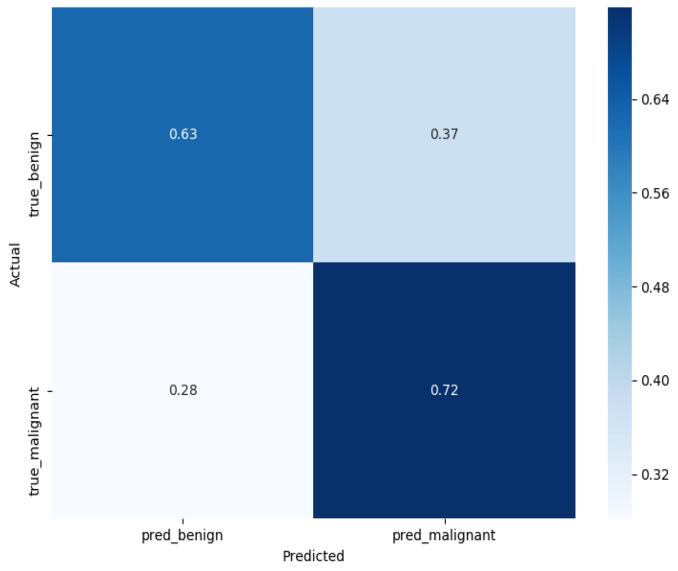
```
Evaluating the model...
Loss: 0.4476394319534302   Accuracy: 0.8
```

```
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)
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 it
  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)
```

Output:



```
sensitivity = sensitivity_score(y_test, y_pred)
specificity = specificity_score(y_test, y_pred)

print("Melanoma Sensitivity:", sensitivity)
print("Melanoma Specificity:", specificity)
```

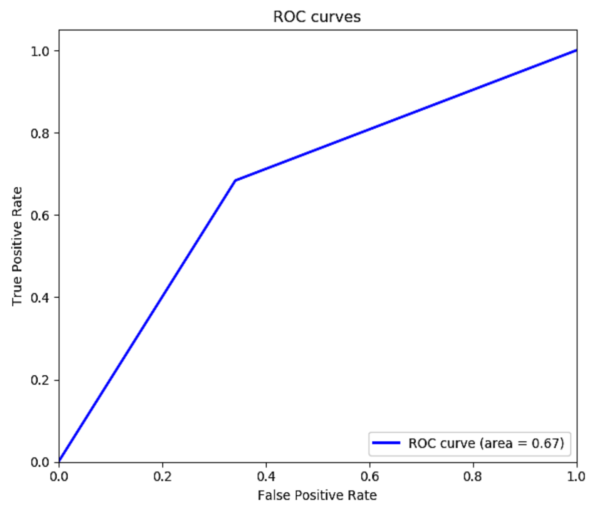
Output:

Melanoma Sensitivity: 0.717948717948718
Melanoma Specificity: 0.6252587991718427

```
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)
```

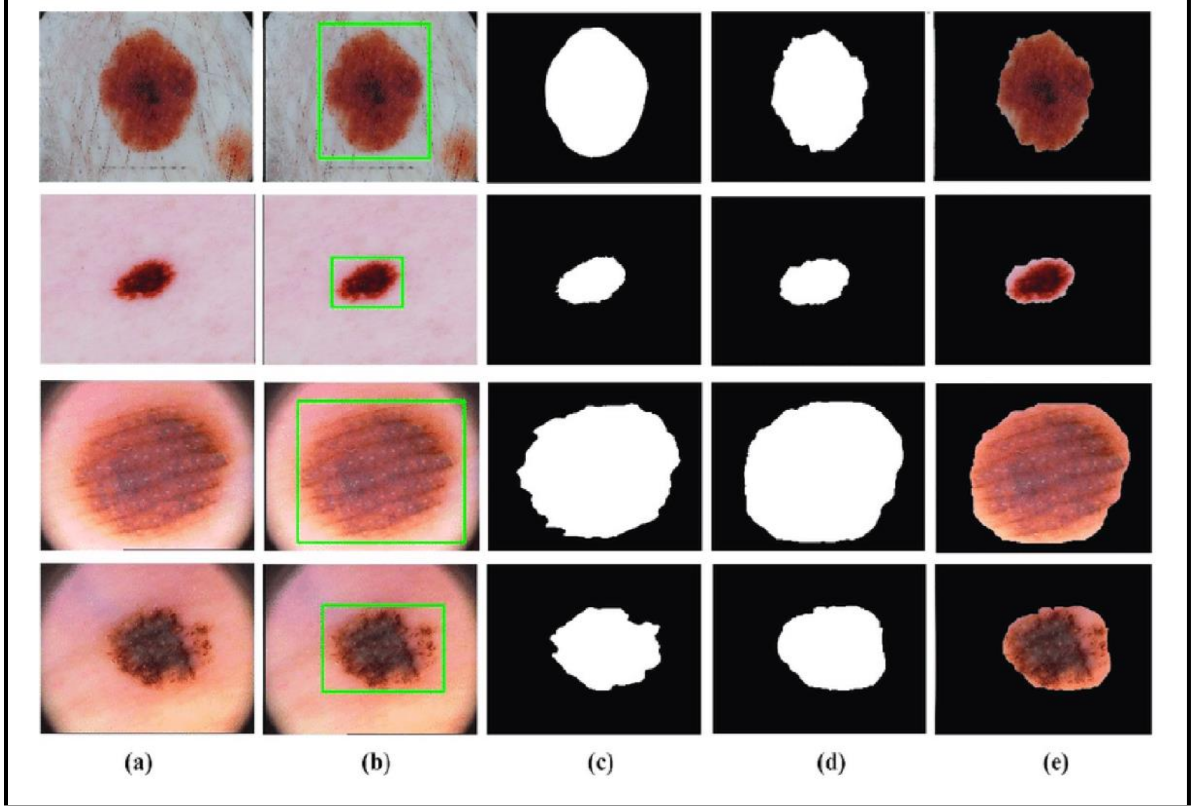
Output:



ROC AUC: 0.671

8. Results

The final results are based on the accuracy results in the form of the melanoma and the non-melanoma skin diseases classifications.



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-19593-1659701859